


```

RN [2]
RP 1-747
RA Hong J., Zhao S., Peng H., Duan J.:
RT Submitted (29-AUG-2002) to the EMBL/GenBank/DBJ databases.
RL Chinese Academy of Sciences, Wuhan Institute of Virology, Wuhan, Hubei
RL 430071, P.R. China
XX
DR SPTREMBL: Q8AYY9; Q8AYY9.
XX
FH Key Location/Qualifiers
FH
FT source 1. .747
FT /db_xref="taxon:208509"
FT /mol_type="genomic DNA"
FT /organism="Dendrolimus punctatus cypovirus 1"
FT /strain="Hunan"
FT 1. .747
FT CDS
FT /codon_start=1
FT /db_xref="SPTREMBL:Q8AYY9"
FT /note="forms crystals/polyhedra"
FT /product="polyhedrin"
FT /protein_id="AA17827.1"
FT /translation="MADVAGTSNDRFGREORLFNSEOYNNNSLNGEVSVMVAYYSD
FT GSVLVINKNSQYKVGISETRFKALKEGREGORNDSTDEYNOSIYYPNGDAHKFHSNA
FT KPAIOLIFSPSVAVRTIKMAKNSVSPDDYLRSHPMWATGIRKRIKRGGEIYGS
FT HYFELPHEYNISLAVSGVHKNPSSYVWGSANHVMDYFQSCDLALRCNRYMAELELVN
FT HYISPNAPYIDINNHSGVALSNHQ"
FT
SQ Sequence 747 BP; 226 A; 188 C; 169 G; 164 T; 0 other;
Query Match 0.1%; Score 13; DB 1; Length 747;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 130468 TGTGTGTGTAGTT 130480
DB 88 TGTGTGTGTAGTT 76

```

```

DR SPTREMBL: Q8AYY9; Q8AYY9.
XX
FH Key Location/Qualifiers
FH
FT source 1. .747
FT /db_xref="taxon:208509"
FT /mol_type="genomic DNA"
FT /note="substitute host"
FT /organism="Dendrolimus punctatus cypovirus 1"
FT /strain="Hunan"
FT /specific_host="Spodoptera exigua"
FT 1. .747
FT CDS
FT /codon_start=1
FT /db_xref="SPTREMBL:Q8AYY9"
FT /note="forms crystals/polyhedra"
FT /product="polyhedrin"
FT /protein_id="AA17828.1"
FT /translation="MADVAGTSNDRFGREORLFNSEOYNNNSLNGEVSVMVAYYSD
FT GSVLVINKNSQYKVGISETRFKALKEGREGORNDSTDEYNOSIYYPNGDAHKFHSNA
FT KPAIOLIFSPSVAVRTIKMAKNSVSPDDYLRSHPMWATGIRKRIKRGGEIYGS
FT HYFELPHEYNISLAVSGVHKNPSSYVWGSANHVMDYFQSCDLALRCNRYMAELELVN
FT HYISPNAPYIDINNHSGVALSNHQ"
FT
SQ Sequence 747 BP; 230 A; 191 C; 166 G; 160 T; 0 other;
Query Match 0.1%; Score 13; DB 1; Length 747;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 130468 TGTGTGTGTAGTT 130480
DB 88 TGTGTGTGTAGTT 76

```

RESULT 4

MMSPRO2 standard; DNA; VRL; 1122 BP.

AC J02261;

SV J02261.1

XX 07-MAY-1992 (Rel. 31, Created)

DT 17-APR-2002 (Rel. 71, Last updated, Version 6)

XX Moloney murine sarcoma virus polyprotein gene, partial cds.

DE proviral gene; terminal repeat.

KM

KX

XX Moloney murine sarcoma virus

OS Viruses; Retroviridae; Gammaretrovirus.

OC

XX

RN [1]

RP 16-1122

RA MEDLINE: 81013872.

RX PUBMED: 6251454.

RX Sutcliffe J.G., Shinnick T.M., Verma I.M., Lerner R.A.;

RT "Nucleotide sequence of Moloney leukemia virus: 3' end reveals details of

RT replication, analogy to bacterial transposons, and an unexpected gene";

RL Proc. Natl. Acad. Sci. U.S.A. 77(6):3302-3306(1980).

XX

RN [2]

RP 1-1122

RA MEDLINE: 81013873.

RX PUBMED: 6251455.

RA Van Beveren C., Goddard J.G., Berns A., Verma I.M.;

RT "Structure of Moloney murine leukemia viral DNA: nucleotide sequence of the

RT 5' long terminal repeat and adjacent cellular sequences";

RL Proc. Natl. Acad. Sci. U.S.A. 77(6):3307-3311(1980).

XX

RN [3]

RP 1-1122

RA MEDLINE: 81052384.


```

RA Fuhrman S.A., Van Beveren C., Verma I.M.;
RT "Identification of a RNA polymerase II initiation site in the long terminal
RL repeat of Moloney murine leukemia viral DNA";
RL Proc. Natl. Acad. Sci. U.S.A. 78(9):5411-5415(1981).
XX
CC On Oct 4, 1994 this sequence version replaced gi:332090.
CC + strand shown. 'LTR' in definition stands for 'long terminal
CC repeat'.
XX
FH Key Location/Qualifiers
FH
FT source 1. .660
FT /db_xref="taxon:11809"
FT /mol_type="genomic DNA"
FT /note="from Balb/mo mouse"
FT /proviral
FT /organism="Moloney murine sarcoma virus"
FT mRNA 486. .>660
FT /product="RNA polII transcript mRNA"
FT
XX
SQ Sequence 660 BP; 155 A; 181 C; 158 G; 166 T; 0 other;
Query Match 0.1%; Score 12; DB 1; Length 660;
Best Local Similarity 100.0%; Pred. No. 7.2;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 119809 GCGCTACTTAA 119820
DB 159 GCGCTACTTAA 148

RESULT 7
MMSPRO2/c
ID MMSPRO2 standard; DNA; VRL; 1122 BP.
XX
AC J02261;
XX
SV J02261.1
XX
DT 07-MAY-1992 (Rel. 31, Created)
DT 17-APR-2002 (Rel. 71, Last updated, Version 6)
XX
DE Moloney murine sarcoma virus polyprotein gene, partial cds.
XX
KW proviral gene; terminal repeat.
XX
OS Moloney murine sarcoma virus
XX OC Viruses; Retroid viruses; Retroviridae; Gammaretrovirus.
XX
RN [1]
RP 16-1122
RX MEDLINE; 81013872.
RX PUBMED; 6251454.
RA Surcliffe J.G., Shinnick T.M., Verma I.M., Lerner R.A.;
RT "Nucleotide sequence of Moloney leukemia virus: 3' reveals details of
RL replications, analogy to bacterial transposons, and an unexpected gene",
RL Proc. Natl. Acad. Sci. U.S.A. 77(6):3302-3306(1980).
XX
XX [2]
RN 1-1122
RP 1-1122
RX MEDLINE; 81013873.
RX PUBMED; 6251455.
RA Van Beveren C., Goddard J.G., Berns A., Verma I.M.;
RT "Structure of Moloney murine leukemia viral DNA: nucleotide sequence of the
RL 5' long terminal repeat and adjacent cellular sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 77(6):3307-3311(1980).
XX
XX [3]
RN 1-1122
RP 1-1122
RX MEDLINE; 81052384.
RX PUBMED; 6159543.
RA Sutcliffe J.G., Shinnick T.M., Green N., Liu F.T., Niman H.L., Lerner R.A.;
RT "Chemical synthesis of a polypeptide predicted from nucleotide sequence

```

```

RT allows detection of a new retroviral gene product";
RL Nature 287(5785):801-805(1980).
XX
DR GOA: Q83401.
DR SPTREMBL: Q83401; Q83401.
XX
FH Key Location/Qualifiers
FH
FT source 1. .1122
FT /db_xref="taxon:11809"
FT /mol_type="genomic DNA"
FT /note="from Balb/mo mouse"
FT /proviral
FT /organism="Moloney murine sarcoma virus"
FT mRNA <1. .1122
FT /product="RNA polII transcript mRNA"
FT CDS <1. .564
FT /codon_start=1
FT /db_xref="GOA:Q83401"
FT /db_xref="SPTREMBL:Q83401"
FT /product="polyprotein"
FT /translation="ILGLTMSGIAGIGTATLMAQFOFOLOAAVODDIBVEKST
FT SNLEKSLTSLSEVVLNRRGLDLFLKEGGICAAIKKECCFYADHGLYRDSMAIKRER
FT LNSVQALVITQGFHQKPRECP"
FT mat_peptide <1. .282
FT /product="p15e protein"
FT mat_peptide 283. .561
FT /product="r protein"
FT 144
FT /note="a may be g ([1])"
FT 302
FT /note="t may be c ([1])"
FT 530
FT /note="t may be a ([1])"
FT 952
FT /note="a may be t ([1])"
XX
SQ Sequence 1122 BP; 307 A; 266 C; 270 G; 279 T; 0 other;
Query Match 0.1%; Score 12; DB 1; Length 1122;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 119809 GCGCTACTTAA 119820
DB 653 GCGCTACTTAA 642

RESULT 8
ADREAR3RE
ID ADREAR3RE standard; DNA; VRL; 1980 BP.
XX
AC M94458;
XX
SV M94458.1
XX
DT 11-DEC-1992 (Rel. 34, Created)
DT 04-MAR-2000 (Rel. 63, Last updated, Version 5)
XX
DE Mastadenovirus serotype 11 early 3 region.
XX
KW early 3 region.
XX
OS Human adenovirus type 11
XX OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus;
XX Human adenovirus B.
XX
XX [1]
RN 1-1980
RP 1-1980
RX MEDLINE; 93033102.
RX PUBMED; 1413499.

```

RA Mel Y.-F., Madell G.;
RT "The nucleotide sequence of adenovirus type 11 early 3 region: comparison
of genome type Ad1p and Ad1a.";
RL Virology 191(1):125-133(1992).
XX
DR GOA; P15140.
DR SWISS-PROT; P15140; E3GL_ADE35.
DR SWISS-PROT; P35768; E320_ADELIP.
DR SWISS-PROT; P35770; E321_ADELIP.
XX
FH Key Location/Qualifiers
FT source 1. 1980
FT /db_xref="taxon:10541"
FT /mol_type="genomic DNA"
FT /organism="Human adenovirus type 11"
FT /strain="Siobitski"
XX
SQ Sequence 1980 BP; 568 A; 466 C; 330 G; 616 T; 0 other;
Query Match 0.1%; Score 12; DB 1; Length 1980;
Best Local Similarity 100.0%; Pred. No. 4.9; Mismatches 0; Gaps 0;
Matches 12; Conservative 0; Indels 0;
QY 131630 ACMAAACCATGT 131641
DB 1331 ACMAAACCATGT 1342
RESULT 9
AF541985 standard; DNA; VRL; 747 BP.
XX AF541985:
XX AF541985.1
SV 26-SEP-2002 (Rel. 73, Created)
DT 26-SEP-2002 (Rel. 73, Last updated, Version 1)
XX Dendrolimus punctatus cypovirus 1 strain Hunan polyhedrin gene, complete
DE cds.
XX
XX Dendrolimus punctatus cypovirus 1
OC Viruses; dsRNA viruses; Reoviridae; Cypovirus; Cypovirus 1.
XX
XX [1]
RN Hong J., Zhao S., Peng H., Duan J.;
RP 1-747
RT "Comparison of C-polyhedrin genes from 5 type 1 cypoviruses";
RL Unpublished.
XX
XX [2]
RN Hong J., Zhao S., Peng H., Duan J.;
RP 1-747
RT Submitted (29-AUG-2002) to the EMBL/GenBank/DBJ databases.
RL Chinese Academy of Sciences, Wuhan Institute of Virology, Wuhan, Hubei
430071, P.R. China
XX
DR SPTREMBL; Q8AYY9; Q8AYY9.
XX
FH Key Location/Qualifiers
FT source 1. 747
FT /db_xref="taxon:208509"
FT /mol_type="genomic DNA"
FT /organism="Dendrolimus punctatus cypovirus 1"
FT /strain="Hunan"
FT 1. 747
FT /codon_start=1
FT CDS

FT /db_xref="SPTREMBL:Q8AYY9"
FT /note="forms crystals/polyhedra"
FT /product="polyhedrin"
FT /protein_id="AA17827.1"
FT /translation="MADVAGTISNRDFRGRQQLFNSQYNNNSLNGEVSWWYAYISD
GSLVINKNSQYKVGISETFKALKEVREGQRNDSDYDEVNOSIYYPNGDAHKFHSNA
KPRALQIIFSPVNWRTIMAKGNSVYPDDYLOHSHPEATGIKRKIRKRGELVGS
HYFELPHEVNSISLAVSGVHKNPSSYVNSAHNMVDVFOCDLALRFQNRWAELELVN
HYSPRAYVLYLDINNHSYGVALSNNHQ"
XX
SQ Sequence 747 BP; 226 A; 188 C; 169 G; 164 T; 0 other;
Query Match 0.1%; Score 11; DB 1; Length 747;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 122009 TTCTGCACCG 122019
DB 628 TTCTGCACCG 638
RESULT 10
AF541986 standard; DNA; VRL; 747 BP.
XX AF541986:
XX AF541986.1
SV 26-SEP-2002 (Rel. 73, Created)
DT 26-SEP-2002 (Rel. 73, Last updated, Version 1)
XX Dendrolimus punctatus cypovirus 1 strain Hunan from Spodoptera exigua
DE polyhedrin gene, complete cds.
XX
XX Dendrolimus punctatus cypovirus 1
OC Viruses; dsRNA viruses; Reoviridae; Cypovirus; Cypovirus 1.
XX
XX [1]
RN Hong J., Zhao S., Peng H., Duan J.;
RP 1-747
RT "Comparison of C-polyhedrin genes from 5 type 1 cypoviruses";
RL Unpublished.
XX
XX [2]
RN Hong J., Zhao S., Peng H., Duan J.;
RP 1-747
RT Submitted (29-AUG-2002) to the EMBL/GenBank/DBJ databases.
RL Chinese Academy of Sciences, Wuhan Institute of Virology, Wuhan, Hubei
430071, P.R. China
XX
DR SPTREMBL; Q8AYY9; Q8AYY9.
XX
FH Key Location/Qualifiers
FT source 1. 747
FT /db_xref="taxon:208509"
FT /mol_type="genomic DNA"
FT /note="substitute-host"
FT /organism="Dendrolimus punctatus cypovirus 1"
FT /strain="Hunan"
FT /specific_host="Spodoptera exigua"
FT 1. 747
FT /codon_start=1
FT /db_xref="SPTREMBL:Q8AYY9"
FT /note="forms crystals/polyhedra"
FT /product="polyhedrin"
FT /protein_id="AA17828.1"
FT /translation="MADVAGTISNRDFRGRQQLFNSQYNNNSLNGEVSWWYAYISD
GSLVINKNSQYKVGISETFKALKEVREGQRNDSDYDEVNOSIYYPNGDAHKFHSNA

```

FT      KPRATIIIESPSVNRITKMAKNSVSPDDYLQSHMEATGIRYKRIRKDEIVGS
FT      HFEELPHEINSLAVSGVHKNPSSITWGSANVMADVQSCDLALRPFGRWAELELVN
FT      HTSPNAPYPIYDINNHSYVALSNHQ"
XX
SQ      Sequence 747 BP; 230 A; 191 C; 166 G; 160 T; 0 other;

Query Match      0.1%; Score 11; DB 1; Length 747;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      122009 TTCTGCACCG 122019
        |||||||
        628 TTCTGCACCG 638

RESULT 11
ADREAR3RE/C
ID      ADREAR3RE standard; DNA; VRL; 1980 BP.
AC      M94458;
XX      M94458.1
SV
DE      11-DEC-1992 (Rel. 34, Created)
DT      04-MAR-2000 (Rel. 63, Last updated, Version 5)
XX
DE      Mastadenovirus serotype 11 early 3 region.
XX      early 3 region.
XX
OS      Human adenovirus type 11
OC      Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus;
XX      Human adenovirus B.
XX
XX      [1]
XX      1-1980
XX      MEDLINE: 93033102.
XX      PUBMED: 1413449.
XX
RA      Mel Y.-F., Wadell G.;
RT      "The nucleotide sequence of adenovirus type 11 early 3 region: comparison
of genome type Ad1p and Ad11a.";
RL      Virology 191(1):125-133(1992).
XX
XX      GOA: P15140.
DR      SWISS-PROT: P15140; E3GL_ADE35.
DR      SWISS-PROT: P35768; E320_ADE1P.
DR      SWISS-PROT: P35770; E321_ADE1P.
XX
XX      Key      Location/Qualifiers
FH      source      1. 1980
FT      /db_xref="taxon:10541"
FT      /mol_type="genomic DNA"
FT      /organism="Human adenovirus type 11"
FT      /strain="Slobitski"
XX
SQ      Sequence 1980 BP; 568 A; 466 C; 330 G; 616 T; 0 other;

Query Match      0.1%; Score 11; DB 1; Length 1980;
Best Local Similarity 100.0%; Pred. No. 7.6;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      123558 GGGTGTGTGG 123568
        |||||||
        1004 GGGTGTGTGG 994

RESULT 12
ADRE3GENE
ID      ADRE3GENE standard; DNA; VRL; 2480 BP.
AC      L08231;
XX
XX

```

```

SV      L08231.1
XX
XX      08-JUL-1993 (Rel. 36, Created)
DT      04-MAR-2000 (Rel. 63, Last updated, Version 3)
XX
DE      Mastadenovirus 11 E3 region encoding fiber gene, complete cds.
XX      fiber protein.
XX
XX      Human adenovirus type 11
OC      Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus;
XX      Human adenovirus B.
XX
XX      [1]
XX      1-2480
XX      MEDLINE: 93276532.
XX      PUBMED: 8503168.
XX
RA      Mel Y.-F., Wadell G.;
RT      "Hemagglutination properties and nucleotide sequence analysis of the fiber
gene of adenovirus genome types 11p and 11a";
RL      Virology 194(2):453-462(1993).
XX
XX      GOA: P35774.
DR      SWISS-PROT: P35774; FIBP_ADE1P.
XX
XX      Key      Location/Qualifiers
FH      source      1. 2480
FT      /db_xref="taxon:10541"
FT      /mol_type="genomic DNA"
FT      /organism="Human adenovirus type 11"
FT      /strain="Slobitski"
FT      1094. 2071
FT      /codon_start=1
FT      /db_xref="GOA:P35774"
FT      /db_xref="SWISS-PROT:P35774"
FT      /gene="E3"
FT      /protein_id="AA42490.1"
FT      /translation="MTKRVRLSDSFNFVPEYDESTSQHPFINPGFISPNGFTOSPNGV
LTKCLIPLATTTGSLQKYGGLVDDTNGFLKENTSATPIYKGTSGILPGLAGIG
TNEKRLCKIKGGGILTFPNSNNICIDDNINFTLMTGVNPPEANCOIMNSSESNDCKLITLIV
KTEGALVAPYVIVIGVSNRNFMETTHRRINTAFELFEDSTGNLTRLSSLEKTPLNHSQO
NMATGATITNKGEMPTTAYPFNDNSREKENYLYGTCTVYASDRTPAIDISVLMNRA
INDETSYICIRITWSMNTGDAPEVQTSATLVTSPEFFYIREDD"
FT
FT
XX
SQ      Sequence 2480 BP; 768 A; 652 C; 418 G; 642 T; 0 other;

Query Match      0.1%; Score 11; DB 1; Length 2480;
Best Local Similarity 100.0%; Pred. No. 6.2;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      124149 TTTAAAGCGCT 124159
        |||||||
        2297 TTTAAAGCGCT 2307

RESULT 13
MMJAI
ID      MMJAI standard; RNA; VRL; 126 BP.
AC      J02243;
XX      J02243.1
SV
XX
XX      01-OCT-1996 (Rel. 49, Created)
DT      11-FEB-1999 (Rel. 58, Last updated, Version 2)
XX
DE      Macaca mulatta and arctoides type C retrovirus, 5' end.
XX      Macaca mulatta and arctoides type C retrovirus;
XX      Viruses; Retroid viruses; Retroviridae; Mammalian type C retroviruses;
OC

```

```

OC 1-Mammalian type C virus group; Macaca mulatta type C retrovirus.
XX
RN [1]
RP 1-126
RX MEDLINE; 80222887.
RA Lovinger G.G., Schochetman G.;
RT "5' terminal nucleotide sequences of type C retroviruses: features common
RL to noncoding sequences of eucaryotic messenger RNAs.";
XX Cell 20(2):441-449(1980).
XX
CC See also <baev5>, <mmcl> & <rd114>.
XX
FH Key Location/Qualifiers
FT source 1.126
FT /db_xref="taxon:11844"
FT /note="Isolated from spleen cells"
FT /organism="Macaca mulatta and arcotoides type C retrovirus"
XX
SQ Sequence 126 BP; 36 A; 33 C; 30 G; 27 T; 0 other;
Query Match 0.1%; Score 10; DB 1; Length 126;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 125409 CCCCGAGAA 125418
Db 24 CCCCGAGAA 33
RESULT 14
MMJAI/C standard; RNA; VRL; 126 BP.
XX
AC J02243;
XX
SV J02243.1
XX
DT 01-OCT-1996 (Rel. 49, Created)
DT 11-FEB-1999 (Rel. 58, Last updated, Version 2)
XX
DE Macaca mulatta and arcotoides type C retrovirus, 5' end.
XX
KM
XX
OS Macaca mulatta and arcotoides type C retrovirus
OC Viruses; Retrovirdae; Retroviridae; Mammalian type C retroviruses;
OC 1-Mammalian type C virus group; Macaca mulatta type C retrovirus.
XX
RN [1]
RP 1-126
RX MEDLINE; 80222887.
RA Lovinger G.G., Schochetman G.;
RT "5' terminal nucleotide sequences of type C retroviruses: features common
RL to noncoding sequences of eucaryotic messenger RNAs.";
XX Cell 20(2):441-449(1980).
XX
CC See also <baev5>, <mmcl> & <rd114>.
XX
FH Key Location/Qualifiers
FT source 1.126
FT /db_xref="taxon:11844"
FT /note="Isolated from spleen cells"
FT /organism="Macaca mulatta and arcotoides type C retrovirus"
XX
SQ Sequence 126 BP; 36 A; 33 C; 30 G; 27 T; 0 other;
Query Match 0.1%; Score 10; DB 1; Length 126;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 127392 AGCTCCAGGT 127401
 Db 99 AGCTCCAGGT 90

Search completed: September 30, 2003, 03:39:07
 Job time : 11 secs

THIS PAGE BLANK (USPTO)

fiber protein.

RA Mel Y.-F., Wadell G.;
RT "The nucleotide sequence of adenovirus type 11 early 3 region: comparison

```
RT of genome type, Ad1p and Ad1a."
RL Virology 191(1):125-133(1992).
XX
DR GOA: P15140.
DR SWISS-PROT: P15140; E3GL_ADE35.
DR SWISS-PROT: P35768; E320_ADE1P.
DR SWISS-PROT: P35770; E321_ADE1P.
XX
FH Key Location/Qualifiers
FH
FT source 1. 1980
FT /db_xref="taxon:10541"
FT /mol_type="genomic DNA"
FT /organism="Human adenovirus type 11"
FT /strain="Siobitski"
XX
SQ Sequence 1980 BP; 568 A; 466 C; 330 G; 616 T; 0 other:
Query Match 0.0%; Score 14; DB 1; Length 1980;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 14; Conservative 0; Mismatches 0; Gaps 0;
Indels 0;
OY 78171 GCCACCGCTGCAAC 78184
DB 1054 GCCACCGCTGCAAC 1041
RESULT 3
AF541985/C
ID AF541985 standard; DNA; VRL; 747 BP.
XX
AC AF541985;
XX
SV AF541985.1
XX
DT 26-SEP-2002 (Rel. 73, Created)
DT 26-SEP-2002 (Rel. 73, Last updated, Version 1)
XX
DE Dendrolimus punctatus cypovirus 1 strain Hunan polyhedrin gene, complete
DE cds.
XX
XX KW
XX OS Dendrolimus punctatus cypovirus 1
XX OC Viruses; dsRNA viruses; Reoviridae; Cypovirus; Cypovirus 1.
XX
RN [1]
RN RP 1-747
RN RA Hong J., Zhao S., Peng H., Duan J.;
RT "Comparison of C-polyhedrin genes from 5 type 1 cypoviruses";
RL unpublished.
XX
XX [2]
XX RP 1-747
XX RA Hong J., Zhao S., Peng H., Duan J.;
RT ;
RL Submitted (29-AUG-2002) to the EMBL/Genbank/DBJ databases.
RL Chinese Academy of Sciences, Wuhan Institute of Virology, Wuhan, Hubei
RL 430071, P.R. China
XX
XX SPTREMBL; Q8AYY9; Q8AYY9.
DR
XX
FH Key Location/Qualifiers
FH
FT source 1. 747
FT /db_xref="taxon:208509"
FT /mol_type="genomic DNA"
FT /organism="Dendrolimus punctatus cypovirus 1"
FT /strain="Hunan"
FT 1. 747
FT /codon_start=1
FT /db_xref="SPTREMBL:Q8AYY9"
FT /note="Forms crystals/polyhedra"
```

```
FT /product="polyhedrin"
FT /protein_id="AAN17827.1"
FT /translation="MADVAGTSNRDPRGQRQLPNSRQYNYNNSLNGEVSVMVAYYS
FT GSVLVINKNSQYKVGISETFKALKEKREGQNDSDYEVEVQSGIYYPNGDAHFEHSA
FT KPAKIQIIFSPSVVVRITKMAKNSVSPDDYLDGRSHPEATGIRKRIKRDGEIVGS
FT HYFELPHEYNISLAVSGVHKRNPSSYNGSAHNMVDFQSCDLALRCNRYMAELELVN
FT HYSFNAVPIYIDINNHSGVALSNHQ"
XX
SQ Sequence 747 BP; 226 A; 188 C; 169 G; 164 T; 0 other:
Query Match 0.0%; Score 13; DB 1; Length 747;
Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 13; Conservative 0; Mismatches 0; Gaps 0;
Indels 0;
OY 64059 TCGAAGTAATGAC 64071
DB 500 TCGAAGTAATGAC 488
RESULT 4
AF541986/C
ID AF541986 standard; DNA; VRL; 747 BP.
XX
AC AF541986;
XX
SV AF541986.1
XX
DT 26-SEP-2002 (Rel. 73, Created)
DT 26-SEP-2002 (Rel. 73, Last updated, Version 1)
XX
DE Dendrolimus punctatus cypovirus 1 strain Hunan from Spodoptera exigua
DE polyhedrin gene, complete cds.
XX
XX KW
XX OS Dendrolimus punctatus cypovirus 1
XX OC Viruses; dsRNA viruses; Reoviridae; Cypovirus; Cypovirus 1.
XX
RN [1]
RN RP 1-747
RN RA Hong J., Zhao S., Peng H., Duan J.;
RT "Comparison of C-polyhedrin genes from 5 type 1 cypoviruses";
RL unpublished.
XX
XX [2]
XX RP 1-747
XX RA Hong J., Zhao S., Peng H., Duan J.;
RT ;
RL Submitted (29-AUG-2002) to the EMBL/Genbank/DBJ databases.
RL Chinese Academy of Sciences, Wuhan Institute of Virology, Wuhan, Hubei
RL 430071, P.R. China
XX
XX SPTREMBL; Q8AYY9; Q8AYY9.
DR
XX
FH Key Location/Qualifiers
FH
FT source 1. 747
FT /db_xref="taxon:208509"
FT /mol_type="genomic DNA"
FT /note="Substitute-host"
FT /organism="Dendrolimus punctatus cypovirus 1"
FT /strain="Hunan"
FT /specific_host="Spodoptera exigua"
FT 1. 747
FT /codon_start=1
FT /db_xref="SPTREMBL:Q8AYY9"
FT /note="Forms crystals/polyhedra"
FT /product="polyhedrin"
FT /protein_id="AAN17828.1"
FT /translation="MADVAGTSNRDPRGQRQLPNSRQYNYNNSLNGEVSVMVAYYS
FT GSVLVINKNSQYKVGISETFKALKEKREGQNDSDYEVEVQSGIYYPNGDAHFEHSA
FT KPAKIQIIFSPSVVVRITKMAKNSVSPDDYLDGRSHPEATGIRKRIKRDGEIVGS
FT HYFELPHEYNISLAVSGVHKRNPSSYNGSAHNMVDFQSCDLALRCNRYMAELELVN
```



```
FT      HYSPNAYPYLDINNHSYGVALSNNHQ"
XX
SQ      Sequence 747 BP; 230 A; 191 C; 166 G; 160 T; 0 other;
Query Match      0.0%; Score 13; DB 1; Length 747;
Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      64059 TCGAGTATATGAC 64071
DB      500 TCGAGTATATGAC 488
RESULT 5
ADREAR3RE standard; DNA; VRL; 1980 BP.
XX      M94458;
XX      M94458.1
SV
XX      11-DEC-1992 (Rel. 34, Created)
DT      04-MAR-2000 (Rel. 63, Last updated, Version 5)
XX
XX      Mastadenovirus serotype 11 early 3 region.
DE      early 3 region.
XX
XX      Human adenovirus type 11
OS      Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus;
OC      Human adenovirus B.
XX
XX      [1]
RN      MEDLINE: 93033102.
RX      PUBMED: 1413499.
RA      Mei Y.-F., Wadell G.;
RT      "The nucleotide sequence of adenovirus type 11 early 3 region: comparison
of genome type Ad1p and Ad11a.";
RL      Virology 191(1):125-133(1992).
XX
XX      GOA: P15140.
DR      SWISS-PROT: P15140; E3GL_ADE35.
DR      SWISS-PROT: P35768; E320_ADE1P.
DR      SWISS-PROT: P35770; E321_ADE1P.
XX
XX      Key      Location/Qualifiers
FH      source      1. 1980
FT      /db_xref="taxon:10541"
FT      /mol_type="genomic DNA"
FT      /organism="Human adenovirus type 11"
FT      /strain="Slobitski"
XX
SQ      Sequence 1980 BP; 568 A; 466 C; 330 G; 616 T; 0 other;
Query Match      0.0%; Score 13; DB 1; Length 1980;
Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      40452 AAAGTTTACAGCG 40464
DB      843 AAAGTTTACAGCG 855
RESULT 6
ADRE3GENE standard; DNA; VRL; 2480 BP.
XX      L08231;
XX      L08231.1
SV
```

```
DT      08-JUL-1993 (Rel. 36, Created)
DT      04-MAR-2000 (Rel. 63, Last updated, Version 3)
XX
XX      Mastadenovirus 11 E3 region encoding fiber gene, complete cds.
DE      Mastadenovirus 11 E3 region encoding fiber gene, complete cds.
XX
XX      fiber protein.
KW
XX
XX      Human adenovirus type 11
OS      Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus;
OC      Human adenovirus B.
XX
XX      [1]
RN      1-2480
RX      MEDLINE: 93276532.
RX      PUBMED: 8503168.
RA      Mei Y.-F., Wadell G.;
RT      "Hemagglutination properties and nucleotide sequence analysis of the fiber
gene of adenovirus genome types 11p and 11a";
RL      Virology 194(2):453-462(1993).
XX
XX      GOA: P35774.
DR      SWISS-PROT: P35774; FIBP_ADE1P.
XX
XX      Key      Location/Qualifiers
FH      source      1. 2480
FT      /db_xref="taxon:10541"
FT      /mol_type="genomic DNA"
FT      /organism="Human adenovirus type 11"
FT      /strain="Slobitski"
FT      1094..2071
FT      /codon_start=1
FT      /db_xref="GOA:P35774"
FT      /db_xref="SWISS-PROT:P35774"
FT      /gene="E3"
FT      /protein_id="AAA42490.1"
FT      /translation="MTKRVRLSDSEPNVYPYDESTSQHPFINPGFISPNGETOSPNGV
LTKCLPTLTGGSLQKVGGLVDDTNGFLKENISATPLVKGHSIGLPLGAGLG
TNBNKLCITLGGGLTFPNSNNICIDNDINLTMLGVNPTFANCOIMNSSESNDCKLITLV
KRGALVTAVYVYIGVSNFMNLTTHNINFTALFPDSTGNLTRSSIKTPLNHSQ
NMAGTATNAKGPMSSTVAIPENDNSREKENTYIGTCYTTASDRTAFPIDISVMLNRA
INDETSYCIRITWSMNTGDAPEVOTSATLVSPFFYIREDQ"
XX
SQ      Sequence 2480 BP; 768 A; 652 C; 418 G; 642 T; 0 other;
Query Match      0.0%; Score 13; DB 1; Length 2480;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      53920 ACGCGGCGCCAA 53932
DB      592 ACGCGGCGCCAA 604
RESULT 7
MMJ1/C
XX      MMJ1 standard; RNA; VRL; 126 BP.
XX      J02243;
AC      J02243.1
SV
XX      01-OCT-1996 (Rel. 49, Created)
DT      11-FEB-1999 (Rel. 58, Last updated, Version 2)
XX
XX      Macaca mulatta and arctoides type C retrovirus, 5' end.
DE      Macaca mulatta and arctoides type C retrovirus, 5' end.
XX
XX      Macaca mulatta and arctoides type C retrovirus
OS      Viruses; Retrovirdae; Retroviridae; Mammalian type C retroviruses;
OC      1-Mammalian type C virus group; Macaca mulatta type C retrovirus.
XX
```

```

RN [1]
RP 1-126
RX MEDLINE; 80222887.
RX PUBMED; 6248246.
RA Lowinger G.G., Schochetman G.;
RT "5' terminal nucleotide sequences of type C retroviruses: features common
RL Cell 20(2):441-449(1980).
XX
XX See also <baev5>, <mmcl> & <rd114>.
XX
XX Key Location/Qualifiers
FH
FH source 1. .126
FT /db_xref="taxon:11844"
FT /note="Isolated from spleen cells"
FT /organism="Macaca mulatta and arcoides type C retrovirus"
XX
XX Sequence 126 BP; 36 A; 33 C; 30 G; 27 T; 0 other;
SO

Query Match 0.0%; Score 12; DB 1; Length 126;
Best Local Similarity 100.0%; Pred. No. 8.6;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 72481 CTCGCGTGTCT 72492
Db 44 CTCGCGTGTCT 33

RESULT 8
MMSPRO2 ID MMSPRO2 standard; DNA; VRL; 1122 BP.
XX
XX J02261;
XX
XX J02261.1
XX
XX 07-MAY-1992 (Rel. 31, Created)
XX 17-APR-2002 (Rel. 71, Last updated, Version 6)
XX
XX Moloney murine sarcoma virus polypeptide gene, partial cds.
XX
XX proviral gene: terminal repeat.
XX
XX Moloney murine sarcoma virus
XX OC Viruses; Retrovirdae; Gammaretrovirus.
XX
XX [1]
XX 16-1122
XX MEDLINE; 81013872.
XX PUBMED; 6251454.
XX
XX Sutcliffe J.G., Shinnick T.M., Verma I.M., Lerner R.A.;
XX "Nucleotide sequence of Moloney leukemia virus: 3' end reveals details of
XX RT replications, analogy to bacterial transposons, and an unexpected gene";
XX Proc. Natl. Acad. Sci. U.S.A. 77(6):3302-3306(1980).
XX
XX [2]
XX 1-1122
XX MEDLINE; 81013873.
XX PUBMED; 6251455.
XX
XX Van Beveren C., Goddard J.G., Berns A., Verma I.M.;
XX "Structure of Moloney murine leukemia viral DNA: nucleotide sequence of the
XX RT 5' long terminal repeat and adjacent cellular sequences";
XX Proc. Natl. Acad. Sci. U.S.A. 77(6):3307-3311(1980).
XX
XX [3]
XX 1-1122
XX MEDLINE; 81052384.
XX PUBMED; 6159543.
XX
XX Sutcliffe J.G., Shinnick T.M., Green N., Liu F.T., Niman H.L., Lerner R.A.;
XX "Chemical synthesis of a polypeptide predicted from nucleotide sequence
XX RT allows detection of a new retroviral gene product";
XX Nature 287(5785):801-805(1980).
XX

```

```

XX GOA: Q83401.
DR SPTREMBL; Q83401; Q83401.
XX
XX Key Location/Qualifiers
FH
FH source 1. .1122
FT /db_xref="taxon:11809"
FT /mol_type="genomic DNA"
FT /note="from Balb/mo mouse"
FT /proviral
FT /organism="Moloney murine sarcoma virus"
XX
XX mRNA
XX 1. .1122
XX /product="RNA polII transcript mRNA"
XX CDS
XX <1. .564
XX /codon_start=1
XX /db_xref="GOA:Q83401"
XX /product="SPTREMBL:Q83401"
XX
XX /product="polypeptide"
XX /protein_id="AA51623.1"
XX /translation="LIGGLTGWGIAIGIGTGTALMATQGFQQLQAAYDDLRREKSI
XX SNIKSLTSEVVLQNRGIDLFLEGGICAAKCECCFYADHTGLVDSMAKLER
XX LNRQKLFESTGCFEGELFNRSPIWFTLLISTIMGPLIVLLMILFPCILNRLVQFVKD
XX RISVQALVLTQCFHQLKPIECEP"
XX mat_peptide
XX <1. .282
XX /product="p15e protein"
XX 283. .561
XX /product="r protein"
XX 144
XX /note="a may be g ([1])"
XX 302
XX /note="t may be c ([1])"
XX 530
XX /note="t may be a ([1])"
XX 952
XX /note="a may be t ([1])"
XX
XX Sequence 1122 BP; 307 A; 266 C; 270 G; 279 T; 0 other;
SO

Query Match 0.0%; Score 12; DB 1; Length 1122;
Best Local Similarity 100.0%; Pred. No. 8.4;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 45978 AAATATAAGATT 45989
Db 568 AAATATAAGATT 579

RESULT 9
MMSPRO1 ID MMSPRO1 standard; DNA; VRL; 660 BP.
XX
XX J02260;
XX
XX J02260.1
XX
XX 05-NOV-1994 (Rel. 41, Created)
XX 12-MAR-2002 (Rel. 71, Last updated, Version 3)
XX
XX Moloney murine sarcoma virus long terminal repeat.
XX
XX terminal repeat.
XX
XX Moloney murine sarcoma virus
XX OC Viruses; Retrovirdae; Gammaretrovirus.
XX
XX [1]
XX 1-660
XX MEDLINE; 81013873.
XX PUBMED; 6251455.
XX
XX Van Beveren C., Goddard J.G., Berns A., Verma I.M.;
XX "Structure of Moloney murine leukemia viral DNA: nucleotide sequence of the
XX RT 5' long terminal repeat and adjacent cellular sequences";
XX

```

```
RL Proc. Natl. Acad. Sci. U.S.A. 77(6):3307-3311(1980).
XX
XX [2]
RP 441-545
RX MEDLINE: 82060256.
RX PUBMED: 6946480.
RA Fuhrman S.A., Van Beveren C., Verma I.M.;
RT "Identification of a RNA polymerase II initiation site in the long terminal
RT repeat of Moloney murine leukemia viral DNA";
RL Proc. Natl. Acad. Sci. U.S.A. 78(9):5411-5415(1981).
XX
XX On Oct 4, 1994 this sequence version replaced g1:332090.
CC + strand shown. 'LTR' in definition stands for 'long terminal
CC repeat'.
XX
FH Key Location/Qualifiers
FH
FT source 1. .660
FT /db_xref="taxon:11809"
FT /mol_type="genomic DNA"
FT /note="from Balb/mo mouse"
FT
FT /proviral
FT /organism="Moloney murine sarcoma virus"
FT mRNA 486. .>660
FT /product="RNA polII transcript mRNA"
XX
SQ Sequence 660 BP; 155 A; 181 C; 158 G; 166 T; 0 other;
Query Match 0.0%; Score 11; DB 1; Length 660;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 41018 CCACACCCCT 41028
Db 467 CCACACCCCT 477
RESULT 10
MMSPRO1/c standard; DNA; VRL; 660 BP.
XX
XX J02260;
XX
XX J02260.1
XX
DT 05-NOV-1994 (Rel. 41, Created)
DT 12-MAR-2002 (Rel. 71, Last updated, Version 3)
XX
XX Moloney murine sarcoma virus long terminal repeat.
XX
XX terminal repeat.
XX
XX Moloney murine sarcoma virus
OC Viruses; Retrovirdae; Retroviridae; Gammaretrovirus.
XX
XX [1]
RP 1-660
RX MEDLINE: 81013873.
RX PUBMED: 6251455.
RA Van Beveren C., Goddard J.G., Berns A., Verma I.M.;
RT "Structure of Moloney murine leukemia viral DNA: nucleotide sequence of the
RT 5' long terminal repeat and adjacent cellular sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 77(6):3307-3311(1980).
XX
XX [2]
RP 441-545
RX MEDLINE: 82060256.
RX PUBMED: 6946480.
RA Fuhrman S.A., Van Beveren C., Verma I.M.;
RT "Identification of a RNA polymerase II initiation site in the long terminal
RT repeat of Moloney murine leukemia viral DNA";
RL Proc. Natl. Acad. Sci. U.S.A. 78(9):5411-5415(1981).
XX
```

```
CC On Oct 4, 1994 this sequence version replaced g1:332090.
CC + strand shown. 'LTR' in definition stands for 'long terminal
CC repeat'.
XX
XX Key Location/Qualifiers
FH
FH source 1. .660
FH /db_xref="taxon:11809"
FH /mol_type="genomic DNA"
FH /note="from Balb/mo mouse"
FH
FH /proviral
FH /organism="Moloney murine sarcoma virus"
FH mRNA 486. .>660
FH /product="RNA polII transcript mRNA"
XX
SQ Sequence 660 BP; 155 A; 181 C; 158 G; 166 T; 0 other;
Query Match 0.0%; Score 11; DB 1; Length 660;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 43290 AGTTCTACCA 43300
Db 85 AGTTCTACCA 75
RESULT 11
AF541985 standard; DNA; VRL; 747 BP.
XX
XX AF541985;
XX
XX AF541985.1
XX
DT 26-SEP-2002 (Rel. 73, Created)
DT 26-SEP-2002 (Rel. 73, Last updated, Version 1)
XX
XX Dendrolimus punctatus cypovirus 1 strain Hunan polyhedrin gene, complete
DE cds.
XX
XX
XX Dendrolimus punctatus cypovirus 1
OC Viruses; dsRNA viruses; Reoviridae; Cypovirus; Cypovirus 1.
XX
XX [1]
RP 1-747
RA Hong J., Zhao S., Peng H., Duan J.;
RT "Comparison of C-polyhedrin genes from 5 type 1 cypoviruses";
RL Unpublished.
XX
XX [2]
RP 1-747
RA Hong J., Zhao S., Peng H., Duan J.;
RT Submitted (29-AUG-2002) to the EMBL/GenBank/DBJ databases.
RL Chinese Academy of Sciences, Wuhan Institute of Virology, Wuhan, Hubei
RL 430071, P.R. China
XX
XX SPTREMBL: Q8AYY9; Q8AYY9.
DR
XX
XX Key Location/Qualifiers
FH
FH source 1. .747
FH /db_xref="taxon:208509"
FH /mol_type="genomic DNA"
FH /organism="Dendrolimus punctatus cypovirus 1"
FH /strain="Hunan"
FH
FH /codon_start=1
FH /db_xref="SPTREMBL:Q8AYY9"
FH /note="forms crystals/polyhedra"
FH /product="polyhedrin"
FT
```

```

FT      /protein_id="AA17827.1"
FT      /translation="MADVAGTSNRDPRGREGQRLNSDQYNNSLNGSEVSWYVAYYS
FT      GSVLVINKNSQYKVGISETFKALKEGREGQNDSDYEYEVNQSIYYPNGDAHKFHSNA
FT      KPRALQIFSPSVWRTIKMAKNSVSPDDYLGSRHPEWATGIKYRKIRKDGELVGS
FT      HYFLPHEYNISLAVSGVHKNSPSYVNGSHANNMDYFGSCDLALRCNRYMAELELVN
FT      HTSPNATPYTIDINNSHYGVALSNHQ"
FT
XX      Sequence 747 BP; 226 A; 188 C; 169 G; 164 T; 0 other;
SQ
Query Match      0.0%; Score 11; DB 1; Length 747;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      45987 ATTCAAACGCC 45997
        |||
        302 ATTCAAACGCC 312

RESULT 12
AF541986 standard; DNA; VRL; 747 BP.
XX      AF541986;
AC      AF541986.1
SV      AF541986.1
XX      26-SEP-2002 (Rel. 73, Created)
DT      26-SEP-2002 (Rel. 73, Last updated, Version 1)
XX      Dendrolimus punctatus cyovirus 1 strain Hunan from Spodoptera exigua
DE      polyhedrin gene, complete cds.
XX
XX      Dendrolimus punctatus cyovirus 1
OS      Viruses; dsRNA viruses; Reoviridae; Cyovirus; Cyovirus 1.
OC      XX
XX      [1]
XX      RP 1-747
XX      RA Hong J., Zhao S., Peng H., Duan J.;
XX      RT "Comparison of C-polyhedrin genes from 5 type 1 cyoviruses";
XX      RL Unpublished.
XX
XX      [2]
XX      RP 1-747
XX      RA Hong J., Zhao S., Peng H., Duan J.;
XX      RT Submitted (29-AUG-2002) to the EMBL/Genbank/DBJ databases.
XX      RL Chinese Academy of Sciences, Wuhan Institute of Virology, Wuhan, Hubei
XX      430071, P.R. China
XX
XX      SPTREMBL; Q8AYY9; Q8AYY9.
DR
XX      SPTREMBL; Q8AYY9; Q8AYY9.
FH
XX      Key      Location/Qualifiers
FH
XX      source      1. 747
FT      /db_xref="taxon:208509"
FT      /mol_type="genomic DNA"
FT      /note="Substitute-host"
FT      /organism="Dendrolimus punctatus cyovirus 1"
FT      /strain="Hunan"
FT      /specific_host="Spodoptera exigua"
FT      1. 747
FT      /codon_start=1
FT      /db_xref="SPTREMBL:Q8AYY9"
FT      /note="forms crystals/polyhedra"
FT      /product="polyhedrin"
FT      /protein_id="AA17828.1"
FT      /translation="MADVAGTSNRDPRGREGQRLNSDQYNNSLNGSEVSWYVAYYS
FT      GSVLVINKNSQYKVGISETFKALKEGREGQNDSDYEYEVNQSIYYPNGDAHKFHSNA
FT      KPRALQIFSPSVWRTIKMAKNSVSPDDYLGSRHPEWATGIKYRKIRKDGELVGS
FT      HYFLPHEYNISLAVSGVHKNSPSYVNGSHANNMDYFGSCDLALRCNRYMAELELVN
FT      HTSPNATPYTIDINNSHYGVALSNHQ"
FT
CDS

```

```

XX      Sequence 747 BP; 230 A; 191 C; 166 G; 160 T; 0 other;
SQ
Query Match      0.0%; Score 11; DB 1; Length 747;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      45987 ATTCAAACGCC 45997
        |||
        302 ATTCAAACGCC 312

RESULT 13
MMSPRO2/c
XX      MMSPRO2 standard; DNA; VRL; 1122 BP.
XX      J02261;
AC      J02261.1
SV      J02261.1
XX      07-MAY-1992 (Rel. 31, Created)
DT      17-APR-2002 (Rel. 71, Last updated, Version 6)
XX      Moloney murine sarcoma virus polyprotein gene, partial cds.
DE      proviral gene; terminal repeat.
XX      Moloney murine sarcoma virus
OS      Viruses; Retroviridae; Gammaretrovirus.
OC      XX
XX      [1]
XX      RP 1-1122
XX      RA MEDLINE; 81013872.
XX      RX PUBMED; 6251454.
XX      RA Sutcliffe J.G., Shinnick T.M., Verma I.M., Lerner R.A.;
XX      RT "Nucleotide sequence of Moloney leukemia virus: 3' end reveals details of
XX      RL Proc. Natl. Acad. Sci. U.S.A. 77(6):3302-3306(1980).
XX
XX      [2]
XX      RP 1-1122
XX      RA MEDLINE; 81013873.
XX      RX PUBMED; 6251455.
XX      RA Van Beveren C., Goddard J.G., Berns A., Verma I.M.;
XX      RT "Structure of Moloney murine leukemia viral DNA: nucleotide sequence of the
XX      RL Proc. Natl. Acad. Sci. U.S.A. 77(6):3307-3311(1980).
XX
XX      [3]
XX      RP 1-1122
XX      RA MEDLINE; 81052384.
XX      RX PUBMED; 6159543.
XX      RA Sutcliffe J.G., Shinnick T.M., Green N., Liu F.T., Nilman H.L., Lerner R.A.;
XX      RT "Chemical synthesis of a polypeptide predicted from nucleotide sequence
XX      RL Nature 287(5785):801-805(1980).
XX
XX      GOA: Q83401.
DR      SPTREMBL; Q83401; Q83401.
FH
XX      Key      Location/Qualifiers
FH
XX      source      1. 1122
FT      /db_xref="taxon:11809"
FT      /mol_type="genomic DNA"
FT      /note="from Balb/mo mouse"
FT      /proviral
FT      /organism="Moloney murine sarcoma virus"
FT      <1. 1122
FT      /product="RNA polII transcript mRNA"
FT      <1. 564
FT      /codon_start=1
FT      /db_xref="GOA:Q83401"
FT
CDS

```

FT	/db_xref="SPRMBL:083401"
FT	/product="polyprotein"
FT	/protein_id="AA51623.1"
FT	/translation="LUGGLMGGIAAGTGTATTMAATQOFOQLAAVYODDLREYKSI
FT	STNKSILTSLEIVLQNRRLDLFLKEGGLAALKECCFYADHTGVLVROMAKLRER
FT	LNMRKQLFESTQWFEGLNRSRWFFPTLLSTIMGPLVLMLLPGPILNVLQFVXD
FT	RISVVALVLTQOFHQLKPIECP"
FT	<1..282
FT	/product="p15e protein"
FT	283..561
FT	mat_peptide
FT	/product="r protein"
FT	144
FT	/note="a may be g ([1])"
FT	302
FT	/note="t may be c ([1])"
FT	530
FT	/note="t may be a ([1])"
FT	952
FT	/note="a may be t ([1])"
XX	
50	Sequence 1122 BP; 307 A; 266 C; 270 G; 279 T; 0 other;

```

OY      44535 AAGACCACCA 44544
        |||||
DB      32  AAGACCACCA 41

```

Search completed: September 30, 2003, 03:37:45
Job time : 28 secs

	Query Match	0.0%	Score 11	DB 1	Length 1122
	Best Local Similarity	100.0%	Pred. No. 13		
	Matches 11	Conservative 0	Mismatches 0	Indels 0	Gaps 0
OY	57720	ACCATCTGTTTC	57730		
Db	798	ACCATCTGTTTC	788		

Search completed: September 30, 2003, 03:37:45
job time : 28 secs

RESULT 14	
MMJ1	
ID MMJ1	standard; RNA; VRL; 126 BP.
...	

AC	J02243;
XX	
SV	J02243.1
XX	
DT	01-OCT-1996 (Rel. 49, Created)
LT	11-FEB-1999 (Rel. 58, Last updated, Version 2)
XX	
DE	Macaca mulatta and arcoides type C retrovirus, 5' end.
KW	.
XX	
OS	Macaca mulatta and arcoides type C retrovirus
OC	Viruses; Retroel viruses; Retroviridae; Mammalian type C retroviruses;
MC	1-Mammalian type C virus group; Macaca mulatta type C retrovirus.
XX	
[1]	
RN	1-126
RP	MEDLINE: 80222887.
RX	PUBMED: 6248246.
RA	Lovinger G.G., Schochetman G.;
RT	"5' terminal nucleotide sequences of type C retroviruses: features common
RL	to noncoding sequences of eucaryotic messenger RNAs.";
XX	Cell 20(2):441-449(1980).
CC	
XX	See also <brev5>, <mml> & <rdl1>.
FH	
EH	Key Location/Qualifiers
FT	source 1..126
FT	/db_xref="taxon:11844"
FT	/note="Isolated from spleen cells"
FT	/organism="Macaca mulatta and arcoides type C retrovirus
QD	Sequence 126 BP; 36 A; 33 C; 30 G; 27 T; 0 other;

```
Query Match          0.0%; Score 10; DB 1; Length 126;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 30, 2003, 03:37:48 ; Search time 18 seconds
(without alignments)
34.943 Million cell updates/sec

Title: us-09-831-000-1
Perfect score: 40001
Sequence: 1 tcccacgagtcgtcacacg.....agcgttgataatcacgac 40001

Scoring table: OLIGO-NUC
Gapop 60.0 , Gapext 60.0

Searched: 7 seqs, 7862 residues

Word size : 0

Total number of hits satisfying chosen parameters: 14

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : em_vi.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15	0.0	2480	1	L08231 Mastadenovl
2	14	0.0	747	1	AF541985 Dendrolim
3	14	0.0	747	1	AF541986 Dendrolim
4	14	0.0	1122	1	MMSPRO2 J02261 Moloney mur
5	14	0.0	1980	1	ADREAR3RE M94458 Mastadenovl
6	13	0.0	1980	1	ADREAR3RE L08231 Mastadenovl
7	13	0.0	2480	1	ADRE3GENE L08231 Mastadenovl
8	12	0.0	126	1	MMJAI J02243 Macaca mula
9	12	0.0	660	1	MMSPRO1 J02260 Moloney mur
10	12	0.0	1122	1	MMSPRO2 J02261 Moloney mur
11	12	0.0	126	1	MMJAI J02243 Macaca mula
12	11	0.0	747	1	AF541985 Dendrolim
13	11	0.0	747	1	AF541986 Dendrolim
14	11	0.0	747	1	AF541986 Dendrolim

ALIGNMENTS

RESULT 1
ADRE3GENE standard; DNA: VRL; 2480 BP.

XX L08231;

XX L08231.1

XX 08-JUL-1993 (Rel. 36, Created)

XX 04-MAR-2000 (Rel. 63, Last updated, Version 3)

XX Mastadenovirus 11 E3 region encoding fiber gene, complete cds.

XX fiber protein.

XX Human adenovirus type 11
OS Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus;
OC Human adenovirus B.

XX [1]
RX 1-2480
RX MEDLINE: 93276532.
RX PUBMED: 8503168.
RA Mei Y.-F., Madell G.;
RT "Hemagglutination properties and nucleotide sequence analysis of the fiber
gene of adenovirus genome types 11p and 11a".
RL Virology 194(2):453-462(1993).

XX GOA: P35774.
XX SWISS-PROT: P35774; FIBP_ADE1P.

XX Key Location/Qualifiers

XX source 1..2480
XX /db_xref="taxon:10541"
XX /mol_type="genomic DNA"
XX /organism="Human adenovirus type 11"
XX /strain="Slobitski"
XX 1094..2071
XX CDS
XX /codon_start=1
XX /db_xref="GOA:P35774"
XX /db_xref="SWISS-PROT:P35774"
XX /gene="E3"
XX /protein_id="AAA42490.1"
XX /translation="MTKRVRLSDSFNPVYDEDESTQHPFINPGFISPNGFQSPNGV
LILKCLPTTTGGSLQKLVGGGLVDDPTNGFLKENSATTPLYKTHSGISGLPGLG
TNEKLCITLGGGLFENSNNICIDQINLTMVGNPTPEANCOIMNSPESDCKLITLV
KIGALVTAVYVIGISNNFMULTTHRNINFTALPFDPSGNLTLRLSSIKTPLNRSQ
NMTAGITNAKGFMPSTAVPFDNSRERENITVGYTASDRTAFPIDISVMLNRA
INDETSYCIIRITWMTGDAPEVQTSATTLVTSPTFYIRDD"

XX SQ Sequence 2480 BP; 768 A; 652 C; 418 G; 642 T; 0 other;

XX Query Match 0.0%; Score 15; DB 1; Length 2480;
XX Best Local Similarity 100.0%; Pred. No. 0.36;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 96973 AGATAAAATCCATC 96987
DB 2272 AGATAAAATCCATC 2286

RESULT 2
ID AF541985 standard; DNA: VRL; 747 BP.

XX AF541985;

XX AF541985.1

XX 26-SEP-2002 (Rel. 73, Created)
XX 26-SEP-2002 (Rel. 73, Last updated, Version 1)

XX Dendrolimus punctatus cypovirus 1 strain Human polyhedrin gene, complete
XX cds.

XX Dendrolimus punctatus cypovirus 1
XX Viruses; dsRNA viruses; Reoviridae; Cypovirus; Cypovirus 1.

XX [1]
XX 1-747

XX Hong J., Zhao S., Peng H., Duan J.;
XX "Comparison of C-polyhedrin genes from 5 type 1 cypoviruses";
XX unpublished.

```
RN [2]
RP 1-747
RA Hong J., Zhao S., Peng H., Duan J.;
RT ;
RL Submitted (29-AUG-2002) to the EMBL/GenBank/DBJ databases.
RU Chinese Academy of Sciences, Wuhan Institute of Virology, Wuhan, Hubei
RL 430071, P.R. China
XX
DR SPTREMBL: O8AYY9; O8AYY9.
XX
FH Key Location/Qualifiers
FH
FT source 1..747
FT /db_xref="taxon:208509"
FT /mol_type="genomic DNA"
FT /organism="Dendrolimus punctatus cypovirus 1"
FT /strain="Hunan"
FT 1..747
FT /codon_start=1
FT /db_xref="SPTREMBL:O8AYY9"
FT /note="forms crystals/polymheda"
FT /product="polyhedrin"
FT /protein_id="AA17827.1"
FT /translation="MADVAGTSNDPFGREORLFSNQYNNNSLNGEVSVMYAYYSD
FT GSVLVYKNSQYKVGISETRKALKETREGORNDSDYEYNQSTIYNGDARFHSNA
FT KPRAIQIIFSPSVNVRTIKAKGNSVSPDDYLQSRHPWEATGIKYRKIRDEIVGYS
FT HYELPHEVNSISLAVSGVHKNPSSYVNGSAHNMDVFOCDLALRRCNRYMALELVN
FT HTSPNAYPYLDINNHSGVALSNHQ"
XX
SO Sequence 747 BP: 226 A; 188 C; 169 G; 164 T; 0 other;

Query Match 0.0%; Score 14; DB 1; Length 747;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 97258 ACAACAGCTTAAC 97271
DB 83 ACAACAGCTTAAC 96

RESULT 3
AF541986 standard; DNA; VRL: 747 BP.
AC AF541986;
XX
SV AF541986.1
XX
DT 26-SEP-2002 (Rel. 73, Created)
DT 26-SEP-2002 (Rel. 73, Last updated, Version 1)
XX
DE Dendrolimus punctatus cypovirus 1 strain Hunan from Spodoptera exigua
DE polyhedrin gene, complete cds.
XX
KW
XX
OS Dendrolimus punctatus cypovirus 1
OC Viruses; dsRNA viruses; Reoviridae; Cypovirus; Cypovirus 1.
XX
RN [1]
RP 1-747
RA Hong J., Zhao S., Peng H., Duan J.;
RT "Comparison of C-polyhedrin genes from 5 type 1 cypoviruses";
RT unpublished.
XX
RN [2]
RP 1-747
RA Hong J., Zhao S., Peng H., Duan J.;
RT Submitted (29-AUG-2002) to the EMBL/GenBank/DBJ databases.
RU Chinese Academy of Sciences, Wuhan Institute of Virology, Wuhan, Hubei
RL 430071, P.R. China
XX
```

```
DR SPTREMBL: O8AYY9; O8AYY9.
XX
FH Key Location/Qualifiers
FH
FT source 1..747
FT /db_xref="taxon:208509"
FT /mol_type="genomic DNA"
FT /note="substitute-host"
FT /organism="Dendrolimus punctatus cypovirus 1"
FT /strain="Hunan"
FT /specific_host="Spodoptera exigua"
FT 1..747
FT /codon_start=1
FT /db_xref="SPTREMBL:O8AYY9"
FT /note="forms crystals/polymheda"
FT /product="polyhedrin"
FT /protein_id="AA17828.1"
FT /translation="MADVAGTSNDPFGREORLFSNQYNNNSLNGEVSVMYAYYSD
FT GSVLVYKNSQYKVGISETRKALKETREGORNDSDYEYNQSTIYNGDARFHSNA
FT KPRAIQIIFSPSVNVRTIKAKGNSVSPDDYLQSRHPWEATGIKYRKIRDEIVGYS
FT HYELPHEVNSISLAVSGVHKNPSSYVNGSAHNMDVFOCDLALRRCNRYMALELVN
FT HTSPNAYPYLDINNHSGVALSNHQ"
XX
SO Sequence 747 BP: 230 A; 191 C; 166 G; 160 T; 0 other;

Query Match 0.0%; Score 14; DB 1; Length 747;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 97258 ACAACAGCTTAAC 97271
DB 83 ACAACAGCTTAAC 96

RESULT 4
MMSPRO2/C
ID MMSPRO2 standard; DNA; VRL: 1122 BP.
AC J02261;
XX
SV J02261.1
XX
DT 07-MAY-1992 (Rel. 31, Created)
DT 17-APR-2002 (Rel. 71, Last updated, Version 6)
XX
DE Moloney murine sarcoma virus polyprotein gene, partial cds.
DE proviral gene; terminal repeat.
XX
KW
XX
OS Moloney murine sarcoma virus
OC Viruses; Retroid viruses; Retroviridae; Gammaretrovirus.
XX
RN [1]
RP 16-1122
RX MEDLINE; 81013872.
RX PUBMED; 6251454.
RA Sutcliffe J.G., Shinnick T.M., Verma I.M., Lerner R.A.;
RT "Nucleotide sequence of Moloney leukemia virus: 3' end reveals details of
RT replications, analogy to bacterial transposons, and an unexpected gene";
RT Proc. Natl. Acad. Sci. U.S.A. 77(6):3302-3306(1980).
XX
RN [2]
RP 1-1122
RX MEDLINE; 81013873.
RX PUBMED; 6251455.
RA Van Beveren C., Goddard J.G., Berns A., Verma I.M.;
RT "Structure of Moloney murine leukemia viral DNA: nucleotide sequence of the
RT 5' long terminal repeat and adjacent cellular sequences";
RT Proc. Natl. Acad. Sci. U.S.A. 77(6):3307-3311(1980).
XX
RN [3]
RP 1-1122
RX MEDLINE; 81052384.
RX
```


RX PubMed: 6159543.
 RA Sutcliffe J.G., Shinnick T.M., Green N., Liu F.T., Niman H.L., Lerner R.A.;
 RT "Chemical synthesis of a polypeptide predicted from nucleotide sequence
 RL allows detection of a new retroviral gene product";
 RX Nature 287(5785):801-805(1980).
 DR GOA: Q83401.
 DR SPTREMBL: Q83401; Q83401.
 XX
 XX
 FH Key Location/Qualifiers
 FH source
 FT 1..1122
 FT /db_xref="taxon:11809"
 FT /mol_type="genomic DNA"
 FT /note="from Balb/mo mouse"
 FT /proviral
 FT /organism="Moloney murine sarcoma virus"
 FT <1..1122
 FT /product="RNA polII transcript mRNA"
 FT <1..564
 FT CDS
 FT /codon_start=1
 FT /db_xref="GOA:Q83401"
 FT /db_xref="SPTREMBL:Q83401"
 FT /product="polyprotein"
 FT /protein_id="AA51623.1"
 FT /translation="LLGLTMCIGIAIGTGTALMATQFOQLQAAYDDDLREVEKSI
 FT SNLEKSLTSEVVLNRRGLDLFLKEGGLCAALKECCFYADHGLVDSNAKLRR
 FT LNRKSLFESTGCPGEGLEPFRSPFTLLISTINGPLVLMLILFGCIINRLVQFVKD
 FT RISVVALVLTQGFHQKPTCECP"
 FT <1..282
 FT mat_peptide
 FT /product="p15e protein"
 FT 283..561
 FT mat_peptide
 FT /product="r protein"
 FT 144
 FT unsure
 FT /note="a may be g (11)"
 FT 302
 FT unsure
 FT /note="t may be c (11)"
 FT 530
 FT unsure
 FT /note="t may be a (11)"
 FT 952
 FT unsure
 FT /note="a may be t (11)"
 FT
 XX
 SQ Sequence 1122 BP; 307 A; 266 C; 270 G; 279 T; 0 other;
 Query Match 0.0%; Score 14; DB 1; Length 1122;
 Best Local Similarity 100.0%; Pred. No. 1.4; Mismatches 0; Gaps 0;
 Matches 14; Conservative 0; Indels 0; Gaps 0;
 OY 83765 TCCCTGTTCCTATT 83778
 Db 52 TCCCTGTTCCTATT 39
 RESULT 5
 ADREAR3RE/c
 ID ADREAR3RE standard; DNA; VRL; 1980 BP.
 XX
 AC M94458;
 XX
 SV M94458.1
 XX
 XX 11-DEC-1992 (Rel. 34, Created)
 DT 04-MAR-2000 (Rel. 63, Last updated, Version 5)
 XX
 DE Mastadenovirus serotype 11 early 3 region.
 XX
 XX early 3 region.
 KW
 XX
 OS Human adenovirus type 11
 OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus;
 OC Human adenovirus B.
 XX [1]

RP 1-1980
 RX MEDLINE; 93033102.
 RX PubMed: 1413499.
 RA Mel Y.-F., Madell G.;
 RT "The nucleotide sequence of adenovirus type 11 early 3 region: comparison
 RL of genome type Ad1p and Ad1a.";
 RL Virology 191(1):125-133(1992).
 XX
 XX
 DR GOA: P15140.
 DR SWISS-PROT; P15140; E3GL_ADE35.
 DR SWISS-PROT; P35768; E320_ADE1P.
 DR SWISS-PROT; P35770; E321_ADE1P.
 XX
 FH Key Location/Qualifiers
 FH source
 FT 1..1980
 FT /db_xref="taxon:10541"
 FT /mol_type="genomic DNA"
 FT /organism="Human adenovirus type 11"
 FT /strain="Slobitski1"
 XX
 SQ Sequence 1980 BP; 568 A; 466 C; 330 G; 616 T; 0 other;
 Query Match 0.0%; Score 14; DB 1; Length 1980;
 Best Local Similarity 100.0%; Pred. No. 1.6;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 94028 TAAAGAGAAATTAA 94041
 Db 1167 TAAAGAGAAATTAA 1154
 RESULT 6
 ADREAR3RE
 ID ADREAR3RE standard; DNA; VRL; 1980 BP.
 XX
 AC M94458;
 XX
 SV M94458.1
 XX
 XX 11-DEC-1992 (Rel. 34, Created)
 DT 04-MAR-2000 (Rel. 63, Last updated, Version 5)
 XX
 DE Mastadenovirus serotype 11 early 3 region.
 XX
 XX early 3 region.
 KW
 XX
 OS Human adenovirus type 11
 OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus;
 OC Human adenovirus B.
 XX
 RN [1]
 RP 1-1980
 RX MEDLINE; 93033102.
 RX PubMed: 1413499.
 RA Mel Y.-F., Madell G.;
 RT "The nucleotide sequence of adenovirus type 11 early 3 region: comparison
 RL of genome type Ad1p and Ad1a.";
 RL Virology 191(1):125-133(1992).
 XX
 XX
 DR GOA: P15140.
 DR SWISS-PROT; P15140; E3GL_ADE35.
 DR SWISS-PROT; P35768; E320_ADE1P.
 DR SWISS-PROT; P35770; E321_ADE1P.
 XX
 FH Key Location/Qualifiers
 FH source
 FT 1..1980
 FT /db_xref="taxon:10541"
 FT /mol_type="genomic DNA"
 FT /organism="Human adenovirus type 11"
 FT /strain="Slobitski1"

SO Sequence 1980 BP; 568 A; 466 C; 330 G; 616 T; 0 other;

Query Match 0.0%; Score 13; DB 1; Length 1980;
Best Local Similarity 100.0%; Pred. No. 5.5;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 83126 ACAGTACTCATTA 83138
|||||
DB 880 ACAGTACTCATTA 892

RESULT 7

ADRE3GENE/c
ID ADRE3GENE standard; DNA; VRL; 2480 BP.

XX L08231;
XX L08231.1

DT 08-JUL-1993 (Rel. 36, Created)
DT 04-MAR-2000 (Rel. 63, Last updated, Version 3)

XX Mastadenovirus 11 E3 region encoding fiber gene, complete cds.

XX fiber protein.

XX Human adenovirus type 11

OS Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus;

OC Human adenovirus B.

XX [1]

RP 1-2480
RX MEDLINE; 93276532.
RX PUBMED; 8503168.

RA Mel Y.-F., Wadell G.;

RT "Hemagglutination properties and nucleotide sequence analysis of the fiber gene of adenovirus genome types 11p and 11a";

RL Virology 194(2):453-462(1993).

XX GOA: P35774.

DR SWISS-PROT; P35774; FIBP_ADE1P.

XX key Location/Qualifiers

XX source

1. 2480
/db_xref="taxon:10541"

/mol_type="genomic DNA"

/organism="Human adenovirus type 11"

/strain="Slobitski"

1094. 2071

/codon_start=1

/db_xref="GOA:P35774"

/db_xref="SWISS-PROT:P35774"

/gene="E3"

/protein_id="AAA2490.1"

/translation="MTRKRVRLSDSFNVPYEPEDSTQHPINPGFISPNCFQSPNGV

LTKCLPLPTTGGSLQIKVGGGLVDFTNGELKENISATPLVKTGHSIGLPGAGLG

TNENKLCIKIGOGILTFPNSNNICIDNINITLMTGVNPTEANQILNNSSESDCKLITLV

KTGALVAFVYVIGVSNPNMLTTHRNINFTFAELFDSGTMLTRLSLKPILNHSQO

NMAGALTAKGEMSPSTAYPENSREKENYIYGCYVYASDRTAPPIDISVMLNRRRA

INDETSICIRLTMSMNTGDAPVQTSATTLVTSPTTYIREDP"

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

RESULT 8

MMJAI/c
ID MMJAI standard; RNA; VRL; 126 BP.

XX J02243;

XX J02243.1

SV J02243.1

DT 01-OCT-1996 (Rel. 49, Created)

DT 11-FEB-1999 (Rel. 58, Last updated, Version 2)

XX Macaca mulatta and arcoides type C retrovirus, 5' end.

DE Macaca mulatta and arcoides type C retrovirus, 5' end.

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

RESULT 9

MMSPRO1
ID MMSPRO1 standard; DNA; VRL; 660 BP.

XX J02260;

XX J02260.1

SV J02260.1

DT 05-NOV-1994 (Rel. 41, Created)

DT 12-MAR-2002 (Rel. 71, Last updated, Version 3)

XX Mooney murine sarcoma virus long terminal repeat.

DE Mooney murine sarcoma virus long terminal repeat.

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

```

RL Proc. Natl. Acad. Sci. U.S.A. 77(6):3307-3311(1980).
XX
XX [2]
RP 441-545
RX MEDLINE: 82060256.
RX PUBMED: 6946480.
RA Fuhrman S.A., Van Beveren C., Verma I.M.;
RT "Identification of a RNA polymerase II initiation site in the long terminal
RL repeat of Moloney murine leukemia viral DNA";
XX Proc. Natl. Acad. Sci. U.S.A. 78(9):5411-5415(1981).
CC On Oct 4, 1994 this sequence version replaced g1:332090.
CC + strand shown. 'LTR' in definition stands for 'long terminal
CC repeat'.
XX
XX Key Location/Qualifiers
FH
FH source 1..660
FT /db_xref="taxon:11809"
FT /mol_type="genomic DNA"
FT /note="from Balb/mo mouse"
FT /proviral
FT /organism="Moloney murine sarcoma virus"
FT mRNA 486..>660
FT /product="RNA polII transcript mRNA"
SQ
SQ Sequence 660 BP; 155 A; 181 C; 158 G; 166 T; 0 other;
Query Match 0.0%; Score 12; DB 1; Length 660;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 88221 TATGATCTCCTT 88232
DB 5 TATGATCTCCTT 16
RESULT 10
MMSPRO1/c
ID MMSPRO1 standard; DNA; VRL; 660 BP.
XX
XX J02260;
XX
XX J02260.1
XX
XX 05-NOV-1994 (Rel. 41, Created)
DT 12-MAR-2002 (Rel. 71, Last updated, Version 3)
XX
XX Moloney murine sarcoma virus long terminal repeat.
XX terminal repeat.
XX
XX Moloney murine sarcoma virus
OS
OC Viruses; Retrovirdae; Retroviridae; Gammaretrovirus.
XX
XX [1]
RP 1-660
RX MEDLINE: 81013873.
RX PUBMED: 6251455.
RA Van Beveren C., Goddard J.G., Berns A., Verma I.M.;
RT "Structure of Moloney murine leukemia viral DNA: nucleotide sequence of the
RL 5' long terminal repeat and adjacent cellular sequences";
XX Proc. Natl. Acad. Sci. U.S.A. 77(6):3307-3311(1980).
XX
XX [2]
RP 441-545
RX MEDLINE: 82060256.
RX PUBMED: 6946480.
RA Fuhrman S.A., Van Beveren C., Verma I.M.;
RT "Identification of a RNA polymerase II initiation site in the long terminal
RL repeat of Moloney murine leukemia viral DNA";
XX Proc. Natl. Acad. Sci. U.S.A. 78(9):5411-5415(1981).
XX

```

```

CC On Oct 4, 1994 this sequence version replaced g1:332090.
CC + strand shown. 'LTR' in definition stands for 'long terminal
CC repeat'.
XX
XX Key Location/Qualifiers
FH
FH source 1..660
FT /db_xref="taxon:11809"
FT /mol_type="genomic DNA"
FT /note="from Balb/mo mouse"
FT /proviral
FT /organism="Moloney murine sarcoma virus"
FT mRNA 486..>660
FT /product="RNA polII transcript mRNA"
SQ
SQ Sequence 660 BP; 155 A; 181 C; 158 G; 166 T; 0 other;
Query Match 0.0%; Score 12; DB 1; Length 660;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 93698 ACCATCTGTTCT 93709
DB 304 ACCATCTGTTCT 293
RESULT 11
MMSPRO2
ID MMSPRO2 standard; DNA; VRL; 1122 BP.
XX
XX J02261;
XX
XX J02261.1
XX
XX 07-MAY-1992 (Rel. 31, Created)
DT 17-APR-2002 (Rel. 71, Last updated, Version 6)
XX
XX Moloney murine sarcoma virus polyprotein gene, partial cds.
XX
XX proviral gene; terminal repeat.
XX
XX Moloney murine sarcoma virus
OS
OC Viruses; Retrovirdae; Retroviridae; Gammaretrovirus.
XX
XX [1]
RP 16-1122
RX MEDLINE: 81013872.
RX PUBMED: 6251454.
RA Sutcliffe J.G., Shinnick T.M., Verma I.M., Lerner R.A.;
RT "Nucleotide sequence of Moloney leukemia virus: 3' end reveals details of
RL replications, analogy to bacterial transposons, and an unexpected gene";
XX Proc. Natl. Acad. Sci. U.S.A. 77(6):3302-3306(1980).
XX
XX [2]
RP 1-1122
RX MEDLINE: 81013873.
RX PUBMED: 6251455.
RA Van Beveren C., Goddard J.G., Berns A., Verma I.M.;
RT "Structure of Moloney murine leukemia viral DNA: nucleotide sequence of the
RL 5' long terminal repeat and adjacent cellular sequences";
XX Proc. Natl. Acad. Sci. U.S.A. 77(6):3307-3311(1980).
XX
XX [3]
RP 1-1122
RX MEDLINE: 81052384.
RX PUBMED: 6159543.
RA Sutcliffe J.G., Shinnick T.M., Green N., Liu F.T., Niman H.L., Lerner R.A.;
RT "Chemical synthesis of a polypeptide predicted from nucleotide sequence
RL allows detection of a new retroviral gene product";
XX Nature 287(5785):801-805(1980).
XX
XX GOA: Q83401.
XX SPTREMBL: Q83401; Q83401.
DR

```

```

XX Key Location/Qualifiers
FH 1..1122
FT source /db_xref="taxon:11809"
FT /mol_type="genomic DNA"
FT /note="from Balb/mo mouse"
FT /providal
FT /organism="Moloney murine sarcoma virus"
FT 1..1122
FT /product="RNA polII transcript mRNA"
FT <1..564
FT /codon_start=1
FT /db_xref="GOA:Q83401"
FT /db_xref="SPTREMBL:Q83401"
FT /product="polyprotein"
FT /protein_id="AA51623.1"
FT /translation="ILGGLTMCITAGTGTATMAATQPOLOAAVDDIPEVEKSI
FT SNIKSLTISEVYLNRRGLDLFLKEGGLCAALKECCFYADHTGLVDSMAKLER
FT LNRQKLFESTQGWFEGLFNRSPTTLTISTIMGPLVLLMLILFGPCILNRLVQFVKD
FT RISVVALVLTQGFHQLEKPECEP"
FT <1..282
FT mat_peptide
FT /product="p15e protein"
FT 283..561
FT /product="r protein"
FT 144
FT /note="a may be g ([1])"
FT 302
FT /note="t may be c ([1])"
FT 530
FT /note="t may be a ([1])"
FT 952
FT /note="a may be t ([1])"
FT unsure
FT
XX
SQ Sequence 1122 BP; 307 A; 266 C; 270 G; 279 T; 0 other;
Query Match 0.0%; Score 12; DB 1; Length 1122;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 117086 CTGTAGCTTTGG 117097
|||||
Db 621 CTGTAGCTTTGG 632

RESULT 12
MMJAL standard; RNA; VRL; 126 BP.
XX J02243;
XX J02243.1
SV
XX
DT 01-OCT-1996 (Rel. 49, Created)
DT 11-FEB-1999 (Rel. 58, Last updated, Version 2)
XX
DE Macaca mulatta and arctoides type C retrovirus, 5' end.
XX
XX
OS Macaca mulatta and arctoides type C retrovirus
OC Viruses; Retroviridae; Retroviridae; Mammalian type C retroviruses;
OC 1-Mammalian type C virus group; Macaca mulatta type C retrovirus.
XX
XX [1]
RN 1-126
RP MEDLINE; 80222887.
RX PUBMED; 6248246.
RA Løvinger G.G., Schochetman G.;
RT "5' terminal nucleotide sequences of type C retroviruses: features common
RL to noncoding sequences of eucaryotic messenger RNAs.";
Cell 20(2):441-449(1980).
XX

```

```

CC See also <baev5>, <mmcl> & <rd114>.
XX
XX Key Location/Qualifiers
FH 1..126
FT source /db_xref="taxon:11844"
FT /note="isolated from spleen cells"
FT /organism="Macaca mulatta and arctoides type C retrovirus"
FT
XX
SQ Sequence 126 BP; 36 A; 33 C; 30 G; 27 T; 0 other;
Query Match 0.0%; Score 11; DB 1; Length 126;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 82201 CTTTATTACAG 82211
|||||
Db 73 CTTTATTACAG 83

RESULT 13
AF541985/C
ID AF541985 standard; DNA; VRL; 747 BP.
XX AF541985;
XX AF541985.1
SV
XX
DT 26-SEP-2002 (Rel. 73, Created)
DT 26-SEP-2002 (Rel. 73, Last updated, Version 1)
XX
DE Dendrolimus punctatus cypovirus 1 strain Hunan polyhedrin gene, complete
DE cds.
XX
XX
KW
XX
OS Dendrolimus punctatus cypovirus 1
OC Viruses; dsRNA viruses; Reoviridae; Cypovirus; Cypovirus 1.
XX
XX [1]
RN 1-747
RP Hong J., Zhao S., Peng H., Duan J.;
RA "Comparison of C-polyhedrin genes from 5 type 1 cypoviruses";
RL Unpublished.
XX
XX [2]
RN 1-747
RP Hong J., Zhao S., Peng H., Duan J.;
RA Submitted (29-AUG-2002) to the EMBL/GenBank/DBJ databases.
RL Chinese Academy of Sciences, Wuhan Institute of Virology, Wuhan, Hubei
RL 430071, P.R. China
XX
XX SPTREMBL: Q8AYY9; Q8AYY9.
XX
XX
FH key Location/Qualifiers
FH source 1..747
FT /db_xref="taxon:208509"
FT /mol_type="genomic DNA"
FT /organism="Dendrolimus punctatus cypovirus 1"
FT /strain="Hunan"
FT 1..747
FT /codon_start=1
FT /db_xref="SPTREMBL:Q8AYY9"
FT /note="forms crystals/polyhedra"
FT /product="polyhedrin"
FT /protein_id="AA117827.1"
FT /translation="MADVACTSNRDFRGREORLPSNQRYNNNSLNGEVSVWYAYYSD
FT GSVLVTKNSQYKVGISETKALKEVREGGRNDSDYEYVNSITYPNGDAHKEFHSNA
FT KPAKIQIIFSPSNVVRTIKMAKNSVSPDDYLRSHPWGATGIRKIRKIRDEIYGV
FT HPELPEYNSISLAVSGVHKNSVSGSAHNVMDVFGCDLALRRCNRYMALELVN
FT HTSPNAPYPLDINNHSYVALSNHQ"

```

XX Sequence 747 BP; 226 A; 188 C; 169 G; 164 T; 0 other;

SO Query Match 0.0%; Score 11; DB 1; Length 747;

Best Local Similarity 100.0%; Pred. No. 21;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 85686 CCATCTTGATG 85696

Db 373 CCATCTTGATG 363

QY 85686 CCATCTTGATG 85696
 Db 373 CCATCTTGATG 363

Search completed: September 30, 2003, 03:38:35
 Job time : 28 secs

RESULT 14

AF541986/c standard; DNA; VRL: 747 BP.

AC AF541986;

SV AF541986.1

XX 26-SEP-2002 (Rel. 73, Created)

DT 26-SEP-2002 (Rel. 73, Last updated, Version 1)

XX Dendrolimus punctatus cypovirus 1 strain Hunan from Spodoptera exigua
 DE polyhedrin gene, complete cds.

XX Dendrolimus punctatus cypovirus 1

OC Viruses; dsRNA viruses; Reoviridae; Cypovirus; Cypovirus 1.

XX [1]

RP 1-747

RA Hong J., Zhao S., Peng H., Duan J.;

RT "Comparison of C-polyhedrin genes from 5 type 1 cypoviruses";

RL unpublished.

XX [2]

RA Hong J., Zhao S., Peng H., Duan J.;

RT Submitted (29-AUG-2002) to the EMBL/GenBank/DBJ databases.

RL Chinese Academy of Sciences, Wuhan Institute of Virology, Wuhan, Hubei

RL 430071, P.R. China

XX SPTREMBL: Q8AYY9; Q8AYY9.

DR SPTREMBL: Q8AYY9; Q8AYY9.

XX Key

Location/Qualifiers

source

1. 747

/db_xref="taxon:208509"

/mol_type="genomic DNA"

/note="substitute-host"

/organism="Dendrolimus punctatus cypovirus 1"

/strain="Hunan"

/specific_host="Spodoptera exigua"

1. 747

/codon_start=1

/db_xref="SPTREMBL:Q8AYY9"

/note="forms crystals/polyhedra"

/product="polyhedrin"

/protein_id="AA017828.1"

/translation="MADVAGTSNRDPRGRORLFRNSFOYNNNSLNGEVSVMVYAYSD

GSVYVIRKNSQYKVGISETRKALKETREGQRNDYDEYVNSQITYPNGDPAKFSNA

KPRAIQITFSPSVAVRTIKAKGNSVSPDDYLDORSHPEWATGIRKIRKIRKDEIGVGS

HYELPHEVNSISLAVSGVHKNPSSYVNGSAHNVMDVFOCDLALRRCNRYWAELELVN

HYISPNAYPYLDINNHSHSYVALSNHQ"

Sequence 747 BP; 230 A; 191 C; 166 G; 160 T; 0 other;

Query Match 0.0%; Score 11; DB 1; Length 747;

Best Local Similarity 100.0%; Pred. No. 21;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 26, 2003, 17:57:32 ; Search time 16 Seconds
(without alignments)
39.310 Million cell updates/sec

Title: us-09-831-000-1
Perfect score: 40000
Sequence: 1 gatcggaacacgcgagggg.....acctatgatactcgttt 40000

Scoring table: OLIGO_NUC
Gapop 60.0 , Capext 60.0

Searched: 7 segs, 7862 residues

Word size: 0

Total number of hits satisfying chosen parameters: 14

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database: em_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	16	0.0	1980	1	M94458 Mastadenov
2	15	0.0	2480	1	L08231 Mastadenov
3	13	0.0	1980	1	M94458 Mastadenov
4	12	0.0	660	1	MMSPRO1
5	12	0.0	747	1	AF541985
6	12	0.0	747	1	AF541985 Dendrolim
7	12	0.0	747	1	AF541985 Dendrolim
8	12	0.0	747	1	AF541986 Dendrolim
9	12	0.0	1122	1	MMSPRO2
10	12	0.0	1122	1	MMSPRO2
11	12	0.0	2480	1	ADRE3GENE
12	11	0.0	660	1	MMSPRO1
13	10	0.0	126	1	MMUAI
14	10	0.0	126	1	MMUAI
					J02243 Macaca mula

ALIGNMENTS

RESULT 1
ADRE3GENE/C
ID ADRE3GENE standard; DNA; VRL; 1980 BP.

XX M94458;

SV M94458.1

XX 11-DEC-1992 (Rel. 34, Created)

DT 04-MAR-2000 (Rel. 63, Last updated, Version 5)

DE Mastadenovirus serotype 11 early 3 region.

XX early 3 region.

XX Human adenovirus type 11
OS Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus;
OC Human adenovirus B.
XX
XX [1]
RN 1-1980
RP MEDLINE: 93033102.
RX PUBMED: 1413499.
RA Wei Y.-F., Wadell G.;
RT "The nucleotide sequence of adenovirus type 11 early 3 region: comparison of genome type Ad1p and Ad1a";
RL Virology 191(1):125-133(1992).
XX
XX GOA: P15140.
DR SWISS-PROT: P15140; E3GL_ADE35.
DR SWISS-PROT: P35768; E320_ADE1P.
DR SWISS-PROT: P35770; E321_ADE1P.
XX
XX Key Location/Qualifiers
FH
FH source 1.1980
FT /db_xref="taxon:10541"
FT /mol_type="genomic DNA"
FT /organism="Human adenovirus type 11"
FT /strain="Slobitski"

Query Match 0.0%; Score 16; DB 1; Length 1980;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27171 ATGTGTCGATAGGT 27186
DB 311 ATGTGTCGATAGGT 296

RESULT 2

ADRE3GENE
ID ADRE3GENE standard; DNA; VRL; 2480 BP.

XX L08231;

AC L08231.1

SV 08-JUL-1993 (Rel. 36, Created)

DT 04-MAR-2000 (Rel. 63, Last updated, Version 3)

DE Mastadenovirus 11 E3 region encoding fiber gene, complete cds.

XX fiber protein.

XX Human adenovirus type 11

OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus;

XX Human adenovirus B.

XX [1]

RP 1-2480

XX MEDLINE: 93276532.

XX PUBMED: 8503168.

XX Wei Y.-F., Wadell G.;

RT "Hemagglutination properties and nucleotide sequence analysis of the fiber gene of adenovirus genome types 11p and 11a";

VL 194(2):453-462(1993).
XX
XX GOA: P35774.
DR SWISS-PROT: P35774; FIBP_ADE1P.
XX
XX Key Location/Qualifiers
FH
FH source 1.2480
FT /db_xref="taxon:10541"

```

FT      /mol_type="genomic DNA"
FT      /organism="Human adenovirus type 11"
FT      /strain="Siobitski"
FT      1094..2071
FT      /codon_start=1
FT      /db_xref="GOA:P35774"
FT      /db_xref="SWISS-PROT:P35774"
FT      /gene="E3"
FT      /protein_id="AAA42490.1"
FT      /translation="MTKRVRLSDSFNPYPYPEDESTSOHPFNPFGFISPNGETOSPNCV
FT      LTKCIPPLTGGSLKVGGLVDDTNGFLKENTSATPLVKTGSHSLGPIGAGG
FT      TNEKCKICKGCGEPFNNNICIDNNITLMTGYNPFPANQIMSSSNCKILITIV
FT      KTGALVAVFYVIGVSNFNNLTNRNINFTAELEFDSGTMLRLSLKTPLNHSGQ
FT      NMARGALITNAGFMPSTTAYPFNDNSREKENYIGCYCTASDRTAFIDISVMLNRA
FT      INDETSYICRITWMSMNTGDAPVQTSATLVTSPTFPYIREDQ"
FT      XX
SQ      Sequence 2480 BP; 768 A; 652 C; 418 G; 642 T; 0 other;

Query Match
Best Local Similarity 0.0%; Score 15; DB 1; Length 2480;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      20378 ATGTTTACCCCACT 20392
DB      1240 ATGTTTACCCCACT 1254

RESULT 3
ADREAR3RE standard; DNA; VRL; 1980 BP.
XX      AC M94458;
XX      SV M94458.1
XX      DT 11-DEC-1992 (Rel. 34, Created)
XX      DT 04-MAR-2000 (Rel. 63, Last updated, Version 5)
XX      DE Mastadenovirus serotype 11 early 3 region.
XX      KW early 3 region.
XX      OS Human adenovirus type 11
XX      OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus;
XX      CC Human adenovirus B.
XX      [1]
XX      RP 1-1980
XX      RX MEDLINE; 93033102.
XX      RX PUBMED; 1413499.
XX      RA Mel Y.-F., Madell G.;
RT      "The nucleotide sequence of adenovirus type 11 early 3 region: comparison
RT      of genome type Ad1p and Ad1a."
RL      Virology 191(1):125-133(1992).
XX      DR GOA: P15140.
XX      DR SWISS-PROT: P15140; E3GL_ADE35.
XX      DR SWISS-PROT: P35768; E320_ADE1P.
XX      DR SWISS-PROT: P35770; E321_ADE1P.
XX      FH Key
XX      FH Location/Qualifiers
FT      source
FT      1..1980
FT      /db_xref="taxon:10541"
FT      /mol_type="genomic DNA"
FT      /organism="Human adenovirus type 11"
FT      /strain="Siobitski"
XX      SQ Sequence 1980 BP; 568 A; 466 C; 330 G; 616 T; 0 other;

Query Match
Best Local Similarity 0.0%; Score 13; DB 1; Length 1980;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

OY      9929 GAACCGGCTCTG 9941
DB      134 GAACCGGCTCTG 146

RESULT 4
MMSPRO1
ID      MMSPRO1 standard; DNA; VRL; 660 BP.
XX      AC J02260;
XX      SV J02260.1
XX      DT 05-NOV-1994 (Rel. 41, Created)
XX      DT 12-MAR-2002 (Rel. 71, Last updated, Version 3)
XX      DE Moloney murine sarcoma virus long terminal repeat.
XX      KW terminal repeat.
XX      OS Moloney murine sarcoma virus
XX      OC Viruses; Retroid viruses; Retroviridae; Gammaretrovirus.
XX      [1]
XX      RP 1-660
XX      RX MEDLINE; 81013873.
XX      RX PUBMED; 6251455.
XX      RA Van Beveren C., Goddard J.G., Berns A., Verma I.M.;
RT      "Structure of Moloney murine leukemia viral DNA: nucleotide sequence of the
RT      5' long terminal repeat and adjacent cellular sequences";
RL      Proc. Natl. Acad. Sci. U.S.A. 77(6):3307-3311(1980).
XX      [2]
XX      RP 441-545
XX      RX MEDLINE; 82060256.
XX      RX PUBMED; 6946480.
XX      RA Fuhrman S.A., Van Beveren C., Verma I.M.;
RT      "Identification of a RNA polymerase II initiation site in the long terminal
RT      repeat of Moloney murine leukemia viral DNA";
RL      Proc. Natl. Acad. Sci. U.S.A. 78(9):5411-5415(1981).
XX      CC On Oct 4, 1994 this sequence version replaced gi:332090.
XX      CC + strand shown. 'LTR' in definition stands for 'long terminal
XX      CC repeat'.
XX      FH Key
XX      FH Location/Qualifiers
FT      source
FT      1..660
FT      /db_xref="taxon:11809"
FT      /mol_type="genomic DNA"
FT      /note="from Balb/mo mouse"
FT      /proviral
FT      /organism="Moloney murine sarcoma virus"
FT      FT mRNA
FT      486..>660
FT      /product="RNA polII transcript mRNA"
XX      SQ Sequence 660 BP; 155 A; 181 C; 158 G; 166 T; 0 other;

Query Match
Best Local Similarity 0.0%; Score 12; DB 1; Length 660;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      28892 CAGGCCAAGAA 28903
DB      285 CAGGCCAAGAA 296

RESULT 5
AF541985 standard; DNA; VRL; 747 BP.
XX      AC AF541985;

```



```
XX AF541985.1
SV
XX
XX 26-SEP-2002 (Rel. 73, Created)
DT 26-SEP-2002 (Rel. 73, Last updated, Version 1)
XX
DE Dendrolimus punctatus cypovirus 1 strain Hunan polyhedrin gene, complete
DE cds.
XX
XX Dendrolimus punctatus cypovirus 1
OS
XX Viruses; dsRNA viruses; Reoviridae; Cypovirus; Cypovirus 1.
XX
XX [1]
RP 1-747
RA Hong J., Zhao S., Peng H., Duan J.;
RT "Comparison of C-polyhedrin genes from 5 type 1 cypoviruses";
RL Unpublished.
XX
XX [2]
RP 1-747
RA Hong J., Zhao S., Peng H., Duan J.;
RT Submitted (29-AUG-2002) to the EMBL/GenBank/DBJ databases.
RL Chinese Academy of Sciences, Wuhan Institute of Virology, Wuhan, Hubei
RL 430071, P.R. China
XX
XX SPTREMBL: Q8AY9; Q8AY9.
DR
XX
XX Key Location/Qualifiers
FH
FH 1. .747
FT /db_xref="taxon:208509"
FT /mol_type="genomic DNA"
FT /organism="Dendrolimus punctatus cypovirus 1"
FT /strain="Hunan"
FT 1. .747
FT /codon_start=1
FT /db_xref="SPTREMBL:Q8AY9"
FT /note="forms crystals/polyhedra"
FT /product="polyhedrin"
FT /protein_id="AA17827.1"
FT /translation="MADVAGTSNRDFRGREORLNFSEQYNNNSLNGEVSVMYYAYSD
FT GSVLVNKKSOYKVGISETFKALKEVREGQNDSDYDEYENOSIYYPNGDAKHFHNSA
FT KPAIOIIFSPSVNVRTIKMAKNSVSPDDYQDRSHPEATGIRKIKRQGEIYGS
FT HYELPHEYNISLAVSGVHKNSSYNVSANHVMDVFGCDLALRRCNRYMALELVN
FT HTSPNAYPYLDNNHSYGVALSNHQ"
FT
XX
SQ Sequence 747 BP; 226 A; 188 C; 169 G; 164 T; 0 other;

Query Match 0.0%; Score 12; DB 1; Length 747;
Best Local Similarity 100.0%; Pred. No. 8.6;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5686 CCGGAACTAAGT 5697
Db 437 CCGGAACTAAGT 448

RESULT 6
AF541985/C
ID AF541985 standard; DNA; VRL; 747 BP.
XX
XX AF541985;
AC
XX
XX AF541985.1
SV
XX
XX 26-SEP-2002 (Rel. 73, Created)
DT 26-SEP-2002 (Rel. 73, Last updated, Version 1)
XX
DE Dendrolimus punctatus cypovirus 1 strain Hunan polyhedrin gene, complete
DE cds.
```

```
XX
XX
XX Dendrolimus punctatus cypovirus 1
OS
XX Viruses; dsRNA viruses; Reoviridae; Cypovirus; Cypovirus 1.
XX
XX [1]
RP 1-747
RA Hong J., Zhao S., Peng H., Duan J.;
RT "Comparison of C-polyhedrin genes from 5 type 1 cypoviruses";
RL Unpublished.
XX
XX [2]
RP 1-747
RA Hong J., Zhao S., Peng H., Duan J.;
RT Submitted (29-AUG-2002) to the EMBL/GenBank/DBJ databases.
RL Chinese Academy of Sciences, Wuhan Institute of Virology, Wuhan, Hubei
RL 430071, P.R. China
XX
XX SPTREMBL: Q8AY9; Q8AY9.
DR
XX
XX Key Location/Qualifiers
FH
FH 1. .747
FT /db_xref="taxon:208509"
FT /mol_type="genomic DNA"
FT /organism="Dendrolimus punctatus cypovirus 1"
FT /strain="Hunan"
FT 1. .747
FT /codon_start=1
FT /db_xref="SPTREMBL:Q8AY9"
FT /note="forms crystals/polyhedra"
FT /product="polyhedrin"
FT /protein_id="AA17827.1"
FT /translation="MADVAGTSNRDFRGREORLNFSEQYNNNSLNGEVSVMYYAYSD
FT GSVLVNKKSOYKVGISETFKALKEVREGQNDSDYDEYENOSIYYPNGDAKHFHNSA
FT KPAIOIIFSPSVNVRTIKMAKNSVSPDDYQDRSHPEATGIRKIKRQGEIYGS
FT HYELPHEYNISLAVSGVHKNSSYNVSANHVMDVFGCDLALRRCNRYMALELVN
FT HTSPNAYPYLDNNHSYGVALSNHQ"
FT
XX
SQ Sequence 747 BP; 226 A; 188 C; 169 G; 164 T; 0 other;

Query Match 0.0%; Score 12; DB 1; Length 747;
Best Local Similarity 100.0%; Pred. No. 8.6;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 35841 GTTTAAGCTGTT 35852
Db 96 GTTTAAGCTGTT 85

RESULT 7
AF541986
ID AF541986 standard; DNA; VRL; 747 BP.
XX
XX AF541986;
AC
XX
XX AF541986.1
SV
XX
XX 26-SEP-2002 (Rel. 73, Created)
DT 26-SEP-2002 (Rel. 73, Last updated, Version 1)
XX
DE Dendrolimus punctatus cypovirus 1 strain Hunan from Spodoptera exigua
DE polyhedrin gene, complete cds.
XX
XX
XX Dendrolimus punctatus cypovirus 1
OS
XX Viruses; dsRNA viruses; Reoviridae; Cypovirus; Cypovirus 1.
XX
XX [1]
RP 1-747
```

```

RA Hong J., Zhao S., Peng H., Duan J.;
RT "Comparison of C-polyhedrin genes from 5 type 1 cypoviruses";
RL Unpublished.
XX
XX [2]
XX 1-747
XX Hong J., Zhao S., Peng H., Duan J.;
RA Submitted (29-AUG-2002) to the EMBL/Genbank/DBJ databases.
RL Chinese Academy of Sciences, Wuhan Institute of Virology, Wuhan, Hubei
RL 430071, P.R. China
XX
XX SPTREMBL; Q8AY9; Q8AY9.
DR
XX
XX Key Location/Qualifiers
FH
FH source
FT 1. 747
FT /db_xref="taxon:208509"
FT /mol_type="genomic DNA"
FT /note="Substitute-host"
FT /organism="Dendrolimus punctatus cypovirus 1"
FT /strain="Hunan"
FT /specific_host="Spodoptera exigua"
FT 1. 747
FT /codon_start=1
FT /db_xref="SPTREMBL:Q8AY9"
FT /note="Forms crystals/polyhedra"
FT /product="polyhedrin"
FT /protein_id="AA17828.1"
FT /translation="MADYAGTSNRDFRGREORLFPNSROYNNNSLNGEVSVMVAYYSD
FT GSVLVINKNSQYKVGISEFTFKALKEVREGQNDSDYDEEVNOSTIYYPGGAHKFHSNA
FT KPRAIQIIFSPSVAVRTITKAKGNSVSPDYILORSHPEWATGIKRKIKRKGELVGS
FT HYPELPHENYNSISLAVSGVHKNPSSYNGSAHNMVDYFQCDLALRFCNRYMAELELVN
FT HYISPNAPYPIDINNHSYGVALSNHQ"
XX
XX CDS
SQ Sequence 747 BP; 230 A; 191 C; 166 G; 160 T; 0 other:

Query Match 0.0%; Score 12; DB 1; Length 747;
Best Local Similarity 100.0%; Pred. No. 8.6;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5686 CCGGATTACG 5697
DB 437 CCGGATTACG 448

RESULT 8
AF541986/C
ID AF541986 standard; DNA; VRL; 747 BP.
XX
XX AF541986;
AC
XX
XX SV AF541986.1
XX
XX 26-SEP-2002 (Rel. 73, Created)
DT 26-SEP-2002 (Rel. 73, Last updated, Version 1)
XX
XX Dendrolimus punctatus cypovirus 1 strain Hunan from Spodoptera exigua
DE polyhedrin gene, complete cds.
XX
XX
XX Dendrolimus punctatus cypovirus 1
OS Viruses; dsRNA viruses; Reoviridae; Cypovirus; Cypovirus 1.
XX
XX [1]
XX 1-747
XX Hong J., Zhao S., Peng H., Duan J.;
RA "Comparison of C-polyhedrin genes from 5 type 1 cypoviruses";
RT Unpublished.
XX
XX [2]
XX 1-747

```

```

RA Hong J., Zhao S., Peng H., Duan J.;
RT Submitted (29-AUG-2002) to the EMBL/Genbank/DBJ databases.
RL Chinese Academy of Sciences, Wuhan Institute of Virology, Wuhan, Hubei
RL 430071, P.R. China
XX
XX SPTREMBL; Q8AY9; Q8AY9.
DR
XX
XX Key Location/Qualifiers
FH
FH source
FT 1. 747
FT /db_xref="taxon:208509"
FT /mol_type="genomic DNA"
FT /note="Substitute-host"
FT /organism="Dendrolimus punctatus cypovirus 1"
FT /strain="Hunan"
FT /specific_host="Spodoptera exigua"
FT 1. 747
FT /codon_start=1
FT /db_xref="SPTREMBL:Q8AY9"
FT /note="Forms crystals/polyhedra"
FT /product="polyhedrin"
FT /protein_id="AA17828.1"
FT /translation="MADYAGTSNRDFRGREORLFPNSROYNNNSLNGEVSVMVAYYSD
FT GSVLVINKNSQYKVGISEFTFKALKEVREGQNDSDYDEEVNOSTIYYPGGAHKFHSNA
FT KPRAIQIIFSPSVAVRTITKAKGNSVSPDYILORSHPEWATGIKRKIKRKGELVGS
FT HYPELPHENYNSISLAVSGVHKNPSSYNGSAHNMVDYFQCDLALRFCNRYMAELELVN
FT HYISPNAPYPIDINNHSYGVALSNHQ"
XX
XX CDS
SQ Sequence 747 BP; 230 A; 191 C; 166 G; 160 T; 0 other:

Query Match 0.0%; Score 12; DB 1; Length 747;
Best Local Similarity 100.0%; Pred. No. 8.6;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 27303 ACTGCGAGCGAA 27314
DB 536 ACTGCGAGCGAA 525

RESULT 9
MMSPRO2
ID MMSPRO2 standard; DNA; VRL; 1122 BP.
XX
XX J02261;
AC
XX
XX SV J02261.1
XX
XX 07-MAY-1992 (Rel. 31, Created)
DT 17-APR-2002 (Rel. 71, Last updated, Version 6)
XX
XX Moloney murine sarcoma virus polyprotein gene, partial cds.
DE proviral gene; terminal repeat.
XX
XX Moloney murine sarcoma virus
OS Viruses; Retroid viruses; Retroviridae; Gammaretrovirus.
XX
XX [1]
XX 16-1122
XX MEDLINE; 81013872.
XX PUBMED; 6251454.
XX Sutcliffe J.G., Shinnick T.M., Verma I.M., Lerner R.A.;
RA "Nucleotide sequence of Moloney leukemia virus: 3' end reveals details of
RT replication, analogy to bacterial transposons, and an unexpected gene";
RL Proc. Natl. Acad. Sci. U.S.A. 77(6):3302-3306(1980).
XX
XX [2]
XX 1-1122
XX MEDLINE; 81013873.
XX PUBMED; 6251455.
XX Van Beveren C., Goddard J.G., Berns A., Verma I.M.;
RA "Structure of Moloney murine leukemia viral DNA: nucleotide sequence of the

```

```

RT 5' long terminal repeat and adjacent cellular sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 77(6):3307-3311(1980).
RN
RX [3]
RX MEDLINE: 81052384.
RX PUBMED: 6159543.
RA Sutcliffe J.G., Shimnick T.M., Green N., Liu F.T., Niman H.L., Lerner R.A.;
RT "Chemical synthesis of a polypeptide predicted from nucleotide sequence
RT allows detection of a new retroviral gene product";
RL Nature 287(5785):801-803(1980).
XX
DR GOA: Q83401.
DR SPTREMBL: Q83401.
XX
FH Key Location/Qualifiers
FH
FT source 1. .1122
FT /db_xref="taxon:11809"
FT /mol_type="genomic DNA"
FT /note="from Balb/mo mouse"
FT /proviral
FT /organism="Moloney murine sarcoma virus"
FT mRNA
FT <1. .1122
FT /product="RNA polII transcript mRNA"
FT <1. .564
FT CDS
FT /codon_start=1
FT /db_xref="GOA:Q83401"
FT /db_xref="SPTREMBL:Q83401"
FT /product="polyprotein"
FT /protein_id="AA51623.1"
FT /translation="LIGGLTMGIGAGTGTALMATQFOLOAAVODDLREVERKSI
FT SNIKSLTSLSEVYLNRRGLDLFLKEGGLCAALKECCFYADHRTGLVDSMAKLRER
FT LNRQRLFTSTQGWFEGLFNRSFMTTLSTINGPLIVLMLILFPCILNRLVQFVKD
FT RISVQALVLTQGFHQLKPECEP"
FT <1. .282
FT mat_peptide
FT /product="p15e protein"
FT 283. .561
FT mat_peptide
FT /product="r protein"
FT 144
FT unsure
FT /note="a may be g ([1])"
FT 302
FT unsure
FT /note="t may be c ([1])"
FT 530
FT unsure
FT /note="t may be a ([1])"
FT 952
FT unsure
FT /note="a may be t ([1])"
FT
FT
XX Sequence 1122 BP; 307 A; 266 C; 270 G; 279 T; 0 other;
SQ
Query Match 0.0%; Score 12; DB 1; Length 1122;
Best Local Similarity 100.0%; Pred. No. 8.9;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 28892 CAGGGCCAGAA 28903
Db 779 CAGGGCCAGAA 790
RESULT 10
MMSPRO2/c standard; DNA; VRL: 1122 BP.
XX
XX J02261;
XX
XX J02261.1
XX
XX
XX 07-MAY-1992 (Rel. 31, Created)
XX 17-APR-2002 (Rel. 71, Last updated, Version 6)
XX
XX Moloney murine sarcoma virus polyprotein gene, partial cds.
XX
XX proviral gene; terminal repeat.

```

```

XX
XX Moloney murine sarcoma virus
OS
XX Viruses; Retroid viruses; Retroviridae; Gammaretrovirus.
XX
XX [1]
XX 16-1122
XX MEDLINE: 81013872.
XX PUBMED: 6251454.
RA Sutcliffe J.G., Shimnick T.M., Verma I.M., Lerner R.A.;
RT "Nucleotide sequence of Moloney leukemia virus: 3' end reveals details of
RT replications, analogy to bacterial transposons, and an unexpected gene";
RL Proc. Natl. Acad. Sci. U.S.A. 77(6):3302-3306(1980).
XX
XX [2]
XX 1-1122
XX MEDLINE: 81013873.
XX PUBMED: 6251455.
RA Van Beveren C., Goddard J.G., Berns A., Verma I.M.;
RT "Structure of Moloney murine leukemia viral DNA: nucleotide sequence of the
RT 5' long terminal repeat and adjacent cellular sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 77(6):3307-3311(1980).
XX
XX [3]
XX 1-1122
XX MEDLINE: 81052384.
XX PUBMED: 6159543.
RA Sutcliffe J.G., Shimnick T.M., Green N., Liu F.T., Niman H.L., Lerner R.A.;
RT "Chemical synthesis of a polypeptide predicted from nucleotide sequence
RT allows detection of a new retroviral gene product";
RL Nature 287(5785):801-803(1980).
XX
DR GOA: Q83401.
DR SPTREMBL: Q83401.
XX
FH Key Location/Qualifiers
FH
FH source 1. .1122
FH /db_xref="taxon:11809"
FH /mol_type="genomic DNA"
FH /note="from Balb/mo mouse"
FH /proviral
FH /organism="Moloney murine sarcoma virus"
FH <1. .1122
FH /product="RNA polII transcript mRNA"
FH <1. .564
FH CDS
FH /codon_start=1
FH /db_xref="GOA:Q83401"
FH /db_xref="SPTREMBL:Q83401"
FH /product="polyprotein"
FH /protein_id="AA51623.1"
FH /translation="LIGGLTMGIGAGTGTALMATQFOLOAAVODDLREVERKSI
FH SNIKSLTSLSEVYLNRRGLDLFLKEGGLCAALKECCFYADHRTGLVDSMAKLRER
FH LNRQRLFTSTQGWFEGLFNRSFMTTLSTINGPLIVLMLILFPCILNRLVQFVKD
FH RISVQALVLTQGFHQLKPECEP"
FH <1. .282
FH mat_peptide
FH /product="p15e protein"
FH 283. .561
FH mat_peptide
FH /product="r protein"
FH 144
FH unsure
FH /note="a may be g ([1])"
FH 302
FH unsure
FH /note="t may be c ([1])"
FH 530
FH unsure
FH /note="t may be a ([1])"
FH 952
FH unsure
FH /note="a may be t ([1])"
FH
FH
XX Sequence 1122 BP; 307 A; 266 C; 270 G; 279 T; 0 other;
SQ
Query Match 0.0%; Score 12; DB 1; Length 1122;
Best Local Similarity 100.0%; Pred. No. 8.9;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

OY      1890 TTCTATTCTCAG 1901
        |||
DB       693 TTCTATTCTCAG 682

RESULT 11
ADRE3GENE/c
ID      ADRE3GENE standard; DNA; VRL; 2480 BP.
XX      L08231;
XX      L08231;
XX      L08231.1
XX      08-JUL-1993 (Rel. 36, Created)
DT      04-MAR-2000 (Rel. 63, Last updated, Version 3)
XX      Mastadenovirus 11 E3 region encoding fiber gene, complete cds.
DE      Mastadenovirus 11 E3 region encoding fiber gene, complete cds.
XX      fiber protein.
KM      Human adenovirus type 11
XX      Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus;
OC      Human adenovirus B.
XX      [1]
RN      1-2480
RP      MEDLINE; 93276532.
RX      PUBMED; 8503168.
RA      Mei Y.-F., Madell G.;
RT      "Hemagglutination properties and nucleotide sequence analysis of the fiber
RL      gene of adenovirus genome types 11p and 11a";
XX      Virology 194(2):453-462(1993).
DR      GOA; P35774.
DR      SWISS-PROT; P35774; FIBP_ADELP.
XX      Key Location/Qualifiers
FH      1. 2480
FT      /db_xref="taxon:10541"
FT      /mol_type="genomic DNA"
FT      /organism="Human adenovirus type 11"
FT      /strain="Siobitski"
FT      1094..2071
FT      /codon_start=1
FT      /db_xref="GOA:P35774"
FT      /db_xref="SWISS-PROT:P35774"
FT      /gene="E3"
FT      /protein_id="AAA2490.1"
FT      /translation="MTKRVRLSDSFNPVPEYEDSTSOHPINFGEFISPNGETOSPNGV
FT      LTLACLPLPTTGGSLQKVGGLVDDTNGFLKENSATTPLVKGTSHSISGLPLGAGIG
FT      TNEKLIKIKLGGLFNSNNICIDININTGVTNPTEANQIINSSSNDCKLITLV
FT      KTGLAVTAFFVYIGVSNNNMILTNRNINTEAFLEPDSGTGLRLSLKTPLNHKSQ
FT      NMATGATINAKGEMPTTAYPNDNSREKEVYICGTCYRTASDRTAPPIDISVNLNRA
FT      INDETSICIRITMSMNTGDAPEVOTSATTLVTSPTTYRTREDP"
XX      SQ Sequence 2480 BP; 768 A; 652 C; 418 G; 642 T; 0 other;
XX      Query Match 0.0%; Score 12; DB 1; Length 2480;
XX      Best Local Similarity 100.0%; Pred. No. 6.2;
XX      Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY      5623 GTCCTCAGCAGG 5634
        |||
DB       855 GTCCTCAGCAGG 844

RESULT 12
MMSPRO1/c
ID      MMSPRO1 standard; DNA; VRL; 660 BP.
XX      J02260;
XX      J02260;

```

```

SV      J02260.1
XX      05-NOV-1994 (Rel. 41, Created)
DT      12-MAR-2002 (Rel. 71, Last updated, Version 3)
XX      Moloney murine sarcoma virus long terminal repeat.
DE      Moloney murine sarcoma virus long terminal repeat.
XX      terminal repeat.
XX      Moloney murine sarcoma virus
XX      Viruses; Retroid viruses; Retroviridae; Gammaretrovirus.
OC      [1]
RN      1-660
RP      MEDLINE; 81013873.
RX      PUBMED; 6251455.
RA      Van Beveren C., Goddard J.G., Berns A., Verma I.M.;
RT      "Structure of Moloney murine leukemia viral DNA: nucleotide sequence of the
RL      5' long terminal repeat and adjacent cellular sequences";
XX      Proc. Natl. Acad. Sci. U.S.A. 77(6):3307-3311(1980).
XX      [2]
RN      441-545
RP      MEDLINE; 82060256.
RX      PUBMED; 6946480.
RA      Fuhrman S.A., Van Beveren C., Verma I.M.;
RT      "Identification of a RNA polymerase II initiation site in the long terminal
RL      repeat of Moloney murine leukemia viral DNA";
XX      Proc. Natl. Acad. Sci. U.S.A. 78(9):5411-5415(1981).
XX      On Oct 4, 1994 this sequence version replaced gi:332090.
CC      + strand shown. 'LTR' in definition stands for 'long terminal
XX      repeat'.
XX      Key Location/Qualifiers
FH      1. 660
FT      /db_xref="taxon:11809"
FT      /mol_type="genomic DNA"
FT      /note="from Balb/mo mouse"
FT      /proviral
FT      /organism="Moloney murine sarcoma virus"
FT      mRNA 486..>660
FT      /product="RNA polII transcript mRNA"
XX      SQ Sequence 660 BP; 155 A; 181 C; 158 G; 166 T; 0 other;
XX      Query Match 0.0%; Score 11; DB 1; Length 660;
XX      Best Local Similarity 100.0%; Pred. No. 19;
XX      Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY      1891 TCTATTCTCAG 1901
        |||
DB       198 TCTATTCTCAG 188

RESULT 13
MMJAL
ID      MMJAL standard; RNA; VRL; 126 BP.
XX      J02243;
XX      J02243.1
XX      J02243.1
XX      01-OCT-1996 (Rel. 49, Created)
DT      11-FEB-1999 (Rel. 58, Last updated, Version 2)
XX      Macaca mulatta and arctoides type C retrovirus, 5' end.
DE      Macaca mulatta and arctoides type C retrovirus, 5' end.
XX      Macaca mulatta and arctoides type C retrovirus
XX      Viruses; Retroid viruses; Retroviridae; Mammalian type C retroviruses;
OC

```

```

OC 1-Mammalian type C virus group; Macaca mulatta type C retrovirus.
XX
XX [1]
RN 1-126
RP MEDLINE: 80222887.
RX PUBMED: 6248246.
RA Lovinger G.G., Schochetman G.;
RT "5' terminal nucleotide sequences of type C retroviruses: features common
RL to noncoding sequences of eucaryotic messenger RNAs.";
XX Cell 20(2):441-449(1980).
XX
CC See also <brev5>, <mmcl> & <rd114>.
XX
XX Key Location/Qualifiers
FH
FT source 1. 126
FT /db_xref="taxon:11844"
FT /note="Isolated from spleen cells"
FT /organism="Macaca mulatta and arcotoides type C retrovirus"
XX
SQ .Sequence 126 BP; 36 A; 33 C; 30 G; 27 T; 0 other;

Query Match 0.0%; Score 10; DB 1; Length 126;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2916 CCCAGACCGT 2925
DB 9 CCCAGACCGT 18

RESULT 14
MMJAL/C standard; RNA; VRL; 126 BP.
XX
XX J02243;
XX
XX J02243.1
XX
DT 01-OCT-1996 (Rel. 49, Created)
DT 11-FEB-1999 (Rel. 58, Last updated, Version 2)
XX
XX Macaca mulatta and arcotoides type C retrovirus, 5' end.
XX
XX
XX Macaca mulatta and arcotoides type C retrovirus
OS Viruses; Retrovirdae; Retroviridae; Mammalian type C retroviruses;
OC 1-Mammalian type C virus group; Macaca mulatta type C retrovirus.
XX
XX [1]
RN 1-126
RP MEDLINE: 80222887.
RX PUBMED: 6248246.
RA Lovinger G.G., Schochetman G.;
RT "5' terminal nucleotide sequences of type C retroviruses: features common
RL to noncoding sequences of eucaryotic messenger RNAs.";
XX Cell 20(2):441-449(1980).
XX
CC See also <brev5>, <mmcl> & <rd114>.
XX
XX Key Location/Qualifiers
FH
FT source 1. 126
FT /db_xref="taxon:11844"
FT /note="Isolated from spleen cells"
FT /organism="Macaca mulatta and arcotoides type C retrovirus"
XX
SQ .Sequence 126 BP; 36 A; 33 C; 30 G; 27 T; 0 other;

Query Match 0.0%; Score 10; DB 1; Length 126;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

OY 1738 ACTCTGTGTG 1747
DB 45 ACTCTGTGTG 36

```

Search completed: September 27, 2003, 01:19:19
Job time : 24 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 26, 2003, 11:18:03 ; Search time 1070 Seconds
(without alignments)
12628.907 Million cell updates/sec

Title: us-09-831-000-1
Perfect score: 40000
Sequence: 1 gacgcggaacgcgagaggg.....acctatgatgaactcgttc 40000

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 189188 seqs, 168911627 residues

Word size : 0

Total number of hits satisfying chosen parameters: 378376

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	ID	Description
1	40000	100.0	133719	1 AF083501 Macaca mu
2	10772	26.9	130733	1 AF210726 Macaca mu
3	7957	19.9	10595	1 AF029302 Rhesus ma
4	3804	9.5	3804	1 AF087411 Rhesus ma
5	475	1.2	475	1 AF159033 Macaque g
6	331	0.8	395	1 AF159041 Macaque g
7	106	0.3	320	1 AF159040 Macaque g
8	80	0.2	2708	1 AF159031 Macaque g
9	71	0.2	475	1 AF159031 Macaque g
10	56	0.1	475	1 AF159032 Macaque g
11	50	0.1	475	1 AF159032 Macaque g
12	48	0.1	336	1 AF159036 Macaque g
13	48	0.1	336	1 AF159037 Macaque g
14	47	0.1	336	1 AF159035 Macaque g
15	46	0.1	3144	1 SH1DNAPOLA
16	41	0.1	336	1 AF159038 Macaque g
17	38	0.1	475	1 AF282937 Macaque g
18	38	0.1	475	1 AF282938 Macaque g
19	38	0.1	475	1 AF282939 Macaque g
20	38	0.1	475	1 AF282940 Macaque g
21	33	0.1	130733	1 AF210726 Macaca mu
22	33	0.1	133719	1 AF083501 Macaca mu
23	32	0.1	454	1 CRH251574
24	31	0.1	395	1 AF159037 Macaque g
25	29	0.1	395	1 AF159039 Macaque g
26	29	0.1	469	1 AF031811 Macaque h
27	29	0.1	3638	1 AF005477 Macaque h
28	29	0.1	108873	1 AF318573 Macaque h
29	29	0.1	133661	1 U93872 Macaque h
30	27	0.1	137508	1 K5U75698 Macaque h
31	27	0.1	480	1 AF031808 Macaque h
32	27	0.1	1295	1 AF327830 Macaque h
33	26	0.1	475	1 AF005478 Macaque h

34	26	0.1	3554	1 AF204166 Retroperi
35	23	0.1	475	1 AF250880 Pan trogl
36	23	0.1	1297	1 AF327831 Ovine her
37	23	0.1	1339	1 AF275657 Badger he
38	23	0.1	6165	1 AF376034 Badger he
39	23	0.1	184427	1 EHV020824 Equine herp
40	22	0.1	171096	1 AV037858 Cercopit
41	21	0.1	949	1 AF292063 Unidentif
42	21	0.1	3623	1 AF283477 Caprine h
43	21	0.1	12708	1 AF033822 Walleye d
44	21	0.1	12708	1 TYCGAG
45	21	0.1	130608	1 AF005370 Alcelaphi

ALIGNMENTS

RESULT 1	AF083501	133719 bp	DNA	Linear	VRL 26-JUN-2000
LOCUS	Macaca mulatta rhadinovirus 17577				
DEFINITION	AF083501				
ACCESSION	AF083501.3	GI:8714565			
VERSION					
KEYWORDS					
SOURCE					
ORGANISM	Macaca mulatta rhadinovirus 17577				
REFERENCE	Sealies,R.P., Bergquam,E.P., Axthelm,M.K. and Wong,S.W.				
AUTHORS	Sealies,R.P., Bergquam,E.P., Axthelm,M.K. and Wong,S.W.				
TITLE	Sequence and genomic analysis of a Rhesus macaque rhadinovirus with similarity to Kaposi's sarcoma-associated herpesvirus/human herpesvirus 8				
JOURNAL	J. Virol. 73 (4), 3040-3053 (1999)				
MEDLINE	99174001				
PUBMED	10074154				
REFERENCE	2 (bases 1 to 133719)				
AUTHORS	Sealies,R.P., Bergquam,E.P., Axthelm,M.K. and Wong,S.W.				
TITLE	Direct Submission				
JOURNAL	Submitted (11-AUG-1998) Division of Pathobiology and Immunology, Oregon Health Sciences University/ Oregon Regional Primate Research Center, 505 NW 185th Avenue, Beaverton, OR 97006, USA				
REFERENCE	3 (bases 1 to 133719)				
AUTHORS	Sealies,R.P., Bergquam,E.P., Axthelm,M.K. and Wong,S.W.				
TITLE	Direct Submission				
JOURNAL	Submitted (16-JUL-1999) Division of Pathobiology and Immunology, Oregon Health Sciences University/ Oregon Regional Primate Research Center, 505 NW 185th Avenue, Beaverton, OR 97006, USA				
REFERENCE	4 (bases 1 to 133719)				
AUTHORS	Sealies,R.P., Bergquam,E.P., Axthelm,M.K. and Wong,S.W.				
TITLE	Direct Submission				
JOURNAL	Submitted (26-JUN-2000) Division of Pathobiology and Immunology, Oregon Health Sciences University/ Oregon Regional Primate Research Center, 505 NW 185th Avenue, Beaverton, OR 97006, USA				
REFERENCE	Sequence update by submitter				
AUTHORS	On Jun 26, 2000 this sequence version replaced gi:5508840.				
TITLE	Location/Qualifiers				
JOURNAL	1. 133719				
REMARK	/organism="Macaca mulatta rhadinovirus 17577"				
COMMENT	/mol_type="genomic DNA"				
FEATURES	/db_xref="taxon:83534"				
SOURCE	1. 840				
repeat_region	/note="partial terminal repeat"				
CDS	1353..2624				
	/codon_start=1				
	/product="R1"				
	/protein_id="AAD21330.1"				
	/db_xref="GI:4494908"				
	/translation="MFLVLLFMLQIPVSVLLPAKLISVPTMCPHPHGDITLLTGRGT				
	STARDDSTQWTFNNITLIRGSGNFTGRVLSVTPNATISDRACQRTTTRSNNDIFRS				
	SSRLTLDERSSSYGTYVANNRTRCYSGGVTLLRNVFPLNGNAVITNGTNTNHTFV				
	LTEKTGTYFCSAFIGNKEFYSQTIINVFSTFPTKPTNDIPNESHFNKTCGIDQOTASY				

CDS

OHPENVYFESVPEISGVLTGALISLMCMFLPIRCNENSESTNSAQTSTYQPSH
NQRSTNNECSRHITIRNAHOESESIEELPHQSTEDSCCOLVLEVNKVAVDGEQNTI
NEVMEQYDVVANKNIKQTSYEDNEWEDMSDTINPNNTYSGHILEVEVFEYNLEI
OYHGLILENDHEEYHNLNMLNMEIOYDME"

/note="ORF 2: similar to Kaposi's sarcoma-associated

herpesvirus ORF 2"

/codon_start=1

/product="dihydrofolate reductase"

/protein_id="AAd21331.1"

/db_xref="GI:4494909"

/translation="MDITVNCIAVDEOLGIGKNCMPMPYLRENMYEFOKMTSPSY
VGEKNVYMGKRWPSIPEKKRPILVNRINIISRELREPHGHAPLARLDDAFNRY
QYKKRQMLTWVWIGKSYVESYLNKCPKLITIKIMESFDQDFPSPINFEYTM
SEIPGKDINFEENGIXKFPQYKFNPK"

/note="ORF 4: similar to Kaposi's sarcoma-associated

herpesvirus ORF 4"

/codon_start=1

/product="complement binding protein"

/protein_id="AAd21332.1"

/db_xref="GI:4494910"

/translation="MTFKLPLFLHAIMYVHODENCKPHEFTEYKVSNGTEKCYSV
GEFAELICRGVYVNTKITTEGCIQNGTSTPNPCDRRCRPPADLLAGAHIGHG
NALKSGNSIYECNEGYDILGSNVRCIIQDIENVMWDSNPEYCELOKICRPAYEHG
DYLPMODVNTGDALIFKCSLTTLVGSTTLVCTSKKWSNFPCTLMVCSQPDN
GYIDIGLSRNYHGQSIIVKCSGDNVIVGPELTCTNTWPLPLPCVILVTNPPSM
PEPMEPEPTPYOKINLSTAKTATPNAFTVTVVSPEDKDYCKVCPHERMVKEN
DEKYSVGSVELICRGFTKMOSTVSECLSGMTWATNACHKCKCPOLLENGE
LYTSGEDAFKGTNTYTKCNEGYOLGSMVRLCMKDLKTVDMEKAPICDIECK
PPQITNGKYPHKDPEYOYLDPIVYVTSNDRPSLVGDEMTICSTNTRKPPCEQITC
SAPNIAHGKLLGSSSVYKTGQSVTIGCTGFTLIGSEISTCKDSSMDPLPCVAV
SMSPDKPEKPTMPNTPPEAKRPMTNVGTHPKPPPPNPPIAPPMKMRHVVLY
LPAVASLFLVLAALYCCLK"

/note="ORF 6: similar to Kaposi's sarcoma-associated

herpesvirus ORF 6"

/codon_start=1

/product="ssDNA binding protein"

/protein_id="AAd21333.1"

/db_xref="GI:4494911"

/translation="MASKNAGOPLEDNOGSRAPIGAGCYVAYVSCNRPPEASITG
NRSGSVPSLILYGLTYEHEGPEPLVKAAYKKVDTPTLAVKYTCNRPPEAHNSL
FRPVDGTGLNLCERARALREYTOFIEGPHSTINPLECPQDPKDMELGAVYTE
GKERLNRGCLPAVFOQOQVIAQOAKRVLVDEDLFAPGHHRMPRYHADVSAVL
YDSLFTSLAQLRLKDVAVIAHATEKQEMQDVKIAKIVQAKOFSTLPTKTDGSSHM
IYDSVVAELALSYGMFLPCQDACEILNYSMPJFGDCDSPEARNALERSAEGAV
HVAQOLFANSVLYLTKVOKAPRGQGDVNYNSPELOHGLPLNEATIKENGSEAF
KGVPSNALDGSEFPYHLAASFSPLLAKICYMOFLQHHKSSNOAFNVHYVCT
AANSEKTCIHCNTPATCNTLFTYRLKDRFPVTTTPQRDPYVYVGTAGTFNDLEILG
NFASTRDEEDGNPADEHKYTYWQICQVTEKLSAIGITECHDNHVNLTINIQSELR
VFKGIDSYDGEVMKFNVMINNNFRHRAVSHIILOFCNVYWOACPAFLNLY
KSLMIIODICLPCMIYEODNPMANGILPESEWIKMFOITMNFNAACIDAVLNGE
LKIVHDMKCFDEPDAGSNGMLAPFKMOVRLARAMVYVKSIIKINRIIFNTNGSE
AVQSGFVKPTGDRDYVYVAGPYMKFLSHRALPDTKTAAALYIHWKISQNTKTVYK
DYPDEDLAIVSYVKTNSLAPEETVNDVYVPSLMSYARIKINGALIRACGQIQYAT
TLHCLTPVLIQITDAEETPHVLGSAIATFVAIATRGFTALTVOQTAAQVAAIGRL
RPVITVPMVNVKTYGVNNGNNVFGHGNLGFAGRGVNRMLNEMSSPFKTKPSAMLR
RHVMVMTPIIDRLIKRAAGQITSTFEASVYKRSVQALLEDKNDNLKSVLILHILHG
KGCODLSEDDVOYLGDYCMLEDEVLEFTLDTNIAQSGVPMTIEDAGLIEDRDADDLQ
FYVSDDIATASQPEEQPLTPPSAGALLAGKKRKINALSLDDLT"

/note="ORF 7: similar to Kaposi's sarcoma-associated

herpesvirus ORF 7"

/codon_start=1

/product="transport protein"

/protein_id="AAd21334.1"

/db_xref="GI:4494912"

/translation="WARELAALYVQALSALAVLDSLVIFADPRSIDGARLTKRTQIEN
LNRDLPLIREONSVEYTSLSLEVEHLAKNIEDKGLGELERSLRQYSSSEHETILR
PECHYHVTYFOYGGGLIDVMCLINVELCKRISGLSVYCIKANDELAVLAVLHIL
LSTLRGISPIHPDLVYTSVPCVCLREILVPPNGSSILAVLADRHCDHCKYKRAE
PIHGFEFEIISQIGLKYTKRSDATOHGVRSSADQIRESLIAIQDHNIFKRYASIME

CDS

CDS

LSNLIYWNAGQIGLOTGTENESQARALITHEADHEHALITPKISATHFIDCFERPD
PIESLEFGGLPNTSIDTINALSDCSVTFFQOANVTNVRKQNELETRLNLSILRQSA
GSGKPAATPESEPTVTVAATVAASVIAIKDAQYREQYKAKVARQKFKLPCLOQSAVL
ANALCKRWGVAAYGEASELVNHFLLRREFVALPWACRQRQIILENSKYIKNSLY
ORLSRHEVEITLOEYGLITGPLETROSDEPPGANAVALAOCEPAAGMLPHHKLVS
EMIPQIOPKMIQOTEMRFYOLPEGDINAVOKSAMCFITREILVSVLYNXTWETLRIF
SLAREKLSINLDVKGITSGVILTYTQDAPLVLIISQNTWIKRDLTALLYHHLQSLDS
HODN"

/note="ORF 8: similar to Kaposi's sarcoma-associated

herpesvirus ORF 8"

/codon_start=1

/product="glycoprotein B"

/protein_id="AAd21335.1"

/db_xref="GI:4494913"

/translation="MAITNRTRRLLRANVVIILGAVENGENTTPKATTPKPPGP
STPPEPNPRAEADEFKVCASATGELEFRNLKEKPCPECTEKTQDEGLTAMFKNIV
PHIFKRYRKATSVYVYRGMTETAVTNGKQVIRPVQYELTNHNDTTPQCSSMNV
VNGIVATYIDROPTNVTFLQPEGLNDIQHFFSOPLITTPGMPGITYRTTYVNC
EIVDMTARSABEYSYFVIALGDTVEVSPCHNDSTCSVAEKTENGGARVAVNTYIVD
FATROPTETTRVFAADSGEYTVSMKADBPASVACALITMTFPRAIQTTHASVHEVAN
DVATETSPISQVNETGYPCINDVIQKTNAATIKLSDTHATNGSEQYETEGELF
LIMOPTPLPISLADENRELNGTTPAPPTTSTANRYRRSVGTNEDQATDLAALQLOAF
DKLRASINKVLELSRANCRBOVDYVMYELSKINPSVMTAIGRPAKAFQVDAI
SVTDCVANDQASVTHKSLRTSTPGICSRPVYTRFELNSTTLFKQGLPRNEITITD
NOVEAKETCEHYFLASVNTYVYKDVYKAKNTSETSYLGFIALNLSFENIDFV
IELYSRAEKELGSGVFEDITMPEREYNYVQRAGREDJDNITDNRDLADLSEIV
ADLGDGRTVAVNASVITLFGSIVSGDFINIKSPGGCLMLIYAVLIYFALNMR
TNIAQAPIRMYIYVPOIDKMPQSGGKQVQFNKSLIAGHQIQQEERRRLDEQGRSAPS
LFRASDGRKFRPKCPLENEAQEYEMSK"

/note="ORF 9: similar to Kaposi's sarcoma-associated

herpesvirus ORF 9"

/codon_start=1

/product="DNA polymerase"

/protein_id="AAd21336.1"

/db_xref="GI:4494914"

/translation="MDFENPYLGPNGRPHSRGTDAPAPAGAVVQPPDVCRILPA
CLRTPDAGMIPVITIPPEPTYENARGSVLLANERSMWTADRAKRVADPDQSLTPE
HAYDVETTYAADRCAEVSRFOTDIIPSGVILKILGRTEDSTSCVNFROOVYFA
KVPAGINVTNHILOQALKNTRGACGSFTRRYNRKRLIKTYDVAHEPVEITLSSGML
SRLSDRIVACGEFESNVDAVRVYLHGFTPTPMYSQARATPADAADATLAEFD
CSMEDLSVQADSDMPRYIYVAFDIECTGEAFAFPATRGDAVIOISCFYTYRGAAP
NPNPILFVSQDTPIDPIDVLEFPSEIDMLVSFFKMLRQFEDVLTGINISNDLPLT
ITRAQVQVILRNETYKIKTGSIFEVHEPREGGGGFMRSVSKIAGIYIPDMYOVR
EKLSLSDVYLDLTVAQCLGKKEDVSKNDIPLFSGGGRAKVSCYCMVDVLMVDL
LKMFMHVEISEIAKILAOARVLYDGGQLRVSCLLEAARENDILHPPEEGOG
YOGAVVNIIPGEFDEPVLVQAFSLYSESIOAHNLCTSTMHGBDLHPMLPTPDY
FEFVYSGGVHVRKKHRESLIGLLTYLKKRRAIRRTLAACDPSIKTITDKOLA
IKVTCNAYIGTFVAGSLDCINIAETVILKRYMLNLSKSYVEALITTEDTLRAGRE
VTARHGARRVYVGTDSLETAQDYSAAVASAFCDILAARTIADLPPLIKLEAKT
FECULLLRKRYIGLVLDKMKVMKCAIDLRTKACKEFVQERCAIIDLVLHDEVARAA
RLICRPRKAVYEEGLPGFIKIIVELNLSVLDLNSVYPIQOLFETSELSPVCDYK
TNLPHLAVYQKALSCREELPOVHRIPIVPEVADAGSKSLDAEHPDYVRQIQIVAV
DLYEPDKIVGANIITQCLEGNADTTVALIVFLNVPKLES"

/note="ORF 10: similar to Kaposi's sarcoma-associated

herpesvirus ORF 10"

/codon_start=1

/product="unknown"

/protein_id="AAd21337.1"

/db_xref="GI:4494915"

/translation="MLVNELSVLGDMEVTEFHGRFSFVNLTIRLOTFKHGGYARVRL
PESLDOLHOFAGFLVTRKELPEPSCVVALIADLSDGDAARVAPGLVDSRP
LTVWVNASGRHTIRFCLFLFKPIDLEAVTVYVGGNGASRGCTKPCATCELSLGGP
LRVGEASQTSFHSFVAYAPRANSYASLILRILVPSDDAABHDAITSPYVYFNS
SGVNCYKASVHTLSPSRCKTAOMELIYAPRGNATVYVSGSPVLPHTGGVSLVYA
DAEKTIOGSSAEVAVOLIFQOGAARQDLAVLGVAVPEPLFVTVPLVLSGCTTHL
RLFNPNNGTPTTIKRDITVAAPACPVRVLRSSADAPRDLVAVSPDGLASIVNAFTIPVG
FPGVVASCHVSLIRNGVHERMNH"

/note="ORF 11: similar to Kaposi's sarcoma-associated

herpesvirus ORF 11"

CDS

Query Match		100.0%;	Score 40000;	DB 1;	Length 133719;
Best Local Similarity		100.0%;	Pred. No. 0;		
Matches 40000;		Conservative	0;	Mismatches	0;
				Indels	0;
				Gaps	0;
Qy	1	GATCGGAAAAACGCGAGGAGCGGGGACAGGGGACAGCGGCTGTGCTTGTGAACA 60			
Db	1	GATCGGAAAAACGCGAGGAGCGGGGACAGGGGACAGCGGCTGTGCTTGTGAACA 60			
Qy	61	CCGGGTACGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120			
Db	61	CCGGGTACGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120			
Qy	121	GCTCGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180			
Db	121	GCTCGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180			
Qy	181	GCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240			
Db	181	GCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240			
Qy	241	GCTCGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300			
Db	241	GCTCGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300			
Qy	301	GCTCGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360			
Db	301	GCTCGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360			
Qy	361	GCTCGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420			
Db	361	GCTCGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420			
Qy	421	AGGGGACAGTAGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480			
Db	421	AGGGGACAGTAGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480			
Qy	481	GTAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540			
Db	481	GTAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540			
Qy	541	GTAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600			
Db	541	GTAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600			
Qy	601	GTAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660			
Db	601	GTAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660			
Qy	661	GTAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720			
Db	661	GTAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720			
Qy	721	GCTCGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780			
Db	721	GCTCGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780			
Qy	781	CAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840			
Db	781	CAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840			
Qy	841	AGGACAAACAGTAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900			
Db	841	AGGACAAACAGTAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900			
Qy	901	AGTAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960			
Db	901	AGTAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960			
Qy	961	TTTCCACGAGGAGGAGGAGTAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1020			
Db	961	TTTCCACGAGGAGGAGGAGTAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1020			

Qy	1021	GCTCTGCGGATTTTGTGCTAGCTAGTACAGCAATAGTATTTTCAATCGCATGCG 1080			
Db	1021	GCTCTGCGGATTTTGTGCTAGCTAGTACAGCAATAGTATTTTCAATCGCATGCG 1080			
Qy	1081	CCTGCATAGGCTCCACAGCATCCGAACAGGTTATTTCTATAGCTAATCTTATGTTCT 1140			
Db	1081	CCTGCATAGGCTCCACAGCATCCGAACAGGTTATTTCTATAGCTAATCTTATGTTCT 1140			
Qy	1141	TCTGTGTTGGATCAATTTTGAAGTTTGGCTCCGTTGAATTAATTAAGAAATCCGTTGGT 1200			
Db	1141	TCTGTGTTGGATCAATTTTGAAGTTTGGCTCCGTTGAATTAATTAAGAAATCCGTTGGT 1200			
Qy	1201	TACAAATACCTGCGCAACGATATGGATGTTCTTTTGGCATCAACCTTGTGCAATTC 1260			
Db	1201	TACAAATACCTGCGCAACGATATGGATGTTCTTTTGGCATCAACCTTGTGCAATTC 1260			
Qy	1261	TAACATTTGAATTTTCAATTAACACCTGATGCTGCTGCTGCTGCTGCTGCTGCT 1320			
Db	1261	TAACATTTGAATTTTCAATTAACACCTGATGCTGCTGCTGCTGCTGCTGCTGCT 1320			
Qy	1321	GCTTGTAAATTTTCTACACATTTCTGCGAAATGTTTGTGTTTATTTATGTTAT 1380			
Db	1321	GCTTGTAAATTTTCTACACATTTCTGCGAAATGTTTGTGTTTATTTATGTTAT 1380			
Qy	1381	TGCAACCTGATCGGTGAGCTTTTGGCTGCAAAATTAACCTTGTTCGCAACGTTGCTC 1440			
Db	1381	TGCAACCTGATCGGTGAGCTTTTGGCTGCAAAATTAACCTTGTTCGCAACGTTGCTC 1440			
Qy	1441	CACCACATCCCGGAGATACCTTACTTGTCTAACCTCCGCGGAGCTTACAGGCCAGAAC 1500			
Db	1441	CACCACATCCCGGAGATACCTTACTTGTCTAACCTCCGCGGAGCTTACAGGCCAGAAC 1500			
Qy	1501	AGGACAGCACAAATGGTTTTCGCAACAAACGCTTATGCGGGAGTAATTTTCAACGCA 1560			
Db	1501	AGGACAGCACAAATGGTTTTCGCAACAAACGCTTATGCGGGAGTAATTTTCAACGCA 1560			
Qy	1561	GACTGTATCTGTGACTCCCAATGCTACGATATCTGACCGGATATGCGTTCMAACAAA 1620			
Db	1561	GACTGTATCTGTGACTCCCAATGCTACGATATCTGACCGGATATGCGTTCMAACAAA 1620			
Qy	1621	CAACACGCGGAGATTAACAACTGATTTTGGGGTAAAGCTCATCGCGCTCACGCTCCAG 1680			
Db	1621	CAACACGCGGAGATTAACAACTGATTTTGGGGTAAAGCTCATCGCGCTCACGCTCCAG 1680			
Qy	1681	AACGGTCTCTTCAATAGGCTATACCGGAATTAACAGAGGATTTTGAAGTATTA 1740			
Db	1681	AACGGTCTCTTCAATAGGCTATACCGGAATTAACAGAGGATTTTGAAGTATTA 1740			
Qy	1741	CTGGTGAACAGTAACTTTAAGAAAGTGTCTTCAATTTAAGCGTACAGCGGTCAATCA 1800			
Db	1741	CTGGTGAACAGTAACTTTAAGAAAGTGTCTTCAATTTAAGCGTACAGCGGTCAATCA 1800			
Qy	1801	ACGGTACTAACAAACATATACATTTTGTGTTAAAGAAACAGAGGAGGACGTAAT 1860			
Db	1801	ACGGTACTAACAAACATATACATTTTGTGTTAAAGAAACAGAGGAGGACGTAAT 1860			
Qy	1861	TCTGTGTTGGATTAATGGGAATGAATAATCTTATTCAGACAAATTAATGTTTTTTA 1920			
Db	1861	TCTGTGTTGGATTAATGGGAATGAATAATCTTATTCAGACAAATTAATGTTTTTTA 1920			
Qy	1921	CTTCATTTTACCTTTTAAACGTAACAAAGCATTTCCCAATGATGTCACATTTTAAATAAC 1980			
Db	1921	CTTCATTTTACCTTTTAAACGTAACAAAGCATTTCCCAATGATGTCACATTTTAAATAAC 1980			
Qy	1981	GGCAATATCAACAAACAGTATAGTACAAACATCTGAAAACTACGTTGTCTCTGTC 2040			
Db	1981	GGCAATATCAACAAACAGTATAGTACAAACATCTGAAAACTACGTTGTCTCTGTC 2040			
Qy	2041	CCGTTTCTTATGAGGCTTTTAAACAGGATTTGCAATATGCTGATTTATGTTGGTTAT 2100			
Db	2041	CCGTTTCTTATGAGGCTTTTAAACAGGATTTGCAATATGCTGATTTATGTTGGTTAT 2100			
Qy	2101	TTACAAATACGCTGCAACAGAACTCTGAATCATCACTAATAGTTATGCAAGCCAGACA 2160			

Db 2101 TTACAATACGCTGCAACGAGAACTGGAATCATCACTAATAGTTATGCAAGCAACAA 2160
QY 2161 GCTACATTAACCCCTCCCAATATCAGCGTTCATATGAATGAATGAGCCATACCT 2220
Db 2161 GCTACATTAACCCCTCCCAATATCAGCGTTCATATGAATGAATGAGCCATACCT 2220
QY 2221 ACAGAAATGCTCATCAAGAAGAGATTTGAGAACTACCAACCAACACAAAGTGAAA 2280
Db 2221 ACAGAAATGCTCATCAAGAAGAGATTTGAGAACTACCAACCAACACAAAGTGAAA 2280
QY 2281 CTGATCTGCTGCTCAATTAAGTTTCTTGAAGTGAAGAAATGAGCCCTACGATGAGCCG 2340
Db 2281 CTGATCTGCTGCTCAATTAAGTTTCTTGAAGTGAAGAAATGAGCCCTACGATGAGCCG 2340
QY 2341 AGGAAAAACAATTAACGAAGTTATGAGAACAGATGATGATGTTGTTGAAAAAATATAG 2400
Db 2341 AGGAAAAACAATTAACGAAGTTATGAGAACAGATGATGATGTTGTTGAAAAAATATAG 2400
QY 2401 AACAAACATCATATGAGATTAATGTTGACACATGACATATAGTACTATTAATCCCA 2460
Db 2401 AACAAACATCATATGAGATTAATGTTGACACATGACATATAGTACTATTAATCCCA 2460
QY 2461 ATTTTAATTAACATGACATGACATTAATTTGAGAAAGTACATGAAAGTTTACATGAA 2520
Db 2461 ATTTTAATTAACATGACATGACATTAATTTGAGAAAGTACATGAAAGTTTACATGAA 2520
QY 2521 TAGAAAAATCAATATCATGATTAATCTGAGAAATTTAGATCAATGAGTACATCAT 2580
Db 2521 TAGAAAAATCAATATCATGATTAATCTGAGAAATTTAGATCAATGAGTACATCAT 2580
QY 2581 TTAATGATTAATACATGATGAGAAACATATGATGTTGTTAGATTAATTAATCTG 2640
Db 2581 TTAATGATTAATACATGATGAGAAACATATGATGTTGTTAGATTAATTAATCTG 2640
QY 2641 TTTTAAATTAACATTAACACATTAAGACGATTTTGTGTAATGCTTATTTAT 2700
Db 2641 TTTTAAATTAACATTAACACATTAAGACGATTTTGTGTAATGCTTATTTAT 2700
QY 2701 AAAATTTTTCATATACCTGAAACCTTATATTTTAACTCCATTTCCCAAGTTGTATC 2760
Db 2701 AAAATTTTTCATATACCTGAAACCTTATATTTTAACTCCATTTCCCAAGTTGTATC 2760
QY 2761 TTTGCCCCGATCTGATACATGATGTTGCGTAAATTAATGATGAAAAATAC 2820
Db 2761 TTTGCCCCGATCTGATACATGATGTTGCGTAAATTAATGATGAAAAATAC 2820
QY 2821 ATCACAATCAAAACCTCATATGCGGTAAATATAGTTTAAAGGACACTATATGT 2880
Db 2821 ATCACAATCAAAACCTCATATGCGGTAAATATAGTTTAAAGGACACTATATGT 2880
QY 2881 AAGAACACTGTCATAAACAGATTTTCCCAATAACCCAGACGTTTAAATGTTCTTT 2940
Db 2881 AAGAACACTGTCATAAACAGATTTTCCCAATAACCCAGACGTTTAAATGTTCTTT 2940
QY 2941 TGGTTTGTATGTCATTAAGAAATTAACGCAATGCTACGTTTCGCTAGAAAGTGTG 3000
Db 2941 TGGTTTGTATGTCATTAAGAAATTAACGCAATGCTACGTTTCGCTAGAAAGTGTG 3000
QY 3001 TCCGTGCGGTGTTACGTAATTTCTGTCTCAAAATTAATTAATTTCTTACCAAGG 3060
Db 3001 TCCGTGCGGTGTTACGTAATTTCTGTCTCAAAATTAATTAATTTCTTACCAAGG 3060
QY 3061 GCGCTTCTTTTTCAGGATGGAAGAACATGTTCTTTCCCATTAATACCAATTCCTTT 3120
Db 3061 GCGCTTCTTTTTCAGGATGGAAGAACATGTTCTTTCCCATTAATACCAATTCCTTT 3120
QY 3121 ACCTTCAACCGATGCGGTAGACGATTTTCTGAAAAATACATCATTTCTTCTAAGTA 3180
Db 3121 ACCTTCAACCGATGCGGTAGACGATTTTCTGAAAAATACATCATTTCTTCTAAGTA 3180
QY 3181 CGGCAAGGCAATGTTCCGTTTTCGCAATTTCTATTTGTCATCAACGCAACGATGA 3240
Db 3181 CGGCAAGGCAATGTTCCGTTTTCGCAATTTCTATTTGTCATCAACGCAACGATGA 3240

Db 3181 CGGCAAGGCAATGTTCCGTTTTCGCAATTTCTATTTGTCATCAACGCAACGATGA 3240
QY 3241 GTTAACGTATATGTCATGTTTATGTTCCATGACGAGGTTTAAACAGAAATATTTCA 3300
Db 3241 GTTAACGTATATGTCATGTTTATGTTCCATGACGAGGTTTAAACAGAAATATTTCA 3300
QY 3301 CAATTAATTAACAAATTAACCAACGATGATCTTAATGTAAGTACGTAACGTGATA 3360
Db 3301 CAATTAATTAACAAATTAACCAACGATGATCTTAATGTAAGTACGTAACGTGATA 3360
QY 3361 TAGTTAATCATATGCTTTCATATGAGACAAAACGAAAAAATGCTACGTGTATAG 3420
Db 3361 TAGTTAATCATATGCTTTCATATGAGACAAAACGAAAAAATGCTACGTGTATAG 3420
QY 3421 CCTACCTGTTTGGATGAGATTTATGTTTCAATGAAAAATTAATATATATTAACGTT 3480
Db 3421 CCTACCTGTTTGGATGAGATTTATGTTTCAATGAAAAATTAATATATATTAACGTT 3480
QY 3481 TTTTACGTAAACATATGTTAATTTAATCAGCGTATGTTATGTTGGCTACTACACACA 3540
Db 3481 TTTTACGTAAACATATGTTAATTTAATCAGCGTATGTTATGTTGGCTACTACACACA 3540
QY 3541 ATGTTTGCATTAAGACCTATGTTAGTACGCTCAATCTTATATTTATTTCAATGTG 3600
Db 3541 ATGTTTGCATTAAGACCTATGTTAGTACGCTCAATCTTATATTTATTTCAATGTG 3600
QY 3601 TTTAAGAGGCAATGATATTTAATTAACACGATTCGAATATGAGGCAACGCTGTCCT 3660
Db 3601 TTTAAGAGGCAATGATATTTAATTAACACGATTCGAATATGAGGCAACGCTGTCCT 3660
QY 3661 ATTAAGGTTAAACATGACGTTTAACTTTTCTGTTTATTTATACAGCCATATAG 3720
Db 3661 ATTAAGGTTAAACATGACGTTTAACTTTTCTGTTTATTTATACAGCCATATAG 3720
QY 3721 TAGTCACATGCGATGAAGAAACGTAAACCTCCACATTTACGGAATATGCGTCAAGT 3780
Db 3721 TAGTCACATGCGATGAAGAAACGTAAACCTCCACATTTACGGAATATGCGTCAAGT 3780
QY 3781 AACACGAAAGGACTTATATAGTGTGAGAAACAGCTGAATTAATTTGTGCTGTGT 3840
Db 3781 AACACGAAAGGACTTATATAGTGTGAGAAACAGCTGAATTAATTTGTGCTGTGT 3840
QY 3841 TATGTTACAATTAACAAATTAATTAACACAGATGTTTCAAAATGTTACGTTGTCACA 3900
Db 3841 TATGTTACAATTAACAAATTAATTAACACAGATGTTTCAAAATGTTACGTTGTCACA 3900
QY 3901 CCAAAATTTTCATGCGACAGAAAGATGCTCCACACGCTGCTGATGATGAGCC 3960
Db 3901 CCAAAATTTTCATGCGACAGAAAGATGCTCCACACGCTGCTGATGATGAGCC 3960
QY 3961 GTGACATTCACGAGGAGATTAATGCTTAAATTTGATCCAAATATTTCTATGAGTGT 4020
Db 3961 GTGACATTCACGAGGAGATTAATGCTTAAATTTGATCCAAATATTTCTATGAGTGT 4020
QY 4021 AATGAAGTTATGATTTAATGTTAGTATGTTGCTTTTGTATTTTCAAGACACAAA 4080
Db 4021 AATGAAGTTATGATTTAATGTTAGTATGTTGCTTTTGTATTTTCAAGACACAAA 4080
QY 4081 AACGTAAATGCGATTCAAATGAACACAGCTGTGAAATTTCAAGAAATGATTAACACCG 4140
Db 4081 AACGTAAATGCGATTCAAATGAACACAGCTGTGAAATTTCAAGAAATGATTAACACCG 4140
QY 4141 GCAAGTGAACATGAGGAGCTACCTACCTAACCAAGATGTTTATATGATGAGATCAAT 4200
Db 4141 GCAAGTGAACATGAGGAGCTACCTACCTAACCAAGATGTTTATATGATGAGATCAAT 4200
QY 4201 ACATTTAAATGTTCAATTTGCTGATACACTGCTTGGATCAACAACTTATGATGACGTC 4260
Db 4201 ACATTTAAATGTTCAATTTGCTGATACACTGCTTGGATCAACAACTTATGATGACGTC 4260
QY 4261 AACAAAAAGTGTGCAACCTCTTTCCCAACGTTTAAATGCTGTATGAAAGTCCACAA 4320
Db 4261 AACAAAAAGTGTGCAACCTCTTTCCCAACGTTTAAATGCTGTATGAAAGTCCACAA 4320

4321 ATAGACAATGGGTACATAGACATTTGGCTTCCAGAAATACAACCATGACATCAATTT 4380
4322 ATAGACAATGGGTACATAGACATTTGGCTTCCAGAAATACAACCATGACATCAATTT 4380
4381 ACTGTAAAGTGTACCGACGGGTACACATTTGTTGGCTTGAACATTTAACGTGCACAAC 4440
4381 ACTGTAAAGTGTACCGACGGGTACACATTTGTTGGCTTGAACATTTAACGTGCACAAC 4440
4441 ACAACTTGGGTCCACCATTAACCAAGTGTATTTAGTTACAAATACCCAGACACCC 4500
4441 ACAACTTGGGTCCACCATTAACCAAGTGTATTTAGTTACAAATACCCAGACACCC 4500
4501 ATGCCAGAAACACCCATGCCAGAAACACCCAGCATATATCAAAAATTAATTTGTCA 4560
4501 ATGCCAGAAACACCCATGCCAGAAACACCCAGCATATATCAAAAATTAATTTGTCA 4560
4561 ACCGCTTAAACTGCACACACCAATGCGTTGTTTACAACCTGTTTCTCCAGAGAAA 4620
4561 ACCGCTTAAACTGCACACACCAATGCGTTGTTTACAACCTGTTTCTCCAGAGAAA 4620
4621 GAGGAGCTTACTTGTGAAGCCTCATTTGAGCGATTCATGTTAAAGGCTGAAAAATGAC 4680
4621 GAGGAGCTTACTTGTGAAGCCTCATTTGAGCGATTCATGTTAAAGGCTGAAAAATGAC 4680
4681 AAGGAAAAATACAGTGTGTGCGAGCGTTGAGCTAATATGTCGACGAGATTACTAAA 4740
4681 AAGGAAAAATACAGTGTGTGCGAGCGTTGAGCTAATATGTCGACGAGATTACTAAA 4740
4741 ATGCACTTACAGTCTTCTGTGAATGTTTCCAAAGGAAACATGAGCTGCTCCAAATGCC 4800
4741 ATGCACTTACAGTCTTCTGTGAATGTTTCCAAAGGAAACATGAGCTGCTCCAAATGCC 4800
4801 AAGTGCATATGAAAAAATGTTCCAAACCCCTCAAGAACTTTTAAACGAGATATATAGTT 4860
4801 AAGTGCATATGAAAAAATGTTCCAAACCCCTCAAGAACTTTTAAACGAGATATATAGTT 4860
4861 ACAAGCGAGAAAGTGTGTTTAAAGTACGAAACAAATTAACATATAATTAATGAAGT 4920
4861 ACAAGCGAGAAAGTGTGTTTAAAGTACGAAACAAATTAACATATAATTAATGAAGT 4920
4921 TATCACTTTTAAAGAAATATGTCGCGGATTTGATGCTTAAAGCAGATTTAAAAACAGTT 4980
4921 TATCACTTTTAAAGAAATATGTCGCGGATTTGATGCTTAAAGCAGATTTAAAAACAGTT 4980
4981 GACGCGGAGCAAAAGGCGCTATATGATATGAAAAATGTAAGCCACCGCCACAATTT 5040
4981 GACGCGGAGCAAAAGGCGCTATATGATATGAAAAATGTAAGCCACCGCCACAATTT 5040
5041 ACAAAACGGAATAATACATCCGCGTGAAGAAAGCTTTTATCAGTATTTGAACACGTAATTT 5100
5041 ACAAAACGGAATAATACATCCGCGTGAAGAAAGCTTTTATCAGTATTTGAACACGTAATTT 5100
5101 TCGTGCATGTCGATCTTTTCTTTAGTTGAGATGAAATGACAAACGCTATATGAATACG 5160
5101 TCGTGCATGTCGATCTTTTCTTTAGTTGAGATGAAATGACAAACGCTATATGAATACG 5160
5101 TCGTGCATGTCGATCTTTTCTTTAGTTGAGATGAAATGACAAACGCTATATGAATACG 5160
5161 TGGAAATTAACCGTTTCCAAAGATGAAACAAATCACTGCAAGCGCTCTTAATATGCAAC 5220
5161 TGGAAATTAACCGTTTCCAAAGATGAAACAAATCACTGCAAGCGCTCTTAATATGCAAC 5220
5221 GGAAGCTGCTAACAGGTTCTTCAAGCGTTTACAAATACGTCATGTTTACCATTTGGT 5280
5221 GGAAGCTGCTAACAGGTTCTTCAAGCGTTTACAAATACGTCATGTTTACCATTTGGT 5280
5281 TGTGAACCTGGATTTACTCTAATTTGGCAGTGAATTTCTACATGCAAGATTCATCGTGG 5340
5281 TGTGAACCTGGATTTACTCTAATTTGGCAGTGAATTTCTACATGCAAGATTCATCGTGG 5340
5341 GATCCACCACTTCTTACGTGCGTGCAGCTGTTTCAATGCCCTCTGACACACCTTAACCA 5400
5341 GATCCACCACTTCTTACGTGCGTGCAGCTGTTTCAATGCCCTCTGACACACCTTAACCA 5400

5401 GAAACCAAAAAACCAACACGCCAGCAGAAAGCACCAACCAACCAACCCAAACGTTT 5460
5401 GAAACCAAAAAACCAACACGCCAGCAGAAAGCACCAACCAACCAACCCAAACGTTT 5460
5461 GGAACACATACACCATTTCAAAACCAACCAACCAAAATTCACCAATAGACACCCCAATAGT 5520
5461 GGAACACATACACCATTTCAAAACCAACCAACCAAAATTCACCAATAGACACCCCAATAGT 5520
5521 AAATGGAAAAGGATGCGTGTATGTTCTTTTGCAGATGTCGCGGCTCTTTGTTATTCGTA 5580
5521 AAATGGAAAAGGATGCGTGTATGTTCTTTTGCAGATGTCGCGGCTCTTTGTTATTCGTA 5580
5581 CTTCGTCCTCTTATTTGTTTCTTAAATTAATGTTTGTCTTACAGAGGTTGCC 5640
5581 CTTCGTCCTCTTATTTGTTTCTTAAATTAATGTTTGTCTTACAGAGGTTGCC 5640
5641 AGGCAAACTGCACGCAATTAACCAATTCGCCAACCGCGTGTGATTCGGAAATTAAGTTTA 5700
5641 AGGCAAACTGCACGCAATTAACCAATTCGCCAACCGCGTGTGATTCGGAAATTAAGTTTA 5700
5701 CATTAATCAAGTTTCCCAATTAAGGTTTAAATTAATCTATGTTTCAATGTTTCTT 5760
5701 CATTAATCAAGTTTCCCAATTAAGGTTTAAATTAATCTATGTTTCAATGTTTCTT 5760
5761 ATGTTGACCCGTTTATGTTATGCGCCACCTTGTGCTACATTAATATACAGATCACT 5820
5761 ATGTTGACCCGTTTATGTTATGCGCCACCTTGTGCTACATTAATATACAGATCACT 5820
5821 TTCACGTTATPACTTTCACGTAATGACATCATACGCTTAATGCTCACTGCGGTGCGAT 5880
5821 TTCACGTTATPACTTTCACGTAATGACATCATACGCTTAATGCTCACTGCGGTGCGAT 5880
5881 TGTGGCGGGGGCTGAAAAATACCAAGGGTACATATCATCAGCGGGGACACATTAAG 5940
5881 TGTGGCGGGGGCTGAAAAATACCAAGGGTACATATCATCAGCGGGGACACATTAAG 5940
5941 ACAAGGTTTAAATTAATATCGAGTACGCCCAACATCACTGTCGTAGCGACACTGATA 6000
5941 ACAAGGTTTAAATTAATATCGAGTACGCCCAACATCACTGTCGTAGCGACACTGATA 6000
5941 ACAAGGTTTAAATTAATATCGAGTACGCCCAACATCACTGTCGTAGCGACACTGATA 6000
6001 GAAAAACATTTTAAACGTTTGTGTTAGCGAACTTGATTAACATTAATGCTTCCAAAGCA 6060
6001 GAAAAACATTTTAAACGTTTGTGTTAGCGAACTTGATTAACATTAATGCTTCCAAAGCA 6060
6061 ACCGCGGACAAACCCCTGGAAGATTAATCAGGGGTCTGTCGCCGATAGGTGCGCGGAT 6120
6061 ACCGCGGACAAACCCCTGGAAGATTAATCAGGGGTCTGTCGCCGATAGGTGCGCGGAT 6120
6121 ACGTGTACGCGTATTCGAAACAAAGACTTTTCCCTTGGCGAGGCGTCCATCTCGGCAACA 6180
6121 ACGTGTACGCGTATTCGAAACAAAGACTTTTCCCTTGGCGAGGCGTCCATCTCGGCAACA 6180
6181 GACCATGTGATCTGGCGTTTCTCGCTACCAATCTTTACGCACTTACAGTTGAACAGC 6240
6181 GACCATGTGATCTGGCGTTTCTCGCTACCAATCTTTACGCACTTACAGTTGAACAGC 6240
6241 GACCATGTGATCTGGCGTTTCTCGCTACCAATCTTTACGCACTTACAGTTGAACAGC 6240
6241 GACCATGTGATCTGGCGTTTCTCGCTACCAATCTTTACGCACTTACAGTTGAACAGC 6240
6241 AATTCCTCTCACACGTTAAAGCCGCAATACAAAAAGTTGACACACGACGCTGCGCTTA 6300
6241 AATTCCTCTCACACGTTAAAGCCGCAATACAAAAAGTTGACACACGACGCTGCGCTTA 6300
6301 AGGTGACGTCCTTTCACAGAGAGTTATGTTGTTTCAAAATGCAAGTTTATTCAGGCGCG 6360
6301 AGGTGACGTCCTTTCACAGAGAGTTATGTTGTTTCAAAATGCAAGTTTATTCAGGCGCG 6360
6361 TGTGTAACGCTACCGGCTTAAGCAATATGCGAGGAAGCAGGCGCTCTTTGGGTACA 6420
6361 TGTGTAACGCTACCGGCTTAAGCAATATGCGAGGAAGCAGGCGCTCTTTGGGTACA 6420
6421 CGCAGTTTATAGAAACGGGTCCACCTCAGACATATGGAACCCCTCTGTAATGTCGCAAGT 6480
6421 CGCAGTTTATAGAAACGGGTCCACCTCAGACATATGGAACCCCTCTGTAATGTCGCAAGT 6480
6481 TACCGCAAGAGATGAGATGTTTCTTGGCTTGTGTTTACGGAAGGTTTAAAGAAAGAC 6540
6481 TACCGCAAGAGATGAGATGTTTCTTGGCTTGTGTTTACGGAAGGTTTAAAGAAAGAC 6540

D	6481	TACCGACAAGGTGATGATGTTCTTGCGGCTGTTTACGGAAGGTTTAAGAAAGAC	6540	D	7561	TTCTGGGCAACTTCGCGAGCTTTAGAGACCGGAAAGGAAACCGCGCCAGAGAC	7620
Q	6541	TGTGAGGGGCTGTCTCCTTCCCGGCGTGTCCAGACCCAGACGATGATTCGCCGAC	6600	Q	7621	ACCCAAAGTACAGTACTGGCAGCTATGTACAGCCGTGACAGAAAAGCTATCCGGATG	7680
D	6541	TGTGAGGGGCTGTCTCCTTCCCGGCGTGTCCAGACCCAGACGATGATTCGCCGAC	6600	D	7621	ACCCAAAGTACAGTACTGGCAGCTATGTACAGCCGTGACAGAAAAGCTATCCGGATG	7680
Q	6601	GCCAGCGTTTAAAGTGCCGTTGTACGACGAAGACCTGTTTGCACCTCAACGCTATAGAA	6660	Q	7681	GAATCACGAGAACACAGATTAATCACGTGACCTCTACCAACATCCAAAGTTTCTCA	7740
D	6601	GCCAGCGTTTAAAGTGCCGTTGTACGACGAAGACCTGTTTGCACCTCAACGCTATAGAA	6660	D	7681	GAATCACGAGAACACAGATTAATCACGTGACCTCTACCAACATCCAAAGTTTCTCA	7740
Q	6661	TGCGAAGGTTTACCTTAAGAAGTTAGGCGGCTACCTCTACGACTCCCTTTACAGACA	6720	Q	7741	GGGTGTTCAAGGGTATCGACTCAATTTGTGAGGAGGAGGTCTGTAAGTTCGTTAATGCA	7800
D	6661	TGCGAAGGTTTACCTTAAGAAGTTAGGCGGCTACCTCTACGACTCCCTTTACAGACA	6720	D	7741	GGGTGTTCAAGGGTATCGACTCAATTTGTGAGGAGGAGGTCTGTAAGTTCGTTAATGCA	7800
Q	6721	TGCGCCAGGCGCTGAGACTCAAGAAGCTGAGCGGCTCATCCAGCGCCACAGAAAACAT	6780	Q	7801	TGATTTAAATTAACCTTTAATTTCCCGAGACAGTCGTAATTCGGTCCATCATCTCAAGT	7860
D	6721	TGCGCCAGGCGCTGAGACTCAAGAAGCTGAGCGGCTCATCCAGCGCCACAGAAAACAT	6780	D	7801	TGATTTAAATTAACCTTTAATTTCCCGAGACAGTCGTAATTCGGTCCATCATCTCAAGT	7860
Q	6781	TGATGCAAGACCATTAACAATAATGCCAAGATAGTGCAGGCAAAAACATTTTCAACGACG	6840	Q	7861	TCTGCTGCAACGTGTATTGCGACAGCGCGCTGCGCGGTCTCTGTAATCTGACTCAAAAT	7920
D	6781	TGATGCAAGACCATTAACAATAATGCCAAGATAGTGCAGGCAAAAACATTTTCAACGACG	6840	D	7861	TCTGCTGCAACGTGTATTGCGACAGCGCGCTGCGCGGTCTCTGTAATCTGACTCAAAAT	7920
Q	6841	TGCCGAAAACGACAGCGGGTGTGCCACATGATTTGTGACAGCGTGTGCGCGAGCTCG	6900	Q	7921	CCCTGCTGTGATTCATTCAGATATCTGCTGCGCTGACTGATGATTCAGAACAAAGATA	7980
D	6841	TGCCGAAAACGACAGCGGGTGTGCCACATGATTTGTGACAGCGTGTGCGCGAGCTCG	6900	D	7921	CCCTGCTGTGATTCATTCAGATATCTGCTGCGCTGACTGATGATTCAGAACAAAGATA	7980
Q	6901	CCCTTAGTACGCGCTGTATGTTCTTCGAGTGTCCCGAGACCGCTGCGAGTGTGTAAT	6960	Q	7981	ATCCGGCGATGGGCAATCCCTCCCTCCGAGTGGCTAAAGATGATTTTGAGAGCTTGGA	8040
D	6901	CCCTTAGTACGCGCTGTATGTTCTTCGAGTGTCCCGAGACCGCTGCGAGTGTGTAAT	6960	D	7981	ATCCGGCGATGGGCAATCCCTCCCTCCGAGTGGCTAAAGATGATTTTGAGAGCTTGGA	8040
Q	6961	ACGATAGCTGCGCCATATTGATGTTGTGACTCACACGAGGCTAAGGTTTAAACGCGTTAG	7020	Q	8041	CGAATTTTAAAGCGCGGTGTCTGACACCGCGGGGTCTCACGGGGTGCAGACTGAATTCG	8100
D	6961	ACGATAGCTGCGCCATATTGATGTTGTGACTCACACGAGGCTAAGGTTTAAACGCGTTAG	7020	D	8041	CGAATTTTAAAGCGCGGTGTCTGACACCGCGGGGTCTCACGGGGTGCAGACTGAATTCG	8100
Q	7021	ACGCGTGTGCGGCGCAACGCGGCTTCACTGAGTGGCGGGTCAACTGTTCCGTGCCAATTCGG	7080	Q	8101	TACACCGGACATGTTTCTGCGACTTCTTGAGACACGAGCGGGGTCCAAACGGCTTAATGG	8160
D	7021	ACGCGTGTGCGGCGCAACGCGGCTTCACTGAGTGGCGGGTCAACTGTTCCGTGCCAATTCGG	7080	D	8101	TACACCGGACATGTTTCTGCGACTTCTTGAGACACGAGCGGGGTCCAAACGGCTTAATGG	8160
Q	7081	TGCTGTACTTAACCTTAAAGTGCAGAAAGCAAGCCGACAGGAGCAAAAAGGAGACGTAACG	7140	Q	8161	CCCCCTTTAAATGCAAGTTAGAAATAGCCCGAGCCATGATGTTCTGCGAAATCAATTA	8220
D	7081	TGCTGTACTTAACCTTAAAGTGCAGAAAGCAAGCCGACAGGAGCAAAAAGGAGACGTAACG	7140	D	8161	CCCCCTTTAAATGCAAGTTAGAAATAGCCCGAGCCATGATGTTCTGCGAAATCAATTA	8220
Q	7141	TGTACAACTCTTTTCCCTCCCAACAGGACTGGGGTTTAAATGAGGCGCAGATCAAGG	7200	Q	8221	AAATTAATAATGAAATCATTTTTCACACCGCGGGATCCGAGCGGTGCACTGGGGGT	8280
D	7141	TGTACAACTCTTTTCCCTCCCAACAGGACTGGGGTTTAAATGAGGCGCAGATCAAGG	7200	D	8221	AAATTAATAATGAAATCATTTTTCACACCGCGGGATCCGAGCGGTGCACTGGGGGT	8280
Q	7201	AAAAGGCAAGGCAAGCGCTTAAAGGCGTACCTCAAAACGCGCTCGATGGTTCTTGCTCA	7260	Q	8281	TGCTAAACCGAGCGGGAACCAAGGACACTTACGTGTGGCGGACCTGATGAAGATTTC	8340
D	7201	AAAAGGCAAGGCAAGCGCTTAAAGGCGTACCTCAAAACGCGCTCGATGGTTCTTGCTCA	7260	D	8281	TGCTAAACCGAGCGGGAACCAAGGACACTTACGTGTGGCGGACCTGATGAAGATTTC	8340
Q	7261	GCGCGTATACCTTGCGCTACGCGCGGTCTTCTGCGCCCATCTGCTGGGAGGATTTATGT	7320	Q	8341	TCACCTGCTGATGCGCGGTCTTCCCGAGACCCAAACGCGCGCTGTACCTGTGGC	8400
D	7261	GCGCGTATACCTTGCGCTACGCGCGGTCTTCTGCGCCCATCTGCTGGGAGGATTTATGT	7320	D	8341	TCACCTGCTGATGCGCGGTCTTCCCGAGACCCAAACGCGCGCTGTACCTGTGGC	8400
Q	7321	ATTACATGCACTTGTGCAACACCAAAAAGCTTCACGAACAGGCGTTTAAACATGATCC	7380	Q	8401	ACAAGATCTCCGAGACCAAAAACCCAGTTCTGAAAAGAGTCCCGGACACGAGCTGG	8460
D	7321	ATTACATGCACTTGTGCAACACCAAAAAGCTTCACGAACAGGCGTTTAAACATGATCC	7380	D	8401	ACAAGATCTCCGAGACCAAAAACCCAGTTCTGAAAAGAGTCCCGGACACGAGCTGG	8460
Q	7381	ATTATGTGGCAACCGCGCCCAACTCAGAGATGTGACGCTATGTACAGGCAACAGCGCG	7440	Q	8461	CGAGCTGTGTGCTAGCTAAAGAACCAACAGCTGCGCTTGAGGAAACGAACGCTGGG	8520
D	7381	ATTATGTGGCAACCGCGCCCAACTCAGAGATGTGACGCTATGTACAGGCAACAGCGCG	7440	D	8461	CGAGCTGTGTGCTAGCTAAAGAACCAACAGCTGCGCTTGAGGAAACGAACGCTGGG	8520
Q	7441	CAAGCTGCTCAACACGCTGTTCTATAGACTGAAGATAGGTTTCCCGCCGTAACACACCC	7500	Q	8521	ACGTGTTCCGGATTCACATCATATGTGTACGGAGAGATCAAACTGAACGGGGCAATTCGA	8580
D	7441	CAAGCTGCTCAACACGCTGTTCTATAGACTGAAGATAGGTTTCCCGCCGTAACACACCC	7500	D	8521	ACGTGTTCCGGATTCACATCATATGTGTACGGAGAGATCAAACTGAACGGGGCAATTCGA	8580
Q	7501	CTCAGCGAGGAGACCCCTACGTGTGACGGAACAGCCGGAAGCTTTAAACGACTGGAGA	7560	Q	8581	GGGCAATGTGGCAGATTCAGTTCTACGCGACAGACCTCCTACCTGCTCAGCGCGGTCTAC	8640
D	7501	CTCAGCGAGGAGACCCCTACGTGTGACGGAACAGCCGGAAGCTTTAAACGACTGGAGA	7560	D	8581	GGGCAATGTGGCAGATTCAGTTCTACGCGACAGACCTCCTACCTGCTCAGCGCGGTCTAC	8640
Q	7561	TTCTGGGCAACTTCGCGAGCTTTAGAGACCGGAGAGAGGAAACCGCGCGACGAGC	7620	Q	8641	AGAGATGATGCGAGGAATACCCCAAGTGTGGGTCCGCGCAATTCGCAACCGG	8700
D	7561	TTCTGGGCAACTTCGCGAGCTTTAGAGACCGGAGAGAGGAAACCGCGCGACGAGC	7620	D	8641	AGAGATGATGCGAGGAATACCCCAAGTGTGGGTCCGCGCAATTCGCAACCGG	8700

8701 TGGCTTACCTGGCAGAAATACGGCGCCGACCGCCCTACCGCTCAGACGACGGCGGCTC 8760
8701 TGGCTTACCTGGCAGAAATACGGCGCCGACCGCCCTACCGCTCAGACGACGGCGGCTC 8760
8761 AGCGGCTGCGCCGACAGGGCGCCCTGCGTACCGGTATACCGTTCCCATGGTACTCAACA 8820
8761 AGCGGCTGCGCCGACAGGGCGCCCTGCGTACCGGTATACCGTTCCCATGGTACTCAACA 8820
8821 AATAACAGGGGGCTCAACGGGAACAACGTTTCCACTGCGGGAACCTGGGGTACTTCG 8880
8821 AATAACAGGGGGCTCAACGGGAACAACGTTTCCACTGCGGGAACCTGGGGTACTTCG 8880
8881 CGGGGGCGGGCTGGACCGCAACCTGTGGCGGGAACCTGCCCCCTTTAAGAAAACGGGCG 8940
8881 CGGGGGCGGGCTGGACCGCAACCTGTGGCGGGAACCTGCCCCCTTTAAGAAAACGGGCG 8940
8941 TCAGCGCATGCTAAGAAGAAGACACGTATGATGACCCCATTTATGACCGCCCTAATAA 9000
8941 TCAGCGCATGCTAAGAAGAAGACACGTATGATGACCCCATTTATGACCGCCCTAATAA 9000
9001 AGCGAGCGGGGAGACACAAATCAGCAGCTTCCAGGCGGGAAGCGTTAAAAAGGCGTGC 9060
9001 AGCGAGCGGGGAGACACAAATCAGCAGCTTCCAGGCGGGAAGCGTTAAAAAGGCGTGC 9060
9061 AGCGGCTGTTAGAGATTAAGACAAACCTTAACCTATTGAAGTCGCTAATCTTGGAGCTTA 9120
9061 AGCGGCTGTTAGAGATTAAGACAAACCTTAACCTATTGAAGTCGCTAATCTTGGAGCTTA 9120
9121 TACGACACCTGGGGAAAGGGCTGCCAGACCTTAAGCTCCGAGGAGCTGCAATATTACCTCG 9180
9121 TACGACACCTGGGGAAAGGGCTGCCAGACCTTAAGCTCCGAGGAGCTGCAATATTACCTCG 9180
9181 GTACACTTGTATGTTTACAGCAGAGAGTTTATTTACGTTGATTAATATAGCACAGTCAG 9240
9181 GTACACTTGTATGTTTACAGCAGAGAGTTTATTTACGTTGATTAATATAGCACAGTCAG 9240
9241 GCGTGCCTGAGCTATCAGAGAGCGGCGGCTCCCTAATAGAGATCAGCAGAGCAGACAG 9300
9241 GCGTGCCTGAGCTATCAGAGAGCGGCGGCTCCCTAATAGAGATCAGCAGAGCAGACAG 9300
9301 ATCTTCAAGTTCTGATAGACAGCAGCATATCCACACCGCTTCTGCAACCCCGAGAGAAC 9360
9301 ATCTTCAAGTTCTGATAGACAGCAGCATATCCACACCGCTTCTGCAACCCCGAGAGAAC 9360
9361 AGCTACGACCCCTAGAGCGCGGCGCTACTGCGCGGGAAGAACGAAAAATTAAACGCGC 9420
9361 AGCTACGACCCCTAGAGCGCGGCGCTACTGCGCGGGAAGAACGAAAAATTAAACGCGC 9420
9421 TGCCTGAGCAGATCAGACCTTTAGAAAAACCGTGGCAGCGGCGCAACAATGCCAGGGAAC 9480
9421 TGCCTGAGCAGATCAGACCTTTAGAAAAACCGTGGCAGCGGCGCAACAATGCCAGGGAAC 9480
9481 TCCGACAGATTAATACGGCAGCTGTGCGCCCTCGCGCTGAGCTGATGATCTGTTATCTTTG 9540
9481 TCCGACAGATTAATACGGCAGCTGTGCGCCCTCGCGCTGAGCTGATGATCTGTTATCTTTG 9540
9541 CGGACCGCGGAAGATACGAGGTGCGCGCATTTCTAAAAAACAACAATAGAGAAC 9600
9541 CGGACCGCGGAAGATACGAGGTGCGCGCATTTCTAAAAAACAACAATAGAGAAC 9600
9601 TGAACCGCAGCTTCTGCGCTGCTAGCGCAAAACCTCGGTAAGACGCTCCAGCTGT 9660
9601 TGAACCGCAGCTTCTGCGCTGCTAGCGCAAAACCTCGGTAAGACGCTCCAGCTGT 9660
9661 CGCTCGAAGTGAAGACACCTGGCCAAAAACATCGAGCAAACTCGGAGACTGGAGCGCA 9720
9661 CGCTCGAAGTGAAGACACCTGGCCAAAAACATCGAGCAAACTCGGAGACTGGAGCGCA 9720
9721 GTCTGCGCGAGATATTTGAGCGCGAAGAGATTTTGAACAATACACTGAGACCCCAAT 9780
9721 GTCTGCGCGAGATATTTGAGCGCGAAGAGATTTTGAACAATACACTGAGACCCCAAT 9780
9781 GTCACATACACTGACGTTACTTTTCAGTTTACGGGGCGGGTTAATAGATTAACA 9840
9781 GTCACATACACTGACGTTACTTTTCAGTTTACGGGGCGGGTTAATAGATTAACA 9840
9841 TGTGCTTAATTAACGATGATAGAACTGCTGTGTAAAGACTAAGGAGTGTATTATGCA 9900
9841 TGTGCTTAATTAACGATGATAGAACTGCTGTGTAAAGACTAAGGAGTGTATTATGCA 9900
9901 TCGGTGCAAAAGAACTGTGCGGATTTGAACCGGGTTCTGACCTTTCTGTCAACACTGC 9960
9901 TCGGTGCAAAAGAACTGTGCGGATTTGAACCGGGTTCTGACCTTTCTGTCAACACTGC 9960
9961 GGGGTATCTCCCGATCCGACACCACTATACGTACAGTGCAGTGCCTTGGCTACAGT 10020
9961 GGGGTATCTCCCGATCCGACACCACTATACGTACAGTGCAGTGCCTTGGCTACAGT 10020
10021 GCGTGAAGGAATTCGAACCTGCTGTAACCAATCAGGGGTCAGTTTACTGCGGCTTTGGCAG 10080
10021 GCGTGAAGGAATTCGAACCTGCTGTAACCAATCAGGGGTCAGTTTACTGCGGCTTTGGCAG 10080
10081 ACCGACACCTGCGATCAGCTCTGTTAAGAAAGTTAGGCGGAGCCAAATACAGGCTGTTTG 10140
10081 ACCGACACCTGCGATCAGCTCTGTTAAGAAAGTTAGGCGGAGCCAAATACAGGCTGTTTG 10140
10141 AGACAGAACTGAGCAGCTGGGCTTAAGAAAGTTAAGCAAAACGTTGCGAGCGCACGACAGC 10200
10141 AGACAGAACTGAGCAGCTGGGCTTAAGAAAGTTAAGCAAAACGTTGCGAGCGCACGACAGC 10200
10201 GCGTCCGCTCTCTGAGATCAGTTAAGGAGTCTGCTGGCGGCCATACAAAGATACA 10260
10201 GCGTCCGCTCTCTGAGATCAGTTAAGGAGTCTGCTGGCGGCCATACAAAGATACA 10260
10261 ATATATTCAAAACGGGCTCCGCGCTCAATCATGAACTATGCAATCTTAATTTATTGAAACG 10320
10261 ATATATTCAAAACGGGCTCCGCGCTCAATCATGAACTATGCAATCTTAATTTATTGAAACG 10320
10321 CCGGGCAAAACGGGCTCCGCGCTCAACACCGGAGCCGAAACGAGTCTCAAAATGAGACTGC 10380
10321 CCGGGCAAAACGGGCTCCGCGCTCAACACCGGAGCCGAAACGAGTCTCAAAATGAGACTGC 10380
10381 TAAACACGAGGCGGATATGACAGGACACCGTGGCTTAATTAACCCAACTAAGCGCGA 10440
10381 TAAACACGAGGCGGATATGACAGGACACCGTGGCTTAATTAACCCAACTAAGCGCGA 10440
10441 CTCACCTCTACGAGCTGTTTCCGACCGGATCCCATAGATCCCTGTTCTGCGGCGCTTTT 10500
10441 CTCACCTCTACGAGCTGTTTCCGACCGGATCCCATAGATCCCTGTTCTGCGGCGCTTTT 10500
10501 TTAACCTATAGACGACACCATTAACGCACTGAGCCGGAATTCCTCGGTGACGTTCTTC 10560
10501 TTAACCTATAGACGACACCATTAACGCACTGAGCCGGAATTCCTCGGTGACGTTCTTC 10560
10561 AACAGGCAAACTATACCAACGTTATGCGAAAAACAAAGAGAGCTGTTCAACAGACTCAATA 10620
10561 AACAGGCAAACTATACCAACGTTATGCGAAAAACAAAGAGAGCTGTTCAACAGACTCAATA 10620
10621 GCATCTGCGCTCAGGAGGAGGCGGAGATCGCAAAAACCGGCGCACCCCTCGGAGGACAGGA 10680
10621 GCATCTGCGCTCAGGAGGAGGCGGAGATCGCAAAAACCGGCGCACCCCTCGGAGGACAGGA 10680
10681 CCACACACCTGCGGCAACCGCGGCAACGCGACGTCATCAAAAGACGACATATCGCAAAAG 10740
10681 CCACACACCTGCGGCAACCGCGGCAACGCGACGTCATCAAAAGACGACATATCGCAAAAG 10740
10741 AACAGTACATGAAAAAGGTGCGCAAGGAGCGGCTTTAAAAAACTAACAAGATGCTGCGAGA 10800
10741 AACAGTACATGAAAAAGGTGCGCAAGGAGCGGCTTTAAAAAACTAACAAGATGCTGCGAGA 10800
10801 CCGAGAGCGGCGGTGTTGGCAAAAGCACTCTGCAATGCGCGTATGAGGGGGGCGCTACG 10860
10801 CCGAGAGCGGCGGTGTTGGCAAAAGCACTCTGCAATGCGCGTATGAGGGGGGCGCTACG 10860
10861 GCGAGAGCGGCGGTGTTGGCAAAAGCACTCTGCAATGCGCGTATGAGGGGGGCGCTACG 10860
10861 GCGAGAGCGGCGGTGTTGGCAAAAGCACTCTGCAATGCGCGTATGAGGGGGGCGCTACG 10860
10861 GCGAGGCGTCCGAGCTGTTGAACCATTTTCTCTCAAGGCGGCGCTTCTGTCGCGCTTCCCT 10920

15241 TTTCAGAGGGAGCTTTTAAACCGGCTATTAACATCTCAAACTTCGCTCCCTACTTAATTC 15300
15301 ACGGAGCGTCCAGAGTGTATACACCTTCGATTTAAACGATACACAAAAATAAAAACCGC 15360
15301 ACGGAGCGTCCAGAGTGTATACACCTTCGATTTAAACGATACACAAAAATAAAAACCGC 15360
15361 TCCATCTTTGAAGTTCACGAGCCCGGTGGCGGGGAGGGGGTTCTATGAGTCCGCTCA 15420
15361 TCCATCTTTGAAGTTCACGAGCCCGGTGGCGGGGAGGGGGTTCTATGAGTCCGCTCA 15420
15421 AAAATTAAATAGGGGGGATGTCCCATATACATGTACCAAGTGTGTCCGGAAGAGTTC 15480
15421 AAAATTAAATAGGGGGGATGTCCCATATACATGTACCAAGTGTGTCCGGAAGAGTTC 15480
15481 AGCCTCCGCACTCAAACTGGACACGGTGGCCAGGAGTGTCTGGGGGGAATAAAGAG 15540
15481 AGCCTCCGCACTCAAACTGGACACGGTGGCCAGGAGTGTCTGGGGGGAATAAAGAG 15540
15541 GACGTATGTACAGAGACATTTCCCTCTGTCTGCTCAGTCCGGCGGCGAGGCTTAAG 15600
15541 GACGTATGTACAGAGACATTTCCCTCTGTCTGCTCAGTCCGGCGGCGAGGCTTAAG 15600
15601 GTGGGCGAGCTTTGCGGTGATGAGTCCGCTGCTGATGAGACCTTTAAATGTATTATG 15660
15601 GTGGGCGAGCTTTGCGGTGATGAGTCCGCTGCTGATGAGACCTTTAAATGTATTATG 15660
15661 ATACACGTGAGATTTTGGAGATAGCCAGCTGGCCAAAGATTCAAGGCGAGCGCTCTG 15720
15661 ATACACGTGAGATTTTGGAGATAGCCAGCTGGCCAAAGATTCAAGGCGAGCGCTCTG 15720
15721 ACGGACGGCCAAACAGCTCCGCTGTCTCTCTGCTGCTGAGAGCCGCGGCGAGAGAC 15780
15721 ACGGACGGCCAAACAGCTCCGCTGTCTCTCTGCTGCTGAGAGCCGCGGCGAGAGAC 15780
15781 TTTATCCCTCCGGTTCCAGAGCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGTTC 15840
15781 TTTATCCCTCCGGTTCCAGAGCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGTTC 15840
15841 AACCCCATTTCCGGGGTTTTTACGAGAGCCGCTCTGTGTGATGATTTTTCAGGCTGTAC 15900
15841 AACCCCATTTCCGGGGTTTTTACGAGAGCCGCTCTGTGTGATGATTTTTCAGGCTGTAC 15900
15901 CCGAGCATCATCCAGGCGGACACCTGTGTCTACTCCACATGATACAGGAGAGAGCTGTG 15960
15901 CCGAGCATCATCCAGGCGGACACCTGTGTCTACTCCACATGATACAGGAGAGAGCTGTG 15960
15961 CACCTGACCCCAACCTGAGCGCGGAGGAGTACGAGAGCTGTGTGTGAGGAGGAGGAGCG 16020
15961 CACCTGACCCCAACCTGAGCGCGGAGGAGTACGAGAGCTGTGTGTGAGGAGGAGGAGCG 16020
16021 GTACATTTTGTAAAAAAACACAGCGGAGTCTGTGTGGGAAGACTGCTAACGCTGTGG 16080
16021 GTACATTTTGTAAAAAAACACAGCGGAGTCTGTGTGGGAAGACTGCTAACGCTGTGG 16080
16081 TTAACAAAAGCAAGGCGGATCCGGCGCACCTGTGGCGGCTGATGACCCCTCCCTAAAA 16140
16081 TTAACAAAAGCAAGGCGGATCCGGCGCACCTGTGGCGGCTGATGACCCCTCCCTAAAA 16140
16141 ACCATTTAGTAAACAACACCTGAGCTCAAGGTGATGATGATGATGATGATGATGATGATG 16200
16141 ACCATTTAGTAAACAACACCTGAGCTCAAGGTGATGATGATGATGATGATGATGATGATG 16200
16201 ACCGGGTGGCGACGCGCTCTCCCATGTATTAACATAGCGGAACCGTGAACGCTCCGG 16260
16201 ACCGGGTGGCGACGCGCTCTCCCATGTATTAACATAGCGGAACCGTGAACGCTCCGG 16260
16261 GGGCGCAGATGCTGGAGATGTCAAAGTCTTACGTGGAGGCCCTGACGACGGAAGAGCTG 16320
16261 GGGCGCAGATGCTGGAGATGTCAAAGTCTTACGTGGAGGCCCTGACGACGGAAGAGCTG 16320
16321 CGAAGCGGTCTCGGAGGAGTACCGCCCGTCAAGGCGGGGGTTTCGGGTGCTTAC 16380
16321 CGAAGCGGTCTCGGAGGAGTACCGCCCGTCAAGGCGGGGGTTTCGGGTGCTTAC 16380

16321 CGAAGCGGTCTCGGAGGAGTACCGCCCGTCAAGGCGGGGGTTTCGGGTGCTTAC 16380
16381 GGTGACACGAGCTCCCTCTTTATGCGGTGACGAGGATTAATTCGCGGAACCGCTTCGCT 16440
16381 GGTGACACGAGCTCCCTCTTTATGCGGTGACGAGGATTAATTCGCGGAACCGCTTCGCT 16440
16441 TTTGTGACGATCTGGCGGCGGAGTACTGCGGACCTGTTCCTCCCACTTAAGTA 16500
16441 TTTGTGACGATCTGGCGGCGGAGTACTGCGGACCTGTTCCTCCCACTTAAGTA 16500
16501 GAGGCGGAAAAGAGCTTCAAGT 16560
16501 GAGGCGGAAAAGAGCTTCAAGT 16560
16501 GAGGCGGAAAAGAGCTTCAAGT 16560
16501 GAGGCGGAAAAGAGCTTCAAGT 16560
16561 CTATTGAACGACAAATGTGATGAAAGGGGTGACCTCATTTCCGCAAAACGGCTGCAAG 16620
16561 CTATTGAACGACAAATGTGATGAAAGGGGTGACCTCATTTCCGCAAAACGGCTGCAAG 16620
16621 TTTGTCCAGAGCGATGCGCGGCTATCTGTGACCTGTGTGTGTGTGTGTGTGTGTGTGTGT 16680
16621 TTTGTCCAGAGCGATGCGCGGCTATCTGTGACCTGTGTGTGTGTGTGTGTGTGTGTGTGT 16680
16681 GCTGGGCGGGGCTGT 16740
16681 GCTGGGCGGGGCTGT 16740
16741 GCTGGCTTTATTAATAATGTAGAGTCTCTCAACGAGCTATCTGTGACCTCCGAACAGC 16800
16741 GCTGGCTTTATTAATAATGTAGAGTCTCTCAACGAGCTATCTGTGACCTCCGAACAGC 16800
16801 GTCTGTGCTTATTAATAATGTAGAGTCTCTCAACGAGCTATCTGTGACCTCCGAACAGC 16860
16801 GTCTGTGCTTATTAATAATGTAGAGTCTCTCAACGAGCTATCTGTGACCTCCGAACAGC 16860
16861 AAGACCAACACCTGCGCCACCTGCGGTGTACCAAAAGCTGGGAGAGTGTGAGAGAG 16920
16861 AAGACCAACACCTGCGCCACCTGCGGTGTACCAAAAGCTGGGAGAGTGTGAGAGAG 16920
16921 CTGCCCCAGGTGACAGATAGATATCCCTACGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 16980
16921 CTGCCCCAGGTGACAGATAGATATCCCTACGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 16980
16981 TCGGACCTGGCGGCAACCCCGGATTAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 17040
16981 TCGGACCTGGCGGCAACCCCGGATTAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 17040
17041 CTATATTTCGACAAACCTGT 17100
17041 CTATATTTCGACAAACCTGT 17100
17101 AAGCGGACACACGAGT 17160
17101 AAGCGGACACACGAGT 17160
17161 TCGTGAACGCAATTTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 17220
17161 TCGTGAACGCAATTTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 17220
17161 TCGTGAACGCAATTTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 17220
17221 GAGCTGAGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 17280
17221 GAGCTGAGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 17280
17281 GGTGTCTCTGCGGACGTGGAGGTGACTTTTACCGGGGTGATGATGATGATGATGATGATGATG 17340
17281 GGTGTCTCTGCGGACGTGGAGGTGACTTTTACCGGGGTGATGATGATGATGATGATGATGATG 17340
17341 GGTGTCTCTGCGGACGTGGAGGTGACTTTTACCGGGGTGATGATGATGATGATGATGATGATG 17400
17341 GGTGTCTCTGCGGACGTGGAGGTGACTTTTACCGGGGTGATGATGATGATGATGATGATGATG 17400
17401 CACCGGCTGTGAAACGTTCAAGGGGCGACGAGGGGTGTACGCCAGGGGTGTGACCTCCCTTCTC 17460
17401 CACCGGCTGTGAAACGTTCAAGGGGCGACGAGGGGTGTACGCCAGGGGTGTGACCTCCCTTCTC 17460
17401 GCTGACACGATTTACCCACCAACATTTTCGCTGTGGAGTCTGTGACGCTCTCAAGGAATC 17460
17401 GCTGACACGATTTACCCACCAACATTTTCGCTGTGGAGTCTGTGACGCTCTCAAGGAATC 17460

QY	17461	GC	CCCCCTTC	TCGAC	TGCGGGCCCTTATCGCCCGCTTGGATTCCGGCGCGACGCGGA	17520
Db	17461	GC	CCCCCTTC	TCGAC	TGCGGGCCCTTATCGCCCGCTTGGATTCCGGCGCGACGCGGA	17520
QY	17521	CG	CGCGCGCGGTGGCCCCCGGGTTCTGCTGTGAGTACTCTCTCGCCCGTGAACCGTGGGT			17580
Db	17521	CG	CGCGCGCGGTGGCCCCCGGGTTCTGCTGTGAGTACTCTCTCGCCCGTGAACCGTGGGT			17580
QY	17581	AA	AGCGAGCGGGGGGACACAGATCCGGTTCTGCTCTCTCTTTTAAAGCCGATCGACCT			17640
Db	17581	AA	AGCGAGCGGGGGGACACAGATCCGGTTCTGCTCTCTCTTTTAAAGCCGATCGACCT			17640
QY	17641	GG	AGCGCGCGGGTACAGTACGTTCTGGCGAGAAAGCGCGCGCGCTCGAGAGGGACCCG			17700
Db	17641	GG	AGCGCGCGGGTACAGTACGTTCTGGCGAGAAAGCGCGCGCGCTCGAGAGGGACCCG			17700
QY	17701	AA	AGCCCAACCTGGCGGACCGGAAAGCCCTGGCGGTGAGACCCCTGGCGCTCTCCGGCGAGCG			17760
Db	17701	AA	AGCCCAACCTGGCGGACCGGAAAGCCCTGGCGGTGAGACCCCTGGCGCTCTCCGGCGAGCG			17760
QY	17761	GT	CTCAGACGTGCGCCCATTCCTTTCGTTGCGTATTTTCCACGGCGCAACTCGGTGGCGTG			17820
Db	17761	GT	CTCAGACGTGCGCCCATTCCTTTCGTTGCGTATTTTCCACGGCGCAACTCGGTGGCGTG			17820
QY	17821	CT	TAAGCCTGTGTGGGTATACAGGTAGAGCGGCTTTTTCGATATGACGGCGCACAGAGACGC			17880
Db	17821	CT	TAAGCCTGTGTGGGTATACAGGTAGAGCGGCTTTTTCGATATGACGGCGCACAGAGACGC			17880
QY	17881	GG	GAATCTCCCCGAAATATACGTACAGTTAGTAACTCGGGGGGTAGCTGTGCAAGGGCTC			17940
Db	17881	GG	GAATCTCCCCGAAATATACGTACAGTTAGTAACTCGGGGGGTAGCTGTGCAAGGGCTC			17940
QY	17941	CG	TTACACAGCTGTCCCGCTGCGGTGTAACCGCGCAATGGAATTCATCTACGCTCC			18000
Db	17941	CG	TTACACAGCTGTCCCGCTGCGGTGTAACCGCGCAATGGAATTCATCTACGCTCC			18000
QY	18001	CG	GGGACCCCAACCGCCAGATAGTCTGTGGCCAGTCCGGACCGCTCTGCCACCCACAC			18060
Db	18001	CG	GGGACCCCAACCGCCAGATAGTCTGTGGCCAGTCCGGACCGCTCTGCCACCCACAC			18060
QY	18061	CG	GGGCGCGCGGTATTTGGGGGTCTACGCGCGAGCGCGGAAACCAATCCACCTGGAACTC			18120
Db	18061	CG	GGGCGCGCGGTATTTGGGGGTCTACGCGCGAGCGCGGAAACCAATCCACCTGGAACTC			18120
QY	18121	CG	CGGAAGTCCGGGTTAGTTAATCTTCCAAACAGGAGCGGCGCTCGGGGCGATCTGGC			18180
Db	18121	CG	CGGAAGTCCGGGTTAGTTAATCTTCCAAACAGGAGCGGCGCTCGGGGCGATCTGGC			18180
QY	18181	GT	TTCTGTGTCACGGGCGTGGGACCGGAGCCCTTATTTGTGTGTACCCCCGGGCACTTTGCT			18240
Db	18181	GT	TTCTGTGTCACGGGCGTGGGACCGGAGCCCTTATTTGTGTGTACCCCCGGGCACTTTGCT			18240
QY	18241	TT	TCGGGTGTGACCAACCACTGCGCTATTTCACACCGATCCGCCACGATATATAA			18300
Db	18241	TT	TCGGGTGTGACCAACCACTGCGCTATTTCACACCGATCCGCCACGATATATAA			18300
QY	18301	AA	AGAGACACCTTGTGGCGCGCGCGCGCTTGCCTGGCTGGTAAAGTCTCGCGCA			18360
Db	18301	AA	AGAGAGACACCTTGTGGCGCGCGCGCGCGCTTGCCTGGCTGGTAAAGTCTCGCGCA			18360
QY	18361	CG	AGGCGCGCGGAGAACCTCGTGGGTGACACAGACAGCGGGCGCTCTCAATTAAAGGCTT			18420
Db	18361	CG	AGGCGCGCGGAGAACCTCGTGGGTGACACAGACAGCGGGCGCTCTCAATTAAAGGCTT			18420
QY	18421	CA	CAATCCCGGTGCGTTTCCAGAGGGGTGTCTGGCGGAGTGTACGTGTCCCTACCGCA			18480
Db	18421	CA	CAATCCCGGTGCGTTTCCAGAGGGGTGTCTGGCGGAGTGTACGTGTCCCTACCGCA			18480
QY	18481	CA	ACGCGGGTCCAGACGATGAACATTTGACGGCAACGATGGAGACACCGGTGCTTC			18540
Db	18481	CA	ACGCGGGTCCAGACGATGAACATTTGACGGCAACGATGGAGACACCGGTGCTTC			18540
QY	18541	TT	TCGGGTGTGACGACCTCTGAGATCTAGTGAACAGGACCCGACGATACAGCTTC			18600
Db	18541	TT	TCGGGTGTGACGACCTCTGAGATCTAGTGAACAGGACCCGACGATACAGCTTC			18600
QY	18601	CT	GTGTGGGGCGCCATTTTACAGAGGGCTACGTGACCTGTGACATGTGTAACAGTCTAAGCTG			18660
Db	18601	CT	GTGTGTGGGGCGCCATTTTACAGAGGGCTACGTGACCTGTGACATGTGTAACAGTCTAAGCTG			18660
QY	18661	TG	CGTACAGGAGAGTCTCCGTCTGCGGGATGCCCCAGCATGGGAGATCGTGGCG			18720
Db	18661	TG	CGTACAGGAGAGTCTCCGTCTGCGGGATGCCCCAGCATGGGAGATCGTGGCG			18720
QY	18721	AA	AGGTTTCCGGGCTTCCCTTTTGGCACCGGCACTGTGGGATCGGGGAACAGCAAC			18780
Db	18721	AA	AGGTTTCCGGGCTTCCCTTTTGGCACCGGCACTGTGGGATCGGGGAACAGCAAC			18780
QY	18781	GT	GTGTACGGGTTGCTGACCGCGCAACCCACGTGGATATGTACCCGCGCTGGGTGAG			18840
Db	18781	GT	GTGTGTACGGGTTGCTGACCGCGCAACCCACGTGGATATGTACCCGCGCTGGGTGAG			18840
QY	18841	CG	GGCGGATGCGGAGGTGGTGTGCGGGTTACAGCTCCGCAACCAACCGGGGTGTGCGCA			18900
Db	18841	CG	GGCGGATGCGGAGGTGGTGTGCGGGTTACAGCTCCGCAACCAACCGGGGTGTGCGCA			18900
QY	18901	TA	CGGACTTAAGGTATTCGTGGCGATTCGTTACGGTGTGCGCCCGCGGGGTGTTTCTTA			18960
Db	18901	TA	CGGACTTAAGGTATTCGTGGCGATTCGTTACGGTGTGCGCCCGCGGGGTGTTTCTTA			18960
QY	18961	CA	TTTTCCAAAGACCGCGCTCCGATCGGGGTGACAGAGCGGTGCAAGGAGGGCTCC			19020
Db	18961					

D	b		 TTCCGTGGCCCCGCGGAACCTGCAGACTCCTCGGCCACCAGATCGCGGCCCTCGAGGCTG	19680
O	y	19681	CCGGGCGGGGTGACAGTGCAGACAGCAAAAAGCTGTAGTGGTTTGAGAACCATGTACCTGTTT	19740
D	b	19681	CCGGGCGGGGTGACAGTGCAGACAGCAAAAAGCTGTAGTGGTTTGAGAACCATGTACCTGTTT	19740
O	y	19741	TTCCACGTAATAATTACTAATAAACCGTTTCCTGCTGTATGGCTCACACAACGCCAAACCGTCTC	19800
D	b	19741	TTCCACGTAATAATAATTACTAATAAACCGTTTCCTGCTGTATGGCTCACACAACGCCAAACCGTCTC	19800
O	y	19801	TCATTTTCGSGGGTGCAGCGCTCGCGAACAACAGAAGTGGCTCAAAACCCCCTTCGCG	19860
D	b	19801	TCATTTTCGSGGGTGCAGCGCTCGCGAACAACAGAAGTGGCTCAAAACCCCCTTCGCG	19860
O	y	19861	ACCTTCGCGACAAAAACAGTTAACGCCCTTCGTTAGATGACGTTATTTATTTATTTTA	19920
D	b	19861	ACCTTCGCGACAAAAACAGTTAACGCCCTTCGTTAGATGACGTTATTTATTTATTTTA	19920
O	y	19921	TTTACATCATACACTTTTGGCGGGGGCGCCGTCGCCGAAAAACATCTGTAGATTTCCAGTAT	19980
D	b	19921	TTTACATCATACACTTTTGGCGGGGGCGCCGTCGCCGAAAAACATCTGTAGATTTCCAGTAT	19980
O	y	19981	GCGAAACGCGGTGAGAACACAGTCCCGGGGGCTGTGCCCCAACAGCAGCAGCGGTTTT	20040
D	b	19981	GCGAAACGCGGTGAGAACACAGTCCCGGGGGCTGTGCCCCAACAGCAGCAGCGGTTTT	20040
O	y	20041	TTTCATTAGACTCCGCGCCACCTATCTTTGTTATTTAGGGAAAGCTCCTCAATTAGAGACTC	20100
D	b	20041	TTTCATTAGACTCCGCGCCACCTATCTTTGTTATTTAGGGAAAGCTCCTCAATTAGAGACTC	20100
O	y	20101	GAGGGCGGACAGCACACAGGTACACCGCGAGCCAAATGGCCGCGCTCCGCTCCCGGG	20160
D	b	20101	GAGGGCGGACAGCACACAGGTACACCGCGAGCCAAATGGCCGCGCTCCGCTCCCGGG	20160
O	y	20161	CGCGTCGTCGACGACGACTCCTCAGTGCGCTCAGTAACTCTGTAGGCCCGGAGCCCGGG	20220
D	b	20161	CGCGTCGTCGACGACGACTCCTCAGTGCGCTCAGTAACTCTGTAGGCCCGGAGCCCGGG	20220
O	y	20221	AACCATGGCGTTCTATACACTGCGGCCCGCGCAAACTCGCGCGCTGGCACTCAACGTTTAA	20280
D	b	20221	AACCATGGCGTTCTATACACTGCGGCCCGCGCAAACTCGCGCGCTGGCACTCAACGTTTAA	20280
O	y	20281	CATCAATAATAGGAGAGTGAACAACAACGACATGATGGCGGGTACTCAACGACCCGACAG	20340
D	b	20281	CATCAATAATAGGAGAGTGAACAACAACGACATGATGGCGGGTACTCAACGACCCGACAG	20340
O	y	20341	AGTGAAGTGGTGGCAGAGTGAACGAACGACGCGCTGATGTTAAACCCCACTTCAGACAG	20400
D	b	20341	AGTGAAGTGGTGGCAGAGTGAACGAACGACGCGCTGATGTTAAACCCCACTTCAGACAG	20400
O	y	20401	GCGGCCCTCGTCTGTCTCAAGAGAGGCGCGGTTCGCGGCCCACTGGGGGAGAACGTTTAT	20460
D	b	20401	GCGGCCCTCGTCTGTCTCAAGAGAGGCGCGGTTCGCGGCCCACTGGGGGAGAACGTTTAT	20460
O	y	20461	TCCAGCGGCAAGTGGGGAGGCGCCAGCGTAgGGCTGGCCGCCCAACAGACAGGTAA	20520
D	b	20461	TCCAGCGGCAAGTGGGGAGGCGCCAGCGTAgGGCTGGCCGCCCAACAGACAGGTAA	20520
O	y	20521	CAAACGACACAGCAGAGGGAACATGACCGGTAAATTTACTCGTTTCAATTCGCGGGCGCG	20580
D	b	20521	CAAACGACACAGCAGAGGGAACATGACCGGTAAATTTACTCGTTTCAATTCGCGGGCGCG	20580
O	y	20581	GGCGGGTCAAGCGGAGTTCATTAAAAACACACCGCGCGCAACCCCGCAACGCGGGGCGG	20640
D	b	20581	GGCGGGTCAAGCGGAGTTCATTAAAAACACACCGCGCGCAACCCCGCAACGCGGGGCGG	20640
O	y	20641	CGCCCTGGAACGCGGTTCTTCCAATTCGCAAAAGAACCGGTCACAAAAAGGCTCGTTTT	20700
D	b	20641	CGCCCTGGAACGCGGTTCTTCCAATTCGCAAAAGAACCGGTCACAAAAAGGCTCGTTTT	20700
O	y	20701	GAACCCATTTTGTGTCATGCGGGTTTGGTTTTGATGATAGGAAAGGCTGTCAAAAACA	20760
D	b	20701	GAACCCATTTTGTGTCATGCGGGTTTGGTTTTGATGATAGGAAAGGCTGTCAAAAACA	20760
D	b	20701	GAACCCATTTTGTGTCATGCGGGTTTGGTTTTGATGATAGGAAAGGCTGTCAAAAACA	20760
O	y	20761	CCCAACGGGGGTGTCTCAAACGCGCATCTCTATATGTGGAGATGGGGTGTGTAC	20820
D	b	20761	CCCAACGGGGGTGTGTCTCAAACGCGCATCTCTATATGTGGAGATGGGGTGTGTAC	20820
O	y	20821	CCCTGACACTCAGATCCGCGGGGTAAAGTCTCTCAGACGGCGCACCTTCTCAAAATCT	20880
D	b	20821	CCCTGACACTCAGATCCGCGGGGTAAAGTCTCTCAGACGGCGCACCTTCTCAAAATCT	20880
O	y	20881	TCAGCCCGGAAAGAGAGCGGGGGTCTCCGACGTGAAGCAGCAGGGGATCAACGTGT	20940
D	b	20881	TCAGCCCGGAAAGAGAGCGGGGGTCTCCGACGTGAAGCAGCAGGGGATCAACGTGT	20940
O	y	20941	TGTTGTAAAGTGGGCGTCAACCAAGGTGTGCACAAAGTCTCCGGGGTCAAGCCGTGA	21000
D	b	20941	TGTTGTAAAGTGGGCGTCAACCAAGGTGTGCACAAAGTCTCCGGGGTCAAGCCGTGA	21000
O	y	21001	CGTAGGATCAGATACGTAGAGAGGGCGTAGTGGCGATGTTAAACGGGACCCGAGGC	21060
D	b	21001	CGTAGGATCAGATACGTAGAGAGGGCGTAGTGGCGATGTTAAACGGGACCCGAGGC	21060
O	y	21061	CCATGTGCGGAGACTTGTGTACAGTGTGAGSAGACAGCTCCCGGAGCAGCTAAACT	21120
D	b	21061	CCATGTGCGGAGACTTGTGTACAGTGTGAGSAGACAGCTCCCGGAGCAGCTAAACT	21120
O	y	21121	GACACAAACGTCGAAGAAGAGAGACCATCTCCGCGAGTCTCGCGGGTTCACCGGC	21180
D	b	21121	GACACAAACGTCGAAGAAGAGAGACCATCTCCGCGAGTCTCGCGGGTTCACCGGC	21180
O	y	21181	ACATAAGATAGCGCGCATCTGTTGGGGCGCCCTGTATTAGATCCACAGTAAACGACGT	21240
D	b	21181	ACATAAGATAGCGCGCATCTGTTGGGGCGCCCTGTATTAGATCCACAGTAAACGACGT	21240
O	y	21241	GGTCCACCCCTGACCTCTGATTGGAGCGCGGCCCTCGTACTCCGCCCAAAATGTC	21300
D	b	21241	GGTCCACCCCTGACCTCTGATTGGAGCGCGGCCCTCGTACTCCGCCCAAAATGTC	21300
O	y	21301	TCACACTGGAACCCGTACACCGGCGCCAGATGCGCTTCGCGGGGTGCCGAAGCCCTGCG	21360
D	b	21301	TCACACTGGAACCCGTACACCGGCGCCAGATGCGCTTCGCGGGGTGCCGAAGCCCTGCG	21360
O	y	21361	CCGCGCAAAAGCGCGGAGCCGTTGGCGCTCCCAATTTTATACGCCGCGCGCGACAGTT	21420

Db	20701	GAACCAATTTTGTGGCATTCGGGTTTCGTTTTCAGATACGAGAAAGCGCTGTCACAAAACA	20760
QY	20761	CCCAACGGGGGTGTGCTCTCAAAAGCCCACTCTCCATCTCTATGTGGGGATGGGGGTGTAGC	20820
Db	20761	CCCAACGGGGGTGTGCTCTCAAAAGCCCACTCTCCATCTCTATGTGGGGATGGGGGTGTAGC	20820
QY	20821	CCTGAGACTCAGATTCGGCGGGCGTAAAGTCTCTCAGACGGGCCACTTCTCMAAAACT	20880
Db	20821	CCTGAGACTCAGATTCGGCGGGCGTAAAGTCTCTCAGACGGGCCACTTCTCMAAAACT	20880
QY	20881	TCAGCCGGGAAACGAGACGGGGGTCTCTCCGAGCTGGAAGCAGCAGGGGATCAACGTGT	20940
Db	20881	TCAGCCGGGAAACGAGACGGGGGTCTCTCCGAGCTGGAAGCAGCAGGGGATCAACGTGT	20940
QY	20941	TGTTTAAACGTGGGCTTCACCCAAAGTGTGCACAAAGTCTCCGGGGTCAAGCCCTGTA	21000
Db	20941	TGTTTAAACGTGGGCTTCACCCAAAGTGTGCACAAAGTCTCCGGGGTCAAGCCCTGTA	21000
QY	21001	CGTGAGCATCAGATACGTCAAGAGAGGGGTGACTGCGCATGTTAAACGGGACCCCGAGGC	21060
Db	21001	CGTGAGCATCAGATACGTCAAGAGAGGGGTGACTGCGCATGTTAAACGGGACCCCGAGGC	21060
QY	21061	CCATTCGGCGAGCTCTGTGTACACAGCTGGACAGACGTCCCGCCGAGCCACAGTAAACT	21120
Db	21061	CCATTCGGCGAGCTCTGTGTACACAGCTGGACAGACGTCCCGCCGAGCCACAGTAAACT	21120
QY	21121	GACACAAAACGTGACAGAAGGAGAGCCATCCGCGGAGGTCCGGGGGTTCCACGGC	21180
Db	21121	GACACAAAACGTGACAGAAGGAGAGCCATCCGCGGAGGTCCGGGGGTTCCACGGC	21180
QY	21181	ACATACGATCGCGGATCTGTGGGGCGCCGTTAATTAAGATCCACACAGTAACGCACT	21240
Db	21181	ACATACGATCGCGGATCTGTGGGGCGCCGTTAATTAAGATCCACACAGTAACGCACT	21240
QY	21241	GGTCCACCCCTGACCCCTCTGATGTGGGGTGGGCCCCCTGTATCTACCCGCCCAAAATGTC	21300
Db	21241	GGTCCACCCCTGACCCCTCTGATGTGGGGTGGGCCCCCTGTATCTACCCGCCCAAAATGTC	21300
QY	21301	TCACATGGAAACCCGTAACACGGGCCCAATCGCCCTCGCGGGGTGCCCGGAAAGCCCTGCG	21360
Db	21301	TCACATGGAAACCCGTAACACGGGCCCAATCGCCCTCGCGGGGTGCCCGGAAAGCCCTGCG	21360
QY	21361	CCGCCAAAAGGGCGGGGACCCCTGCGGGTCCCAAAATTTTAAAGCGCGGGCGCGCACTT	21420
Db	21361	CCGCCAAAAGGGCGGGGACCCCTGCGGGTCCCAAAATTTTAAAGCGCGGGCGCGCACTT	21420
QY	21421	CGGTGAGATCGGTGGAGGCCCTGATATTAACACAGCAACTCTCCACAGACGCCCTCCAAA	21480
Db	21421	CGGTGAGATCGGTGGAGGCCCTGATATTAACACAGCAACTCTCTCCACAGACGCCCTCCAAA	21480
QY	21481	ACACCCTTTGGTGTAAACAGAGAAACTGTCCTCTAGAGTTATATCGGGCTGAAACC	21540
Db	21481	ACACCCTTTGGTGTAAACAGAGAAACTGTCCTCTAGAGTTATATCGGGCTGAAACC	21540
QY	21541	CGAACAGGACCTGTGTGCCACAGCCCGTCTCTCTCCCTCTGCACGCGCTGTATTAATA	21600
Db	21541	CGAACAGGACCTGTGTGCCACAGCCCGTCTCTCTCCCTCTGCACGCGCTGTATTAATA	21600
QY	21601	TTAAATCCAGGTGGGCCCAAGTACGTACACTGCGGTGGTGGCCGGGAGCGACGGAGCGGA	21660
Db	21601	TTAAATCCAGGTGGGCCCAAGTACGTACACTGCGGTGGTGGCCGGGAGCGACGGAGCGGA	21660
QY	21661	CGGCGCGGACCTTCCTGGGTCGCGAAAAACCCGGAGTCTGGGGCCGCAATTCAGCA	21720
Db	21661	CGGCGCGGACCTTCCTGGGTCGCGAAAAACCCGGAGTCTGGGGCCGCAATTCAGCA	21720
QY	21721	CGCAACGGGTATATATTTTAAACGTAGCAGATATCCAGATGCAACGAGCAATCATAA	21780
Db	21721	CGCAACGGGTATATATTTTAAACGTAGCAGATATCCAGATGCAACGAGCAATCATAA	21780
QY	21781	TTACACCGAGAGTGTCTTACACATCTAATCCGTTAAAGGCTGAAGACGAACATTAATTTAA	21840
Db	21781	TTACACCGAGAGTGTCTTACACATCTAATCCGTTAAAGGCTGAAGACGAACATTAATTTAA	21840

QY	21841	AGCAGCTTGGGGGGGGCCACACACAGCGCGGCCGGCTGTAGCGATTAAATAACCCA	21900
Db	21841	AGGCACTTGGGGGGGGCCGACACAGCGCGGCCGGCTGTAGCGATTAAATAACCCA	21900
QY	21901	CGTGGTCTCCCCAAGCGTCTCCCGAGCGTGAAGGCTTCCCAACGCCCAAAACAACAC	21960
Db	21901	CGTGGTCTCCCAAGCGTCTCCCGAGCGTGAAGGCTTCCCAACGCCCAAAACAACAC	21960
QY	21961	AGATAATTAATAATAATCATGTTATTTTTTATTAACCTTAACGGGATTAAGCTCTT	22020
Db	21961	AGATAATTAATAATAATCATGTTATTTTTTATTAACCTTAACGGGATTAAGCTCTT	22020
QY	22021	AACAGGGGCCAATAGAAAGCAACGTGCGAGGGCGCATTCGGCGCTCAAAAGCCACCA	22080
Db	22021	AACAGGGGCCAATAGAAAGCAACGTGCGAGGGCGCATTCGGCGCTCAAAAGCCACCA	22080
QY	22081	CACGGGGCGCTGTAAAGCGTTAAACAAACAATTTAGCCATTGTAACCGTTAAATCCCA	22140
Db	22081	CACGGGGCGCTGTAAAGCGTTAAACAAACAATTTAGCCATTGTAACCGTTAAATCCCA	22140
QY	22141	ACCCCTGCGCTCCGAGACCATTCGCCAGCTGAGCTACGTCAGAGGGTGTTCCTAAATCG	22200
Db	22141	ACCCCTGCGCTCCGAGACCATTCGCCAGCTGAGCTACGTCAGAGGGTGTTCCTAAATCG	22200
QY	22201	CATTTTGAGCCCTTTGGCACGGCGCGCTGCGTTAATGTGTCTTAATTCGCGTCCCA	22260
Db	22201	CATTTTGAGCCCTTTGGCACGGCGCGCTGCGTTAATGTGTCTTAATTCGCGTCCCA	22260
QY	22261	AGGCGCTCTTGGGAATGTCATATAGGCTGCGGGGTTCTCTGCGCCCTTTTGGGACGC	22320
Db	22261	AGGCGCTCTTGGGAATGTCATATAGGCTGCGGGGTTCTCTGCGCCCTTTTGGGACGC	22320
QY	22321	TTGTGCACCGGCTGAAGAGATTCTTCACTGCTGCTGCTCCCGGAGATTGGCACACAGCTT	22380
Db	22321	TTGTGCACCGGCTGAAGAGATTCTTCACTGCTGCTGCTCCCGGAGATTGGCACACAGCTT	22380
QY	22381	TTACCGGGGCGAGTGTTTAATATCAGCGCGTCCACGACGACTGCGAGAGGTGGAG	22440
Db	22381	TTACCGGGGCGAGTGTTTAATATCAGCGCGTCCACGACGACTGCGAGAGGTGGAG	22440
QY	22441	TAAAGAACCATTAACCGGGGGGCGGAGATGATGATTACATACCCCAACAGCAGAGTTGC	22500
Db	22441	TAAAGAACCATTAACCGGGGGGCGGAGATGATGATTACATACCCCAACAGCAGAGTTGC	22500
QY	22501	GGCGGGGCTCGTATGAGAGCCCATAGAAAGGCATATCACTACACAGCGCAACCC	22560
Db	22501	GGCGGGGCTCGTATGAGAGCCCATAGAAAGGCATATCACTACACAGCGCAACCC	22560
QY	22561	GCAAAAAAAGCGCACAGAAAAAGCCCTCATGTGTGACAAAAACAAAAACAAGACGGG	22620
Db	22561	GCAAAAAAAGCGCACAGAAAAAGCCCTCATGTGTGACAAAAACAAAAACAAGACGGG	22620
QY	22621	GTCGCTGCTGCTTGGCACAGCGCACAGCGTCCGCGTCTGCGCACAGGTTGAGCGGCTC	22680
Db	22621	GTCGCTGCTGCTTGGCACAGCGCACAGCGTCCGCGTCTGCGCACAGGTTGAGCGGCTC	22680
QY	22681	CATTAAATACCGGGGCCCGGGCGCTCGACGGAACCAAGCGCTGGTTAGCCACTGAC	22740
Db	22681	CATTAAATACCGGGGCCCGGGCGCTCGACGGAACCAAGCGCTGGTTAGCCACTGAC	22740
QY	22741	GCAGTGTCTCCCTCCAGATGTGGCATTTGGAGTCCCAAAACGGGGCTGTAACTACAG	22800
Db	22741	GCAGTGTCTCCCTCCAGATGTGGCATTTGGAGTCCCAAAACGGGGCTGTAACTACAG	22800
QY	22801	GTCGCCCCGGGTTCAAAAGACGGGAGATCCCAAAACAGTTAAACCTTTTGTCCAAA	22860
Db	22801	GTCGCCCCGGGTTCAAAAGACGGGAGATCCCAAAACAGTTAAACCTTTTGTCCAAA	22860
QY	22861	CAGAAAGCCAACAGCAACCGAAGGAATCTCAAAACAGCAAGGAGGTTCCGTCGGCGCA	22920
Db	22861	CAGAAAGCCAACAGCAACCGAAGGAATCTCAAAACAGCAAGGAGGTTCCGTCGGCGCA	22920
QY	22921	TAAACGGAATAATTTCCCTCACTAAACACACAGCGCGCTTAAACGTTTAAACAGCAAT	22980
Db	22921	TAAACGGAATAATTTCCCTCACTAAACACACAGCGCGCTTAAACGTTTAAACAGCAAT	22980
QY	22981	ACTTCTAGGCGTGTGTTAATAAACAACAAGGTTGTATTTTCGGGGGCCCTTTGG	23040
Db	22981	ACTTCTAGGCGTGTGTTAATAAACAACAAGGTTGTATTTTCGGGGGCCCTTTGG	23040
QY	23041	GGCCCGCGGCTGTGGGGGTGCGGTGTCTGTTGTGGTATGCAATCAACACCCGCGTGC	23100
Db	23041	GGCCCGCGGCTGTGGGGGTGCGGTGTCTGTTGTGGTATGCAATCAACACCCGCGTGC	23100
QY	23101	CGAAAAACAGGCAACACCCCTGCGCTAGTTTTTTTAAACTTAACACCGCAAGGGA	23160
Db	23101	CGAAAAACAGGCAACACCCCTGCGCTAGTTTTTTTAAACTTAACACCGCAAGGGA	23160
QY	23161	GAAGGAAAGGGGTGGGCTTAAATGGGCTGTTAGACGCCAACGGGAGGAAAAAAGG	23220
Db	23161	GAAGGAAAGGGGTGGGCTTAAATGGGCTGTTAGACGCCAACGGGAGGAAAAAAGG	23220
QY	23221	GGGCAAAACCGCGGTTAACAACAACAGCAACAGGCGCCAAACCCATATATACACAACGA	23280
Db	23221	GGGCAAAACCGCGGTTAACAACAACAGCAACAGGCGCCAAACCCATATATACACAACGA	23280
QY	23281	TATTCGCTGTGTTTCCGGGGCGGGTCCGTTACGGCTAACCCGCTTGGGCTTTGCACA	23340
Db	23281	TATTCGCTGTGTTTCCGGGGCGGGTCCGTTACGGCTAACCCGCTTGGGCTTTGCACA	23340
QY	23341	AGCAGCCCCCGGCTGCACCCGGGCTCCCGAGGTACCGAAGGGGTCAGAAACAATAGTT	23400
Db	23341	AGCAGCCCCCGGCTGCACCCGGGCTCCCGAGGTACCGAAGGGGTCAGAAACAATAGTT	23400
QY	23401	TTACAGGTGCGCAGTGCAGCGCGTGGCAACATCTTTGCGTGCCTTCGCAACACCCGGA	23460
Db	23401	TTACAGGTGCGCAGTGCAGCGCGTGGCAACATCTTTGCGTGCCTTCGCAACACCCGGA	23460
QY	23461	AAATCCCCCGCGCGGGTCTGTGGAAGGCGCAACGAAGATATCCCAACAGCAACTTA	23520
Db	23461	AAATCCCCCGCGCGGGTCTGTGGAAGGCGCAACGAAGATATCCCAACAGCAACTTA	23520
QY	23521	AAGCATCATGTTTGGGGTTCGGTGTACGGCGCGGAGAGAGAGCGCGGTGGCGCTTG	23580
Db	23521	AAGCATCATGTTTGGGGTTCGGTGTACGGCGCGGAGAGAGAGCGCGGTGGCGCTTG	23580
QY	23581	CGAAGATAGTGGCGCGACAGCAGGGTTTCGGTAGTACGCGCTGTGACGGCTGCACCT	23640
Db	23581	CGAAGATAGTGGCGCGACAGCAGGGTTTCGGTAGTACGCGCTGTGACGGCTGCACCT	23640
QY	23641	GGCAGAGGCGCAAAAAACAGGGGCGCGGACAGGGCGGAGGTGGGCGCGCTTTCCCG	23700
Db	23641	GGCAGAGGCGCAAAAAACAGGGGCGCGGACAGGGCGGAGGTGGGCGCGCTTTCCCG	23700
QY	23701	CACGCGCGATTTTGGCAAAATGGCGGACCGGACGCGCGGTTGGAACGGCGGACGTCA	23760

[illegible]

Qy	26221	CCCCGAGGGTCCCCGGGTCCCGTCCCGAGGGTCCGGGGTCCCGGTTCCCGAGGGT	26280
Db	26222	CCCCGAGGGTCCCCGGGTCCCGTCCCGAGGGTCCGGGGTCCCGGTTCCCGAGGGT	26280
Qy	26281	CCCCGGGTCCCGTCCCGAGGGTCCGGGGTCCCGGTTCCCGAGGGTCCGGGGTCC	26340
Db	26281	CCCCGGGTCCCGTCCCGAGGGTCCGGGGTCCCGGTTCCCGAGGGTCCGGGGTCC	26340
Qy	26341	CCGTTCCCGAGGGTCCCGGGTCCCGGTTCCCGAGGGTCCGGGGTCCCGGTTCCCG	26400
Db	26341	CCGTTCCCGAGGGTCCCGGGTCCCGGTTCCCGAGGGTCCGGGGTCCCGGTTCCCG	26400
Qy	26401	AGGGTCCCGGGTCCCGGTTCCCGAGGGTCCGGGGTCCCGGTTCCCGAGGGTCCCG	26460
Db	26401	AGGGTCCCGGGTCCCGGTTCCCGAGGGTCCGGGGTCCCGGTTCCCGAGGGTCCCG	26460
Qy	26461	GCTCCCGGTTCCCGAGGGTCCCGGGTCCCGGTTCCCGAGGGTCCGGGGTCCCGGTT	26520
Db	26461	GCTCCCGGTTCCCGAGGGTCCCGGGTCCCGGTTCCCGAGGGTCCGGGGTCCCGGTT	26520
Qy	26521	CCCCGATTCAAGGTTAAGGTTTATAGCAAAACAGTTTTCGCGGTTGGG	26580
Db	26521	CCCCGATTCAAGGTTAAGGTTTATAGCAAAACAGGTTTTCGCGGTTGGG	26580
Qy	26581	TTGTACATACACGCGGGTGGCATTTGGCCCGCATCAAAAAATTAAGTTGGGTTCC	26640
Db	26581	TTGTACATACACGCGGGTGGCATTTGGCCCGCATCAAAAAATTAAGTTGGGTTCC	26640
Qy	26641	GAACCGGTAAGTCTTTAGTCTTATAGCAAGTCTTTCGTCACGGTAGAGTGTGA	26700
Db	26641	GAACCGGTAAGTCTTTAGTCTTATAGCAAGTCTTTCGTCACGGTAGAGTGTGA	26700
Qy	26701	GTTTGTGAGGAATGCAACAGTAGTCCGCTACCGGGAAAGGAACGTTTAA	26760
Db	26701	GTTTGTGAGGAATGCAACAGTAGTCCGCTACCGGGAAAGGAACGTTTAA	26760
Qy	26761	CCGAGTGTACCGCGGTGGCATAGGTTTAACTGCAACTCCGGTCCCGGCGTGG	26820
Db	26761	CCGAGTGTACCGCGGTGGCATAGGTTTAACTGCAACTCCGGTCCCGGCGTGG	26820
Qy	26821	TACCTTAAGTTTACGTAGCAATTAAGCGGCTGTTACAGGCGCTCCCGCCCTGA	26880
Db	26821	TACCTTAAGTTTACGTAGCAATTAAGCGGCTGTTACAGGCGCTCCCGCCCTGA	26880
Qy	26881	GGAAGAAATGAATAATCTTGGCAGTTGAGTTATAGTAGAGGCAATCTTCTTA	26940
Db	26881	GGAAGAAATGAATAATCTTGGCAGTTGAGTTATAGTAGAGGCAATCTTCTTA	26940
Qy	26941	CTGTGGCTCGGGAGGCGAGTACTTGACACATCCGTTTAAAGCAAT	27000
Db	26941	CTGTGGCTCGGGAGGCGAGTACTTGACACATCCGTTTAAAGCAAT	27000
Qy	27001	TATCAGGCGCTTCTCAAGACAGCGCTCGCTTACGAGAGGCTCTTGGCCACACGA	27060
Db	27001	TATCAGGCGCTTCTCAAGACAGCGCTCGCTTACGAGAGGCTCTTGGCCACACGA	27060
Qy	27061	TTACCGCTCTGTGGGGAGCTAAAGCCATAGGCCAGAGGATGCTGAATAAACACGA	27120
Db	27061	TTACCGCTCTGTGGGGAGCTAAAGCCATAGGCCAGAGGATGCTGAATAAACACGA	27120
Qy	27121	CGAGCGCACACGCGGGTGGCGTTTGGCGTTTGGTGTGTGTGTGTGTGTGTGTGT	27180
Db	27121	CGAGCGCACACGCGGGTGGCGTTTGGCGTTTGGTGTGTGTGTGTGTGTGTGTGT	27180
Qy	27181	TAAAGTTAAAGACAGACGCTTTTAAAGTTGCCATAGCCGTTTACCGGTGACGC	27240
Db	27181	TAAAGTTAAAGACAGACGCTTTTAAAGTTGCCATAGCCGTTTACCGGTGACGC	27240
Qy	27241	GTCAGAGCGCTGAGTCTAGTGTTCGTTACAGGGGAATGGAGGACACAGAA	27300
Db	27241	GTCAGAGCGCTGAGTCTAGTGTTCGTTACAGGGGAATGGAGGACACAGAA	27300
Qy	27301	TTACTGGACGAATACGTAGGATCGCCGCAACGCGAGAGACATGTCTACGAGT	27360
Db	27301	TTACTGGACGAATACGTAGGATCGCCGCAACGCGAGAGACATGTGTACGAGT	27360
Qy	27361	TGGGCTGTCTTGTGGCGTACTGTGCGCTGTTTGCATCAGCGGATAGTGTCTTGA	27420
Db	27361	TGGGCTGTCTTGTGGCGTACTGTGCGCTGTTTGCATCAGCGGATAGTGTCTTGA	27420
Qy	27421	ACCGGATTTCCCGACCGTAAAGAGCGGATGATATGAGCAATTAACA	27480
Db	27421	ACCGGATTTCCCGACCGTAAAGAGCGGATGATATGAGCAATTAACA	27480
Qy	27481	AAACAACTAAGGATGATTTCTTGAACATTTTATTTAGACATCTCCGAGACA	27540
Db	27481	AAACAACTAAGGATGATTTCTTGAACATTTTATTTAGAGATCTCCGAGACA	27540
Qy	27541	TTTTTTTATCTGTGACACGGGGCGGCTGTGCGCTCCACCGGGCCCGCGG	27600
Db	27541	TTTTTTTATCTGTGACACGGGGCGGCTGTGCGCTCCACCGGGCCCGCGG	27600
Qy	27601	ACTGCGCATTTCTGATCGAGGGGCGGACGCGCCAGCGGGGGGAGAGCTGAG	27660
Db	27601	ACTGCGCATTTCTGATCGAGGGGCGGACGCGCCAGCGGGGGGAGAGCTTAA	27660
Qy	27661	GAATGGGTTGACATTACAGATTCTTGGGCGGGGGGCTGAGTTGCCGCTGCTGG	27720
Db	27661	GAATGGGTTGACATTACAGATTCTTGGGCGGGGGGCTGAGTTGCCGCTGCTGG	27720
Qy	27721	CGAGACGGGCTGTGGCTCGCGGCTGCGGGGGCGTGTGCTTGTGCTGCTGCT	27780
Db	27721	CGAGACGGGCTGTGGCTCGCGGCTGCGGGGGCGTGTGCTTGTGCTGCTGCT	27780
Qy	27781	GCGGCTCTGTTAGGCTGTGGGCGTGGAGATGGTGTGCTCCGGAATACACTGG	27840
Db	27781	GCGGCTCTGTTAGGCTGTGGGCGTGGAGATGGTGTGCTCCGGAATACACTGG	27840
Qy	27841	GTTGTTAGCTAGGTTAGGCGCACAGCGCTGTGTGCGCACAGAACTGAACGGGCG	27900
Db	27841	GTTGTTAGCTAGGTTAGGCGCACAGCGCTGTGTGCGCACAGAACTGAACGGGCG	27900
Qy	27901	GTTGTTAGCTAGGTTAGGCGCACAGCGCTGTGTGCGCACAGAACTGAACGGGCG	27960
Db	27901	GTTGTTAGCTAGGTTAGGCGCACAGCGCTGTGTGCGCACAGAACTGAACGGGCG	27960
Qy	27961	GGTCCCTCAGATCCGCTGAATGTCAATATTTTGAACAGCGCATGACGCTTGT	28020
Db	27961	GGTCCCTCAGATCCGCTGAATGTCAATATTTTGAACAGCGCATGACGCTTGT	28020
Qy	28021	GATGCGGACCTCTCGCTGGAACAACGGGCTGTGGAAGCTCCACGTCCTGTTGC	28080
Db	28021	GATGCGGACCTCTCGCTGGAACAACGGGCTGTGGAAGCTCCACGTCCTGTTGC	28080
Qy	28081	GCTTCTGTGGCGAGCGTCCGAGCGTATAGCCGTAAGTGTGGAGATAGTACGTGGCCG	28140
Db	28081	GCTTCTGTGGCGAGCGTCCGAGCGTATAGCCGTAAGTGTGGAGATAGTACGTGGCCG	28140
Qy	28141	CATACGAGAGGTTGGGGGCAAAACGCTGAAGGAAAGGATGTCGAGCGGGCG	28200
Db	28141	CATACGAGAGGTTGGGGGCAAAACGCTGAAGGAAAGGATGTCGAGCGGGCG	28200
Qy	28201	GTCGTTAGATGGAGGCTACGTCAGCGGGGCTATCCAGATGATACGCGCGCTTG	28260
Db	28201	GTCGTTAGATGGAGGCTACGTCAGCGGGGCTATCCAGATGATACGCGCGCTTG	28260
Qy	28261	CCGCGATCAGAGGTGGCGCAAAACGTAAGTGTGGCTGTGCTGCTGCTATTCGA	28320
Db	28261	CCGCGATCAGAGGTGGCGCAAAACGTAAGTGTGGCTGTGCTGCTGCTATTCGA	28320
Qy	28321	GACTGCTGTGACCATATGATGCAAGAGTCTTGGGAAATGTATGTGTCTCCGGA	28380
Db	28321	GACTGCTGTGACCATATGATGCAAGAGTCTTGGGAAATGTATGTGTCTCCGGA	28380
Qy	28381	GGCGCTCATAGTTCCGGGTGTGCGGTTACCGCAGTGTGACGCGAGGAAACTGGCTTG	28440

D	28381	GGGCGCTCAGGTGTGGGTGTGGGTATCCCGAGTGTGAGGGGAAACCTGGCTTG	28440	
O	28441	CCTTTAAATACGTACTTCTCGGAGACTGGCCACGGCTTATCTGTTTGAGCAGGTCTG	28500	
D	28441	CCTTTAAATACGTACTTCTCGGAGACTGGCCACGGCTTATCTGTTTGAGCAGGTCTG	28500	
O	28501	TGCGATCTCGGATTAATCCGGCGTCGATGCGCTTGCCATCAGTGTCTCAAGAGGGCGG	28560	
D	28501	TGCGATCTCGGATTAATCCGGCGTCGATGCGCTTGCCATCAGTGTCTCAAGAGGGCGG	28560	
O	28561	GGAATTCGCGGTGTGACCTGACGCTTGGCAAAAGATCTAAACATGACCGTTATTTAC	28620	
D	28561	GGAATTCGCGGTGTGACCTGACGCTTGGCAAAAGATCTAAACATGACCGTTATTTAC	28620	
O	28621	CGGCTTCCTCGCGTAAGAGATCAAACTTGAGAGCAGCCATGAGGGTCTGGCTCGT	28680	
D	28621	CGGCTTCCTCGCGTAAGAGATCAAACTTGAGAGCAGCCATGAGGGTCTGGCTCGT	28680	
O	28681	AAACGGCGATTAACCCCTACGCTCCAGTGCGCACAGAGAGAGAGCTGTAACGCGG	28740	
D	28681	AAACGGCGATTAACCCCTACGCTCCAGTGCGCACAGAGAGAGAGCTGTAACGCGG	28740	
O	28741	GGGGGATTTGGGGTCTGACCTGCTTGGGTGGAGGGAGCAGAGAGGAGACTCCGGGA	28800	
D	28741	GGGGGATTTGGGGTCTGACCTGCTTGGGTGGAGGGAGCAGAGAGGAGACTCCGGGA	28800	
O	28801	GCCATGTGTATTAACATCTCCACAGAGGGGTCCGAGAGCATGGGGTTTACCTGATCTGGG	28860	
D	28801	GCCATGTGTATTAACATCTCCACAGAGGGGTCCGAGAGCATGGGGTTTACCTGATCTGGG	28860	
O	28861	CGGCTCGGAGTCCCCCGGAGCGGTGACGCCAGGGCCAAAGAAATGCTGGCTGTTAGCT	28920	
D	28861	CGGCTCGGAGTCCCCCGGAGCGGTGACGCCAGGGCCAAAGAAATGCTGGCTGTTAGCT	28920	
O	28921	TGCCAGGCAATATCCCGTGTACTTGTGAAGAGACCGATGTTGTACCTAGCTAGTGGG	28980	
D	28921	TGCCAGGCAATATCCCGTGTACTTGTGTGAAGAGACCGATGTTGTACCTAGCTAGTGGG	28980	
O	28981	CTTTCGGGGAGTGTCTATGTTTATCGGTAGAGGGGTCCGTATACGGGAGACGAGTCCGA	29040	
D	28981	CTTTCGGGGAGTGTCTATGTTTATCGGTAGAGGGGTCCGTATACGGGAGACGAGTCCGA	29040	
O	29041	CGATTGAGGGCTCTAATATACACTCTCTTCTATCTTGGTAGGCTGACACAGTCCACCT	29100	
D	29041	CGATTGAGGGCTCTAATATACACTCTCTTCTATCTTGGTAGGCTGACACAGTCCACCT	29100	
O	29101	ATCCCCCAACGTACACGGGAGTCAATGTTGGGTGCGTGTGAGGAGGAGATGA	29160	
D	29101	ATCCCCCAACGTACACGGGAGTCAATGTTGGGTGCGTGTGAGGAGGAGATGA	29160	
O	29161	GGGCGGTCCTTCGGGGGCTGATGTGGCGGTTATCCGTTGTGAGATTTAATACGTTTC	29220	
D	29161	GGGCGGTCCTTCGGGGGCTGATGTGGCGGTTATCCGTTGTGAGATTTAATACGTTTC	29220	
O	29221	TGCCCTGGGAGTCAAGTTCCTACCTGTGTGCGAATGTACACTACGCTCTTA	29280	
D	29221	TGCCCTGGGAGTCAAGTTCCTACCTGTGTGCGAATGTACACTACGCTCTTA	29280	
O	29281	ACGTGACCTTCTGAAGAGGAAATGCGCAATACCGGAACGAGGGACGATATTGTCCTG	29340	
D	29281	ACGTGACCTTCTGAAGAGGAAATGCGCAATACCGGAACGAGGGACGATATTGTCCTG	29340	
O	29341	GGCGTAAGGTTCCGGTGAAGTCTGGAATAATCGTTTACGATGGTTAAAGAGATGGGGG	29400	
D	29341	GGCGTAAGGTTCCGGTGAAGTCTGGAATAATCGTTTACGATGGTTAAAGAGATGGGGG	29400	
O	29401	TTTCTGACGCAACGTTGCTCTGAGAAACCAAGGGGGCTGTGGCTTACTTCAACG	29460	
D	29401	TTTCTGACGCAACGTTGCTCTGAGAAACCAAGGGGGCTGTGGCTTACTTCAACG	29460	
O	29461	GGCGTCGCGCTGTAAAGGCTAGGGAGTACGTTTGGCAACGCGGGGTTAAGCC	29520	
D	29461	GGCGTCGCGCTGTAAAGGCTAGGGAGTACGTTTGGCAACGCGGGGTTAAGCC	29520	
D	29461	GGCGTCGCGCTGTAAAGGCTAGGGAGTACGTTTGGCAACGCGGGGTTAAGCC	29520	
O	29521	ACAGCGTACGCGTGTTCGGAAGAAACCTAACGGATGGGAATATCTATTAACCTAGGCA	29580	
D	29521	ACAGCGTACGCGTGTTCGGAAGAAACCTAACGGATGGGAATATCTATTAACCTAGGCA	29580	
O	29581	GGGTATACCATGTGCGCTGCTTGTGGCACTAGCTACTGTTTGGCGTTTGGGGGACG	29640	
D	29581	GGGTATACCATGTGCGCTGCTTGTGGCACTAGCTACTGTTTGGCGTTTGGGGGACG	29640	
O	29641	CTGACACGAGCCGCGGTGAGTGTGGCGGCAAGATTTTATACCTACTTAATTA	29700	
D	29641	CTGACACGAGCCCTGGTGTGAGTGTGGCGGCAAGATTTTATACCTACTTAATTA	29700	
O	29701	TTTTCGGCCACATTAATGCGCAGGAAGTCAATCTTGAACAGGTGGGAAGCTCCGGGTACG	29760	
D	29701	TTTTCGGCCACATTAATGCGCAGGAAGTCAATCTTGAACAGGTGGGAAGCTCCGGGTACG	29760	
O	29761	GTTGCTTGTGAGGAGTGTGTGCGATGTTTCGGCGGTACACGGGATTCGGCGGTGGG	29820	
D	29761	GTTGCTTGTGAGGAGTGTGTGCGATGTTTCGGCGGTACACGGGATTCGGCGGTGGG	29820	
O	29821	ATTTGCGTCGCGGGTCCGGGTTAAGCTCTCAACAGAGGAGTACTGTTTGGCTTCA	29880	
D	29821	ATTTGCGTCGCGGGTCCGGGTTAAGCTCTCAACAGAGGAGTACTGTTTGGCTTCA	29880	
O	29881	ATAACAGCTAGTGTAGGCTCCCTCACACTACCGACGTGGCGAGCGGACGATATCCAG	29940	
D	29881	ATAACAGCTAGTGTAGGCTCCCTCACACTACCGACGTGGCGAGCGGACGATATCCAG	29940	
O	29941	GACCAAAAATTAACCTCTGTGTAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	30000	
D	29941	GACCAAAAATTAACCTCTGTGTAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	30000	
O	30001	GTTGTCACAGCCGGGGGGGAGTGGTGGCAAGAGATGGGGGCGCAGGCTTCTCGCGCT	30060	
D	30001	GTTGTCACAGCCGGGGGGGAGTGGTGGCAAGAGATGGGGGCGCAGGCTTCTCGCGCT	30060	
O	30061	TAAACGTACGACGTTTGAAGCTGATACAGCTGCGCAGCGTCCGTGAACGTAGCTTTTG	30120	
D	30061	TAAACGTACGACGTTTGAAGCTGATACAGCTGCGCAGCGTCCGTGAACGTAGCTTTTG	30120	
O	30121	GTTCAAGATGTAAAGATTTGCTTAATCTGGAACCGGTGACAGTTGGAGCAAGCAAGT	30180	
D	30121	GTTCAAGATGTAAAGATTTGCTTAATCTGGAACCGGTGACAGTTGGAGCAAGCAAGT	30180	
O	30181	GTTTGTAGATGGATATGGCTTGGCTCCAGCCCGCTAGATACGACCCGGGAAACA	30240	
D	30181	GTTTGTAGATGGATATGGCTTGGCTCCAGCCCGCTAGATACGACCCGGGAAACA	30240	
O	30241	AAACGACGTGGGGGCTGTGCGCGCGCAAGAAATGGGGAGATGTAAATTTCTGTGAG	30300	
D	30241	AAACGACGTGGGGGCTGTGCGCGCGCAAGAAATGGGGAGATGTAAATTTCTGTGAG	30300	
O	30301	GAATCAAAAATTTCTCCCTTTTAAGGATGTGTGAACCGGAGGGGTCTTACCTT	30360	
D	30301	GAATCAAAAATTTCTCCCTTTTAAGGATGTGTGAACCGGAGGGGTCTTACCTT	30360	
O	30361	GGAATAATCTCCACCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	30420	
D	30361	GGAATAATCTCCACCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	30420	
O	30421	GATTTGGGCGACGCTCAATAGCAGTAAACCAAACTAAGCCTAGTCCGAGAGGCGC	30480	
D	30421	GATTTGGGCGACGCTCAATAGCAGTAAACCAAACTAAGCCTAGTCCGAGAGGCGC	30480	
O	30481	GGCTCGGAGGTTCCATTTGGTATGCTTGAAGGAGGAGGAGGAGGAGGAGGAGGAGG	30540	
D	30481	GGCTCGGAGGTTCCATTTGGTATGCTTGAAGGAGGAGGAGGAGGAGGAGGAGGAGG	30540	
O	30541	CGCAAGGATGTATACGAGATCTGTGTCAAGTGTGCTGACCGGTACCGGGGTTTGGAAAC	30600	
D	30541	CGCAAGGATGTATACGAGATCTGTGTCAAGTGTGCTGACCGGTACCGGGGTTTGGAAAC	30600	

Qy 30601 GGGTAGAGTCCGCTCTGTGCCAACGTCCGATATCATCAGTGTGTTGTAAGAAGTCCGC 30660
| | | | |
Db 30601 GGGTAGAGTCCGCTCTGTGCCAACGTCCGATATCATCAGTGTGTTGTAAGAAGTCCGC 30660
Qy 30661 GTTGTACTTGTGTTCTTGTGTTAGGGGCGCTAGAGAGCGCGTTGCCCTCGATTCGANT 30720
| | | | |
Db 30661 GTTGTACTTGTGTTCTTGTGTTAGGGGCGCTAGAGAGCGCGTTGCCCTCGATTCGANT 30720
Qy 30721 TGTAACTCGAAGACCGAGCCCTCTGTGTTGTTTAAAGTGAAGAGAACGTCGCGAG 30780
| | | | |
Db 30721 TGTAACTCGAAGACCGAGCCCTCTGTGTTGTTTAAAGTGAAGAGAACGTCGCGAG 30780
Qy 30781 CTGTTGCCGAGTTATCCAGAGCGCGTTTCGAGTTGGCGGCAACGGGGATACCTGTCGC 30840
| | | | |
Db 30841 GTGACAGTAGTACCCGTTGAGAGAGCACAGCGCGCGCTGCCGTGCCATACGTTGGGAC 30900
| | | | |
Qy 30901 ATCCGCGTAAAGTCTGTGTGATCGAGCGCGCTGTGAGATTAAGGACAGCATTAAGCT 30960
| | | | |
Db 30901 ATCCGCGTAAAGTCTGTGTGATCGAGCGCGCTGTGAGATTAAGGACAGCATTAAGCT 30960
Qy 30961 TAGAGAGTGGAGTTTGAAGTTGTTGTGCTCCGCAAAATCTGGGGGAACACCCCTGCG 31020
| | | | |
Db 30961 TAGAGAGTGGAGTTTGAAGTTGTTGTGCTCCGCAAAATCTGGGGGAACACCCCTGCG 31020
Qy 31021 TTGCATGGCGTTATCTGTGAGGCTACTGTACCAAGCGCGCTATTTGTGGACCATTTGCTT 31080
| | | | |
Db 31021 TTGCATGGCGTTATCTGTGAGGCTACTGTACCAAGCGCGCTATTTGTGGACCATTTGCTT 31080
Qy 31081 TTGGTCACTAGACAGGCTTGGCAGAGCTCCAGAGGAGATCTGGTTTACCGTAATCC 31140
| | | | |
Db 31081 TTGGTCACTAGACAGGCTTGGCAGAGCTCCAGAGGAGATCTGGTTTACCGTAATCC 31140
Qy 31141 CGGGTCTCCGGGGCTATTTGACAGAGACGCTCTCCATGTCTCTGCGGGGAGTTT 31200
| | | | |
Db 31141 CGGGTCTCCGGGGCTATTTGACAGAGACGCTCTCCATGTCTCTGCGGGGAGTTT 31200
Qy 31201 GGGTGGGGGTTTGTGATGTTTGGGCAATTTGGCGTTCCCTGCCCGGGGACCCGATGTC 31260
| | | | |
Db 31201 GGGTGGGGGTTTGTGATGTTTGGGCAATTTGGCGTTCCCTGCCCGGGGACCCGATGTC 31260
Qy 31261 CCCGACCATGTTTGAATGTTTCTAGGTCGCGCATGACCACTTCTGTTCCGTTGGTG 31320
| | | | |
Db 31261 CCCGACCATGTTTGAATGTTTCTAGGTCGCGCATGACCACTTCTGTTCCGTTGGTG 31320
Qy 31321 CGTTTGGACGACGTTGCTAGTTCAGCCGAGAGAGTTTTCGACGCTGTGAACCT 31380
| | | | |
Db 31321 CGTTTGGACGACGTTGCTAGTTCAGCCGAGAGAGTTTTCGACGCTGTGAACCT 31380
Qy 31381 TAGCGCCAGCTGTGATTTCCCATCACAACGCGTTCTTCTTCTATCAGAGATG 31440
| | | | |
Db 31381 TAGCGCCAGCTGTGATTTCCCATCACAACGCGTTCTTCTTCTATCAGAGATG 31440
Qy 31441 TTTGTAATTAACAGACGTTGTTGATGTTGGGGGCCCAAAAGTTGGGTAATTTGCGG 31500
| | | | |
Db 31441 TTTGTAATTAACAGACGTTGTTGATGTTGGGGGCCCAAAAGTTGGGTAATTTGCGG 31500
Qy 31501 CGCTGTTTTCGTTGGGTATCTCATACAGCATTTTTCGACGTGGCATCTTCCCATTTGCG 31560
| | | | |
Db 31501 CGCTGTTTTCGTTGGGTATCTCATACAGCATTTTTCGACGTGGCATCTTCCCATTTGCG 31560
Qy 31561 TAAAGAACCCGTTAAGCGCGCGCGAGCTGTGTTGATTAATGTAAGCGGAAACGCTGATG 31620
| | | | |
Db 31561 TAAAGAACCCGTTAAGCGCGCGCGAGCTGTGTTGATTAATGTAAGCGGAAACGCTGATG 31620
Qy 31621 ACTGAGTATGAATGTTTAAAGTGTGTTCTGTTCTTAATAGAGCCAGGCGCTTACG 31680
| | | | |
Db 31621 ACTGAGTATGAATGTTTAAAGTGTGTTCTGTTCTTAATAGAGCCAGGCGCTTACG 31680

Qy 31681 ACCAGTTTCTGTGCTCTTGGCGCGGCTGCTATATATGACAGGAATCTGTCAATT 31740
| | | | |
Db 31681 ACCAGTTTCTGTGCTCTTGGCGCGGCTGCTATATATGACAGGAATCTGTCAATT 31740
Qy 31741 GGTGTAGCCCTGCCATCGCTGTATATTTTATTGGCTTCCGGGAATACACCCCGC 31800
| | | | |
Db 31741 GGTGTAGCCCTGCCATCGCTGTATATTTTATTGGCTTCCGGGAATACACCCCGC 31800
Qy 31801 TTAGCACGTTCTAGTTCAATTAAGTACAGAGCTTTTGTGTTGCTGTTTAAACGGTA 31860
| | | | |
Db 31801 TTAGCACGTTCTAGTTCAATTAAGTACAGAGCTTTTGTGTTGCTGTTTAAACGGTA 31860
Qy 31861 GCACACAATCTGTAATTCGCTACCTAGAGGAACCTCGAAAAAATCCTAAATTTAACG 31920
| | | | |
Db 31861 GCACACAATCTGTAATTCGCTACCTAGAGGAACCTCGAAAAAATCCTAAATTTAACG 31920
Qy 31921 TTTTGTGTTGCCCTAGTGTGGGGGAATGAAAGAACTTAAATATCAAGCGAGC 31980
| | | | |
Db 31921 TTTTGTGTTGCCCTAGTGTGGGGGAATGAAAGAACTTAAATATCAAGCGAGC 31980
Qy 31981 GGTGTTGATTAACCGTCGATACTGCTAAGTGGGCGCGAGTTCCAGCCGTTTGGCGTG 32040
| | | | |
Db 31981 GGTGTTGATTAACCGTCGATACTGCTAAGTGGGCGCGAGTTCCAGCCGTTTGGCGTG 32040
Qy 32041 AGCCCGGAAGGGCTTCGAGGGTCCGACGTCCTTAATGATTTGCAAAACCCATGCGCG 32100
| | | | |
Db 32041 AGCCCGGAAGGGCTTCGAGGGTCCGACGTCCTTAATGATTTGCAAAACCCATGCGCG 32100
Qy 32101 AAGAGGTCCTGGCTTTGGCAGACAGCTTGTCCGTCATATCGGGATCGGAAGCTTAAT 32160
| | | | |
Db 32101 AAGAGGTCCTGGCTTTGGCAGACAGCTTGTCCGTCATATCGGGATCGGAAGCTTAAT 32160
Qy 32161 GGGAGAGTCTTCCGACGATCTGATGACGTTGACACCGAAGACCGATCTTGAGTATG 32220
| | | | |
Db 32161 GGGAGAGTCTTCCGACGATCTGATGACGTTGACACCGAAGACCGATCTTGAGTATG 32220
Qy 32221 ATGATGTGTTCCCGGTGATAGATACGACGGCTTAATGAGCCCTGGAAGTCAAACTATG 32280
| | | | |
Db 32221 ATGATGTGTTCCCGGTGATAGATACGACGGCTTAATGAGCCCTGGAAGTCAAACTATG 32280
Qy 32281 ACGTACCAAGTCTCCGACGTCGCGGAACCGCTGGGAATTAATCTGACCCCGGACCCCTGATG 32340
| | | | |
Db 32281 ACGTACCAAGTCTCCGACGTCGCGGAACCGCTGGGAATTAATCTGACCCCGGACCCCTGATG 32340
Qy 32341 CACATCCGAGGTGCGCGCTTAAAGGGGCTGTGCCGGGGGTGCGCGCTGCCAAGG 32400
| | | | |
Db 32341 CACATCCGAGGTGCGCGCTTAAAGGGGCTGTGCCGGGGGTGCGCGCTGCCAAGG 32400
Qy 32401 TGTCCGCTTCTCGGCTAGACTCAATATGTTGACAGACAGATTTGGGATAGAGAGA 32460
| | | | |
Db 32401 TGTCCGCTTCTCGGCTAGACTCAATATGTTGACAGACAGATTTGGGATAGAGAGA 32460
Qy 32461 CCGCGACCTTAACGGGGCTAGTTCCTCCGAGAGGACACGAAATATGCGGAATAC 32520
| | | | |
Db 32461 CCGCGACCTTAACGGGGCTAGTTCCTCCGAGAGGACACGAAATATGCGGAATAC 32520
Qy 32521 CGGAGCGTACTACTACAGCGCCGCTTGAAGCGGAGACGAAGAAATTTCACTCCGCGC 32580
| | | | |
Db 32521 CGGAGCGTACTACTACAGCGCCGCTTGAAGCGGAGACGAAGAAATTTCACTCCGCGC 32580
Qy 32581 GTAGGGGTGCAATCTCGGGACCTCTGTCGACAAAACTAGTCAGCGTCCGGGTTAACAC 32640
| | | | |
Db 32581 GTAGGGGTGCAATCTCGGGACCTCTGTCGACAAAACTAGTCAGCGTCCGGGTTAACAC 32640
Qy 32641 GTAAAGCTAAAGCTGCTGAGTGTATTTAAAACTTCTGCTCGGATTAAGAGCATG 32700
| | | | |
Db 32641 GTAAAGCTAAAGCTGCTGAGTGTATTTAAAACTTCTGCTCGGATTAAGAGCATG 32700
Qy 32701 ATGCTAAGTGTATGATACCGAGCGCGGTTTACCGTTCATCTCATGACCGCATC 32760
| | | | |
Db 32701 ATGCTAAGTGTATGATACCGAGCGCGGTTTACCGTTCATCTCATGACCGCATC 32760
Qy 32761 CTATGACGAATATGAAGATCCCTTTTAATCTATAGAGGGGCTCATGGGTGTGAA 32820
| | | | |

```
Db 32761 CTAATGCGAATATATGAAATGCTTTTATATCTATCTAGAGGGGGCATGGGCTTGGAA 32820
Qy 32821 AAACAACGCTATTTGAATTCATGACAGCGATGTCGCCAGAGAAACGTTTAAAGTGC 32880
Db 32821 AAACAACGCTATTTGAATTCATGACAGCGATGTCGCCAGAGAAACGTTTAAAGTGC 32880
Qy 32881 CCGAGCCCATGAAATTTTGGAGCTGTGTTTATTCAAATTCCTTAAAGAACAGCGAGA 32940
Db 32881 CCGAGCCCATGAAATTTTGGAGCTGTGTTTATTCAAATTCCTTAAAGAACAGCGAGA 32940
Qy 32941 TATGTTAGCAAGGCAACCCAGGGAATTTATCATCTTCGCTCGCTATACGGGTGCACA 33000
Db 32941 TATGTTAGCAAGGCAACCCAGGGAATTTATCATCTTCGCTCGCTATACGGGTGCACA 33000
Qy 33001 GCAAGTTTGGCTACCGTTTCGTGCGACAGCCGCGCATCGGTCCCAACCTGCACACGT 33060
Db 33001 GCAAGTTTGGCTACCGTTTCGTGCGACAGCCGCGCATCGGTCCCAACCTGCACACGT 33060
Qy 33061 GCGTGGTGGGAAACGGTAGACAAAGCCAGCAATTTGATGTTTGAACAGACCTTAC 33120
Db 33061 GCGTGGTGGGAAACGGTAGACAAAGCCAGCAATTTGATGTTTGAACAGACCTTAC 33120
Qy 33121 TGTCCGCAACGGTGGTTTTCGGTGTGTCAGTTAAGTAAACAGGCTAAGCCGAGATC 33180
Db 33121 TGTCCGCAACGGTGGTTTTCGGTGTGTCAGTTAAGTAAACAGGCTAAGCCGAGATC 33180
Qy 33181 ATCTGTTTCAAAATCCATCTCTTCTTCGCGACAGACGCGCATGTGTGTTTGGCTAA 33240
Db 33181 ATCTGTTTCAAAATCCATCTCTTCTTCGCGACAGACGCGCATGTGTGTTTGGCTAA 33240
Qy 33241 CGCTCAACAGTTGCGAGGCGCACAGGCGCATTCAAAGTGGAGCCGTAAAGAAAGAAAG 33300
Db 33241 CGCTCAACAGTTGCGAGGCGCACAGGCGCATTCAAAGTGGAGCCGTAAAGAAAGAAAG 33300
Qy 33301 GAATCACGCAAAACTACTTGCACAGAGTAGCGTGGGCGTACCATGCGCTGTCTGACGT 33360
Db 33301 GAATCACGCAAAACTACTTGCACAGAGTAGCGTGGGCGTACCATGCGCTGTCTGACGT 33360
Qy 33361 GGGTGTATGATGCAATATCTCACACGAGCAAAATGGTTGAGTGTGTACAAACTGTGT 33420
Db 33361 GGGTGTATGATGCAATATCTCACACGAGCAAAATGGTTGAGTGTGTACAAACTGTGT 33420
Qy 33421 CCATAGAGAGCAATATGCAATATGCAATTCAGATTCGATCGTTTCTAACCTTACAA 33480
Db 33421 CCATAGAGAGCAATATGCAATATGCAATTCAGATTCGATCGTTTCTAACCTTACAA 33480
Qy 33481 AACTACATGAACAGAGATGATACCATGTCGAGAAATGTAGATGGTTAAAGAAC 33540
Db 33481 AACTACATGAACAGAGATGATACCATGTCGAGAAATGTAGATGGTTAAAGAAC 33540
Qy 33541 ACGTGAACCTTAAATGAGGTCTGTTGGGACTCTTTAAAGAGCTACGAAAGCTTCAATTT 33600
Db 33541 ACGTGAACCTTAAATGAGGTCTGTTGGGACTCTTTAAAGAGCTACGAAAGCTTCAATTT 33600
Qy 33601 TTAATGTTGACCCAGAGAGAAACATCTAGATGCGGTGGCTCTGGGGAATATTATAG 33660
Db 33601 TTAATGTTGACCCAGAGAGAAACATCTAGATGCGGTGGCTCTGGGGAATATTATAG 33660
Qy 33661 GGCAGGTGATGTCAAATGAGGTATTTAAACAGAGCAATGAACTGGCCAGCTCTTGAAA 33720
Db 33661 GGCAGGTGATGTCAAATGAGGTATTTAAACAGAGCAATGAACTGGCCAGCTCTTGAAA 33720
Qy 33721 GCTACATTCAAACGCTAACCAATTTGGAAGGCAATGGCGCTATTAATTTT 33780
Db 33721 GCTACATTCAAACGCTAACCAATTTGGAAGGCAATGGCGCTATTAATTTT 33780
Qy 33781 TTTACTATATATAGGTGTTCTGTAACGAGCAAAATCGTGTATGATGAAATCAATGTA 33840
Db 33781 TTTACTATATATAGGTGTTCTGTAACGAGCAAAATCGTGTATGATGAAATCAATGTA 33840
Qy 33841 GAGTGGATTTAATGGAACATTTTACCAATTTATTTGAGAAAGGTAAAGCAATTA 33900
Db 33841 GAGTGGATTTAATGGAACATTTTACCAATTTATTTGAGAAAGGTAAAGCAATTA 33900

Db 33841 GAGTGGATTTAATGGAACATTTTACCAATTTATTTGAGAAAGGTAAAGCAATTA 33900
Qy 33901 ACATCTATTTGTAATGAGAAATGGCTGATGATGATCTTCTTACTGTGGAACATGTCGTG 33960
Db 33901 ACATCTATTTGTAATGAGAAATGGCTGATGATGATCTTCTTACTGTGGAACATGTCGTG 33960
Qy 33961 ACTTTGGAAAAAGAAAAAGTTTGTCTGCATCAAGTATAGTTATATGATATATATGAC 34020
Db 33961 ACTTTGGAAAAAGAAAAAGTTTGTCTGCATCAAGTATAGTTATATGATATATATGAC 34020
Qy 34021 TATACATTTTGTAAATCTTCAAGTGCACATGATATTAACCTTACGGGTGATTTAATAC 34080
Db 34021 TATACATTTTGTAAATCTTCAAGTGCACATGATATTAACCTTACGGGTGATTTAATAC 34080
Qy 34081 ACTTCTTCCAGGTTTACTGGAATTTTAAATGTAATGACATGCTTTTAAACAGAGC 34140
Db 34081 ACTTCTTCCAGGTTTACTGGAATTTTAAATGTAATGACATGCTTTTAAACAGAGC 34140
Qy 34141 GTTTTATTTACGAACAGTCAATTTATTTACCACTCAACAACTTATGATCTTTTTCAC 34200
Db 34141 GTTTTATTTACGAACAGTCAATTTATTTACCACTCAACAACTTATGATCTTTTTCAC 34200
Qy 34201 GCGGAAAAAATTAATGCAAAATGTTCAAGATTACTTTGATTAATTCGAATGAATTT 34260
Db 34201 GCGGAAAAAATTAATGCAAAATGTTCAAGATTACTTTGATTAATTCGAATGAATTT 34260
Qy 34261 TCCGGCATTTATACAGAAATTTGATATGATATGATATGATATGATATGATATGATAT 34320
Db 34261 TCCGGCATTTATACAGAAATTTGATATGATATGATATGATATGATATGATATGATAT 34320
Qy 34321 AATATGCAATGTGTTGCACTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 34380
Db 34321 AATATGCAATGTGTTGCACTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 34380
Qy 34381 TATGATCTTATGCTGATTTATGTCGCTTAAATAATTCAAATGCTGCTGGGTGAAT 34440
Db 34381 TATGATCTTATGCTGATTTATGTCGCTTAAATAATTCAAATGCTGCTGGGTGAAT 34440
Qy 34441 GCGCGGAAATCTTATATCTCTGATGTTGGCATTTTTCACAAAAATTTTACAGAAATG 34500
Db 34441 GCGCGGAAATCTTATATCTCTGATGTTGGCATTTTTCACAAAAATTTTACAGAAATG 34500
Qy 34501 TTTGTTTCAATATGATATGTCGCTTATGTCGCTTATGTCGCTTATGTCGCTTATG 34560
Db 34501 TTTGTTTCAATATGATATGTCGCTTATGTCGCTTATGTCGCTTATGTCGCTTATG 34560
Qy 34561 GCTATTTGAAGCAAAAGGTCCTGTCNAATTCCTTCAAAATGAAATGATATCTTATCTTC 34620
Db 34561 GCTATTTGAAGCAAAAGGTCCTGTCNAATTCCTTCAAAATGAAATGATATCTTATCTTC 34620
Qy 34621 TTTTGTGAAGTATCTGCAATAATTTTATTTATTTATTTATTTATTTATTTATTTATTT 34680
Db 34621 TTTTGTGAAGTATCTGCAATAATTTTATTTATTTATTTATTTATTTATTTATTTATTT 34680
Qy 34681 GTTAAGTGTGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 34740
Db 34681 GTTAAGTGTGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 34740
Qy 34741 AGGCTCTGTACCAACGTTTATGTTATGAGTAAATTTGGAACGTTTGTGCGATAT 34800
Db 34741 AGGCTCTGTGTACCAACGTTTATGTTATGAGTAAATTTGGAACGTTTGTGCGATAT 34800
Qy 34801 GCGAGTCCAGGTTTATTTACTGCGCGCAATATGATGATATGCTTATGATGATATGAT 34860
Db 34801 GCGAGTCCAGGTTTATTTACTGCGCGCAATATGATGATATGCTTATGATGATATGAT 34860
Qy 34861 CAAGAGTCTGTTTATTTTCAATGTTTAAATTTGATATTAATACCTTAAAGGTGTGTA 34920
Db 34861 CAAGAGTCTGTTTATTTTCAATGTTTAAATTTGATATTAATACCTTAAAGGTGTGTA 34920
Qy 34921 ATTTTAAAGCAATTTGATATTTTCAATTTTCAATTTTCAATTTTCAATTTTCAATTTT 34980
Db 34921 ATTTTAAAGCAATTTGATATTTTCAATTTTCAATTTTCAATTTTCAATTTTCAATTTT 34980
```


OY	34981	CAGTAACCAACACATTTAGCGGAGATGTAATGAACATGTATGAAGTTTAAACAATT	35040
Db	34981		
OY	35041	AAATTAAGCGTACAGATTCCTGTGTGTTTATCCGTAATATTTGTCACATCCATGTGT	35100
Db	35041		
OY	35101	AATATGTAGAGATATCATATATGTATTAATAGAAAGCCGATGACATCCACTA	35160
Db	35101		
OY	35161	TTTCGCGTGTTCCTGCTTTGTTTAAAGTTTAAAGTTTGAATTTAGATGAAGAACAGTA	35220
Db	35161		
OY	35221	CGATCCGACGACCGCAGACGTCAAAAGAACCGGCTCGGAACCTGGCAAGAGACGCTCT	35280
Db	35221		
OY	35281	GCTTTTGGCGGCTTTCACAGCCTTTTACGCCACGCGTATTAACGAGTTTTCATCATTA	35340
Db	35281		
OY	35341	AATTTACAGGCTGGCATGGAAGCAAGTAACCGGCTGATCCGCTTACGAACATCCAG	35400
Db	35341		
OY	35401	TACGTCATAGCTCCGTCGCGCCCTGATACAGCTCGCGTTTACGAGTTTCGGAGGTGTC	35460
Db	35401		
OY	35461	CTTAACACCGGATTTTGTCTCGGCGCTTATCCAAATTTGTTTCATTTTACACCGCC	35520
Db	35461		
OY	35521	GATACCGCTTACACATTCGATATTAACCTTTCCGCCCGGAGATAGATGTGCG	35580
Db	35521		
OY	35581	CTGTGTGATTCGATTTGTTTGAAGCTATGATGAGAACGAGCATACAGCATGATGTAC	35640
Db	35581		
OY	35641	GTGTCAACCCACAGTTCAGCCACTGTTTCCCGTATTCCTCTTTTACACAC	35700
Db	35641		
OY	35701	GATATTTTCAATTCATTTTGTGTTAATGAACAAGGATACCGTTGTGAATTTGG	35760
Db	35701		
OY	35761	GGATTTGACAGAGACGACACTCATGTATTCATTAATTTGCTTTTATTTGAACA	35820
Db	35761		
OY	35821	ATGTCTGCTGTATTTTCTGTTAAGCTGTTTCCATTCCTGACCTTAATTAATAA	35880
Db	35821		
OY	35881	GGCTAAACCTTTAAAGTTGTTCCGTTTCTTTTGGATGCTTACGGGGGAGCTGAGA	35940
Db	35881		
OY	35941	TTAGGAGAACCTCGGATAGAGCGTGCCTCATATTTGATTCATCACTCTCGCCA	36000
Db	35941		
OY	36001	ACTTGAATGGCAGCTTCGATTTTGGGAGGAACATTTAAATAATTTTGTGCGTCCG	36060
Db	36001		
OY	36061	GTATTAATTCGTGCGGAGCCCGCAGCAAACTCGAATACTCTGTGAAGTCTGTGGAC	36120
Db	36061		
OY	36121	TCTATGAGTTTAAACAACACATGCTTCACAGCGCTGTTTACCGCGAGACATG	36180
Db	36121		
OY	36181	GATTCGAAGTATTCCTCTGATAGGCGCGCGCTTACAGCTATTTGCGCTATGACATT	36240
Db	36181		
OY	36241	TTAAAGTAACAGATATTTTCCAAACCCAACTGCAATAGGACGTGCTTTAAAAA	36300
Db	36241		
OY	36301	AGCTTTGATAGCTTTAGTTTAAATTAAGTAAACATTAATAGACTTTGTGCGCGC	36360
Db	36301		
OY	36361	TGCATTAATTCACGCTGTTAAACGCGTAATCCGCGCTCTGCGTATTTGTGCGCGC	36420
Db	36361		
OY	36421	GAACCCATGGCAAAATATGTCTCCAGTAACAGTCCGACTGTACATTTGACTCGCTG	36480
Db	36421		
OY	36481	GTGCTGGCGGTTGCTTGAAGATGATGAAAGTTTATTAATCCGCGGAAGCCGCTTA	36540
Db	36481		
OY	36541	CATTAAGTCGCGGGGCAATTTGATGATCTTCTGCGGCTTTGCCAGCTCGTTTATG	36600
Db	36541		
OY	36601	GTTATCTGTTTGTATTTGTAAGATTAACCGGTGGGCTTACCGTCCGCGAGGAA	36660
Db	36601		
OY	36661	AATGCCCTGCAGTCAAAAAAGAGATTAAGTCAATCAATTTTGAAGTTTACGCTA	36720
Db	36661		
OY	36721	ATTGCTGTCTCTCAAGCAAGCACTTCAATTAAGTGGTCTCAACCAATATACGCTT	36780
Db	36721		
OY	36781	CTCTGCGCTTCTCCGCTTCCACGCAAGCAAGCTGTTTACGCGGTAGGATGGGATGAC	36840
Db	36781		
OY	36841	ACCATTAATTCGACATTAATTAATTCGAGCTTTTGGGCGCTACATGCAATGTTT	36900
Db	36841		
OY	36901	GAATAGATGCTCAATTTTAAACAACAGGGAAGGGAAGGCGTCCCGGAACT	36960
Db	36901		
OY	36961	CCGACCATTTGGGCAAGTGCAGAGATACAGCATGACAGACGTACTCGCGTTGAT	37020
Db	36961		
OY	37021	AGCTCACCGCCCGCCCAACTAAGGACCTTTAATGTGAGATTTTATCATTTGATTTT	37080
Db	37021		
OY	37081	CCTTTGATGTTTCAAGAACCGCAGCGGCTTGGCTTGGGCTTATTTTGTGCTTTATG	37140
Db	37081		
OY	37141	TCTCCAGTAAGTCCCAAAACGCTAATAGTGTGCAATTAACCTCGGCTTTAACTTTGA	37200

```
Db 37141 TCTCCAGTAAGTCCCAACGCTCAATAGTGTGCGAATTAACCGCGGTTTAAAGTTTGA 37200
Qy 37201 AAACGCGTACCGGTCGTACGTATGAAGAACATAAATTTGGCGTTGGCTCTTAACGTGC 37260
Db 37201 AAACGCGTACCGGTCGTACGTATGAAGAACATAAATTTGGCGTTGGCTCTTAACGTGC 37260
Qy 37261 TAAACGTAATTTTTTACTTCGACGATATCTTTGGATGAGGTGGCATTTTTTATATCC 37320
Db 37261 TAAACGTAATTTTTTACTTCGACGATATCTTTGGATGAGGTGGCATTTTTTATATCC 37320
Qy 37321 CAGAAATGCGCATTCGTTTGGCTTTGGTGTGATCATATGATGCGTTTAAAGTCAAA 37380
Db 37321 CAGAAATGCGCATTCGTTTGGCTTTGGTGTGATCATATGATGCGTTTAAAGTCAAA 37380
Qy 37381 CGTACCAAGCGGGGCGGCGGCTTCAGAGGCTCCAGATCCAAACGCAAAACGAAACA 37440
Db 37381 CGTACCAAGCGGGGCGGCGGCTTCAGAGGCTCCAGATCCAAACGCAAAACGAAACA 37440
Qy 37441 TTCACCAAAACACTCGATTAAGCCTTGTAGAGTTGTATTTGGCGCTTTATTTCTGT 37500
Db 37441 TTCACCAAAACACTCGATTAAGCCTTGTAGAGTTGTATTTGGCGCTTTATTTCTGT 37500
Qy 37501 CTCACGCGTGTGAATTTGTGTTTTTCACTGCTATCTATCTAGCATATGAAACGCTTAA 37560
Db 37501 CTCACGCGTGTGAATTTGTGTTTTTCACTGCTATCTATCTAGCATATGAAACGCTTAA 37560
Qy 37561 TATTTGGTTCAATTCATCCGAAAGTTTTTTAAAGAGGCTACCGTATATTTTAAAGAT 37620
Db 37561 TATTTGGTTCAATTCATCCGAAAGTTTTTTAAAGAGGCTACCGTATATTTTAAAGAT 37620
Qy 37621 TGTGCGAGTTGGCCGCTTAAACACAGAACGTTGCATCCGTCTTTACTAGAAACACAGA 37680
Db 37621 TGTGCGAGTTGGCCGCTTAAACACAGAACGTTGCATCCGTCTTTACTAGAAACACAGA 37680
Qy 37681 AGGGAATTTAGTGTGCAGAAACGTCGTGCGCCGCCCGCTACATATGATTTGGTTTC 37740
Db 37681 AGGGAATTTAGTGTGCAGAAACGTCGTGCGCCGCCCGCTACATATGATTTGGTTTC 37740
Qy 37741 AAGCCGCTGAGGCTTAACGCTAGAGTTCCAGTTCCGANTCGAAACCGGGAATTTGCTT 37800
Db 37741 AAGCCGCTGAGGCTTAACGCTAGAGTTCCAGTTCCGANTCGAAACCGGGAATTTGCTT 37800
Qy 37801 CACCGGTAAACACACCTGAGGTTTCCATAGCGAATTAAGTGCACACTGTCGCCGCT 37860
Db 37801 CACCGGTAAACACACCTGAGGTTTCCATAGCGAATTAAGTGCACACTGTCGCCGCT 37860
Qy 37861 TATGTTAAGCTTAATTCAGACCCCGTTGCACAGGTTGTGGAGTAGAACACACACGCT 37920
Db 37861 TATGTTAAGCTTAATTCAGACCCCGTTGCACAGGTTGTGGAGTAGAACACACACGCT 37920
Qy 37921 GAATGACGCTTCTTTCACGAGAAATTTTTTCAATACAAAGTATATGAGGCTGGGAT 37980
Db 37921 GAATGACGCTTCTTTCACGAGAAATTTTTTCAATACAAAGTATATGAGGCTGGGAT 37980
Qy 37981 GTGGAATTAATTCAGACGCTGAGGCTGAGACACACGCTGATTTTGGTATTAATTC 38040
Db 37981 GTGGAATTAATTCAGACGCTGAGGCTGAGACACACGCTGATTTTGGTATTAATTC 38040
Qy 38041 CATATTGATTAATTAACAGATTTTGAAGTTGTGAACCTGATGCTTAATCTGATC 38100
Db 38041 CATATTGATTAATTAACAGATTTTGAAGTTGTGAACCTGATGCTTAATCTGATC 38100
Qy 38101 GAACATGCTGGAAGAGTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 38160
Db 38101 GAACATGCTGGAAGAGTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 38160
Qy 38161 GTTTTATGCGGCTTAAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTCG 38220
Db 38161 GTTTTATGCGGCTTAAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTCG 38220
Qy 38221 CGAAACATGCGCTTAGAGACGAGGCTTTGGCTGGCCCAAGAACTCGGTTAGG 38280
Db 38221 CGAAACATGCGCTTAGAGACGAGGCTTTGGCTGGCCCAAGAACTCGGTTAGG 38280
Db 38281 ATACAGCCTGTGCGACGAATGACACAGCTTTCGCCACAGACATGACATTTGCGAGCG 38340
Qy 38281 ATACAGCCTGTGCGACGAATGACACAGCTTTCGCCACAGACATGACATTTGCGAGCG 38340
Db 38341 GAATTAATGTAATCTGCGGCTGGAACGTTAGATATGATGATTTGACTTTGGCTCAACAAAC 38400
Qy 38341 GAATTAATGTAATCTGCGGCTGGAACGTTAGATATGATGATTTGACTTTGGCTCAACAAAC 38400
Db 38401 GAATTAATGTAATCTGCGGCTGGAACGTTAGATATGATGATTTGACTTTGGCTCAACAAAC 38400
Qy 38401 TACCTGTAGCGTTTTTGGCGGAGTCTTTTGTATTTTCAATTCACCTGATTTTACGTC 38460
Db 38401 TACCTGTAGCGTTTTTGGCGGAGTCTTTTGTATTTTCAATTCACCTGATTTTACGTC 38460
Qy 38461 AAGGATGATTTACTATGTTTGTGATGATGATTAATTCCTGCCACTTTGATGATC 38520
Db 38461 AAGGATGATTTACTATGTTTGTGATGATGATTAATTCCTGCCACTTTGATGATC 38520
Qy 38521 CTGAAATTTGTTTTGCTTTCAGAGGTTTTTAAAGTACCGGATTTGATTCGATTTGTG 38580
Db 38521 CTGAAATTTGTTTTGCTTTCAGAGGTTTTTAAAGTACCGGATTTGATTCGATTTGTG 38580
Qy 38581 AATTAATGCGTTTGGACGCGATGCGATGCGGATGCGGAATCCAAATCCGAAGTAAACC 38640
Db 38581 AATTAATGCGTTTGGACGCGATGCGATGCGGATGCGGAATCCAAATCCGAAGTAAACC 38640
Qy 38641 CAATAATGTTAAATTTTAAATTAATTCAGATGATGATGATGATGATGATGATGATGATG 38700
Db 38641 CAATAATGTTAAATTTTAAATTAATTCAGATGATGATGATGATGATGATGATGATGATG 38700
Qy 38701 TACGCTGAGATTTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 38760
Db 38701 TACGCTGAGATTTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 38760
Qy 38761 CAGATGTTCCGCGAGTGTGCGGTAAAGGAGCAAAACATTCCTCGAATTTCCATATTTG 38820
Db 38761 CAGATGTTCCGCGAGTGTGCGGTAAAGGAGCAAAACATTCCTCGAATTTCCATATTTG 38820
Qy 38821 AAGTAAAGCAGAGATTTGAAACATGCTTTGATTAATTTACGCAATACATTAATG 38880
Db 38821 AAGTAAAGCAGAGATTTGAAACATGCTTTGATTAATTTACGCAATACATTAATG 38880
Qy 38881 CGAAACATACAGGACCGGTAGATGCTGCTGCTGCTTGAACCAAAACGCTGCGAGAC 38940
Db 38881 CGAAACATACAGGACCGGTAGATGCTGCTGCTGCTTGAACCAAAACGCTGCGAGAC 38940
Qy 38941 TTTGAGGTGAATAAGGTTGGAATAAGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 39000
Db 38941 TTTGAGGTGAATAAGGTTGGAATAAGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 39000
Qy 39001 GATAGCATCATTAATTAATTAACCCGCTCCGCGTACTGCTTACCGGCTTTCGCAACGAT 39060
Db 39001 GATAGCATCATTAATTAATTAACCCGCTCCGCGTACTGCTTACCGGCTTTCGCAACGAT 39060
Qy 39061 ACCACCTTGGCGGTGATTAATAAGGATATGCTTCTCCCAATACAGAGCGCGAGCGC 39120
Db 39061 ACCACCTTGGCGGTGATTAATAAGGATATGCTTCTCCCAATACAGAGCGCGAGCGC 39120
Qy 39121 ACGGCAAGCTTAATAAGGTTGCTGCTTTCATAGCCCTGCAAGGCTCTGAGCGAGAC 39180
Db 39121 ACGGCAAGCTTAATAAGGTTGCTGCTTTCATAGCCCTGCAAGGCTCTGAGCGAGAC 39180
Qy 39181 GTTTTCAAGATCTAATTTATGTTGCTGCGACGACGCAAAATTTGCCAGTTGAGTTTAA 39240
Db 39181 GTTTTCAAGATCTAATTTATGTTGCTGCGACGACGCAAAATTTGCCAGTTGAGTTTAA 39240
Qy 39241 ATCGAATTTGCGCGGTGACGCGGCTTTCGCTGCGACCGGTAGACAGACGCGGCGAGAG 39300
Db 39241 ATCGAATTTGCGCGGTGACGCGGCTTTCGCTGCGACCGGTAGACAGACGCGGCGAGAG 39300
Qy 39301 AACAGGCGCTGCAACAGATTAATGAGGCGGCTGAGAGTACGACCTTTCCATATAT 39360
Db 39301 AACAGGCGCTGCAACAGATTAATGAGGCGGCTGAGAGTACGACCTTTCCATATAT 39360
```

OY	39361	GGCAGCGAGAGCCCAATTCGTTGCTGCTAAATGAAGAAGCTGGCGACCCAGCGACTTTTAA	39420
Db	39361	GGCAGCGAGAGCCCAATTCGTTGCTGCTAAATGAAGAAGCTGGCGACCCAGCGACTTTTAA	39420
OY	39421	AAGTTTTCAACCTGCTGTTGGGAAAACACGCCAGAGGAGAGAGTTCATTTGAGGGTCT	39480
Db	39421	AAGTTTTCAACCTGCTGTTGGGAAAACACGCCAGAGGAGGAGAGTTCATTTGAGGGTCT	39480
OY	39481	TTTGGCGGTGTATACCAAGTAATTCAGTTTGTGAAGTTTCTGGAAAGCTCCGTACGGT	39540
Db	39481	TTTGGCGGTGTATACCAAGTAATTCAGTTTGTGAAGTTTCTGGAAAGCTCCGTACGGT	39540
OY	39541	TGCGTGGCTTAAACCGAGTTTAAAGACCCCAACGAAATGACAGATGAGAAAATTCAGTT	39600
Db	39541	TGCGTGGCTTAAACCGAGTTTAAAGACCCCAACGAAATGACAGATGAGAAAATTCAGTT	39600
OY	39601	TAAAGTATCTGTACCGACATCTCGGTATGGGGAGCGGACGCGCCACAAAACAAAACA	39660
Db	39601	TAAAGTATCTGTACCGACATCTCGGTATGGGGAGCGGACGCGCCACAAAACAAAACA	39660
OY	39661	ATACATATATGATGAAGCCCTGCAATTAAGCATTCATTTGGTCCCGAATATGACCTGTGCAC	39720
Db	39661	ATACATATATGATGAAGCCCTGCAATTAAGCATTCATTTGGTCCCGAATATGACCTGTGCAC	39720
OY	39721	TGATGACATCGAGCTGTTATTCATTTGACAGAGAAACCCACTGATTTACACAGAAATACGC	39780
Db	39721	TGATGACATCGAGCTGTTATTCATTTGACAGAGAAACCCACTGATTTACACAGAAATACGC	39780
OY	39781	CGGGGCGGTAAAGACATTAACCGCTCTCTCCAGTTTGGCGTGTGACCGCGCTGGAGAGGG	39840
Db	39781	CGGGGCGGTAAAGACATTAACCGCTCTCTCCAGTTTGGCGTGTGACCGCGCTGGAGAGGG	39840
OY	39841	CTGTGTGATACCGTATTTGAATGTTTAAAGCTTACGTCGCCGCCGATGTTTATCTTAA	39900
Db	39841	CTGTGTGATACCGTATTTGAATGTTTAAAGCTTACGTCGCCGCCGATGTTTATCTTAA	39900
OY	39901	AACATATTCAGACCGGCTCTACACCGAAGCGGGCTCTAAAGAGAGGCTGTTTAAGTCAGACAT	39960
Db	39901	AACATATTCAGACCGGCTCTACACCGAAGCGGGCTCTAAAGAGAGGCTGTTTAAGTCAGACAT	39960
OY	39961	GGTGTCCATGTTCAAAAGCTACCTTATGATTAAGTCTGTTT	40000
Db	39961	GGTGTCCATGTTCAAAAGCTACCTTATGATTAAGTCTGTTT	40000
RESULT 2			
AF210726	130733 bp	DNA	linear
LOCUS	Macaca mulatta rhadinovirus 26-95	long unique region L-DNA,	
DEFINITION	complete sequence.		
ACCESSION	AF210726		
VERSION	AF210726.1		
KEYWORDS	Macaca mulatta rhadinovirus 26-95		
SOURCE	Macaca mulatta rhadinovirus 26-95		
ORGANISM	viruses; dsDNA viruses, no RNA stage; Herpesviridae; Gammaherpesvirinae; Rhadinovirus.		
REFERENCE	1 (bases 1 to 130733)		
AUTHORS	Alexander, L., Denekamp, L., Knapp, A., Auerbach, M. R., Damania, B. and Desrosiers, R. C.		
TITLE	The primary sequence of rhesus monkey rhadinovirus isolate 26-95: sequence similarities to Kaposi's sarcoma-associated herpesvirus and rhesus monkey rhadinovirus isolate 17577		
JOURNAL	J. Virol. 74 (7), 3388-3398 (2000)		
MEDLINE	20173730		
PUBMED	10708456		
REFERENCE	2 (bases 1 to 130733)		
AUTHORS	Alexander, L., Denekamp, L. M., Knapp, A., Auerbach, M., Czajak, S., Damania, B. and Desrosiers, R. C.		
TITLE	Direct Submission		
JOURNAL	Submitted (02-DEC-1999) Microbiology, New England Regional Primate Research Center, One Pinehill Dr, Southborough, MA 01772, USA		

FEATURES	SOURCE	Location/Qualifiers
		1. .130733
		/organism="Macaca mulatta rhadinovirus 26-95"
		/mol_type="genomic DNA"
		/isolate="Macaca mulatta rhadinovirus isolate 26-95"
		/db_xref="taxon:119193"
		513. .1784
gene		/gene="R1"
CDS		513. .1784
		/gene="R1"
		/codon_start=1
		/product="ORF1"
		/protein_id="AAFS9980.1"
		/db_xref="GI:7329991"
		/translation="MFVLYLPHLLQSVYVELLPAKLITVPMCPBPHRGDTVLLTQCT
		STARDSTOMFRRNLTMRSSNFTGLRIVYSTPAPNATISDRACQTKTTRTSNNIDFRS
		SSRITLDERCSSIGETIYANNTRVALRCSGGGNVLRNVPHLNGAVLNGTTRNIRHTEV
		LTEKPTGGTFCASAFIGNEKFFSQTINVEFTSFEPKPNDI PNESHFKKTOIIOOTQSH
		QHEPNVYFVPVAFSIGLVGLIAISLIMCMLPTIRCMENSSSTNSYASQTSYIOESH
		NORSTNECSRHYTYRNAHOESIEIIEELNOSTSEDSQCVLLLEKVAADGQENIT
		NEWEOYQDVVVENIIEQTSYEDNEHNDYSDTINPNPNYISGLILEVDVFPNLEEN
		QYHLILENDHNENYHNLNLEMLIEQDYLE"
		complement(1852. .2418)
gene		/gene="ORF02"
CDS		complement(1852. .2418)
		/gene="ORF02"
		/codon_start=1
		/product="DHRP"
		/protein_id="AAFS9981.1"
		/db_xref="GI:7329992"
		/translation="MDIAVNCIAVAVDQLGKNGTIPMPVYLRNEMKYFOKWTSPSY
		VGEKNVIMKRTWFSIPERKRPVLRNINILSELSEPHGAFHFLRTLDDAFNEFR
		QYKLEQNLNTVMVIGSKSVESYVNLCSPLKLYITRMISFDPCDPSFINSIEYTWL
		SELGDKDFNEENQIKKKFOYERKENFK"
		2595. .3782
gene		/gene="ORF04"
CDS		2595. .3782
		/gene="ORF04"
		/codon_start=1
		/product="complement binding protein"
		/protein_id="AAFS9982.1"
		/db_xref="GI:7329993"
		/translation="MFWIPITLFCICVILVSDGDSNVTCLRPDPRENVKTRANDNE
		NVAAGTRVELICRPGFATLQANVYBELCSNGWTTTPVAECRRKCSNPEDILNGEVI
		TSDONARFGLSNITIKYCNCTGYLLGAVRVCILKLYSDNLVDQPPAATPCIECKQAP
		DIENGGYVPOEAFNYLETITFTCNKDFSLIGNTTTCMTNGTSSPVCQOQITGSA
		PNDHGTLLVGGSSRVYKHGQSVTIGCGEDVTLNKKKCTCEYSILMNPRLTQVINT
		DPMPSEYSPGTRKQEMPTREPNRSHSETTTETPTQIHNKSTSPKPKVNETHRP
		TTTPAGISQKQTTTRNSKAPSONPFIAPRPSKKRHYVLVLFASVSLVLVAALAYC
		FLK"
		4213. .7611
gene		/gene="ORF06"
CDS		4213. .7611
		/gene="ORF06"
		/codon_start=1
		/product="sdbp"
		/protein_id="AAFS9983.1"
		/db_xref="GI:7329994"
		/translation="MASKGNAGQPLEDNOGSRATGACGYYVAYSKODPFAEASITLG
		NRPSSGVFSPLIYGLTVEHEPFIYKAAVYKADDTLLAVKYCFREYIVFIMSLI
		FRPVEDGTNLNCEEARALEGYTOLEPDPHSINPLRSCQPLDDEMEVLLVLE
		GFKRILARGCLPAVPOTQOVOLAGRAFAFVLTDELLPHGHRMPRAHKDVSALV
		YDSLEFSLAALRLKDYTYIHATERQPMODHYKIAITYAKQOSTLLPRTTDOSSIM
		IVDSVVELALSTGCMFLCECPDQACELNDTSNFIPOGDSPEARVNALEKWSMEDAV
		HVAQSLAANSVLYLTIRVQAPRGQGDVNVNNSFLQHGLEFLNPAITKEGSEAF
		KGPSNALDSSFTPYHLAYAAASPSPLAKLCYMFLOHKKSSITQANVMYHYVT
		AAENSEMTLCHGNTPATCLMTLEFYRLDRPRAVTPQRPDYPVVTGAGTFNDLEILG
		NFSFQRREDGNADDEPKYTYWQLOQVTEKLSAIGIEDHNNHNLITLNOSFLR
		VFGCITSDVGEYMKFVNSMTIKNNENREHKVGHNTLOECNVYUQAAPAVLNIYY
		KSULTIQTDCIPLPCATYEDDNPAMGLISBEWYLMKHQTLPTNFNKACDRGLVTCGE
		LKTVHRMFCDFPDYDAGSNGLAAPFMQVRIAAAMNVPRSTIKIRITLISFNAGE
		AVDSGEKPTGTRDTYVAGPYMKFLNLSLRALFPDRTAALYLHMKISQTNKTPVLK
		DVDPDELAELAVSYKTNLSAEEETINVDVVDLSMSYARIKGLNGALILRACGOIQFYAT

gene
CDS
7636..9696
/gene="ORF07"
7636..9696
/gene="ORF07"
/product="transport protein"
/protein_id="AAF59984.1"
/db_xref="GI:7329995"
/translation="MARELAALYAOISALAVLSLVTFFADPPSIDARILKTKQTEN
LNRDLPLREONSVETSSLSEVEHLANIDKLGELERSLRORSKEHEETLRL
PCGHYSTVFQFQGGGLIDVNMCLINDVELCKRGVFCIGANEALSGDRLVTE
LSTLRGISIP1PHPDLYTVSPVCQCIKRETELVPNOSSSLAVADRCHOLCKVAE
PIHGLETELSQLGKVKTRSDATOHGVSSADOLBRESSLA1IODHNIRKVSASME
LSNLIYMNAGGOTGLOTGTEPNECSOMARLLTHEADMEHRLITPKLSATHFYDCPRD
PIESLFCGGLFNSIDDTINALRDCSVTFEQANTNNRKONELTRNLTRLSRQSA
GSOKPATPSEPRITTVAAADSVIKDAQYRKQYWKVARGFKILTCLOTQAVL
ANALCMRWGVGVAEGASELVNHFLLRRFVALPWARCSDOILFENSKYIKNSLYS
ORLSREHVEIITLOFYGILTGPLTRSDLPGPANVLAQFEAGMLPHHMLYSEM
IMPOLOPKMIDOTFNREYOLPEGDINAOKSAMCP1RELVSVALYNTRWKTURIF
SLAREKLSINLDVKGIYSGILTYEQDAPVLVISQNTGIMIKDLIALLIHHLOLSDG
HSDN"
9683..12172
/gene="ORF08"
9683..12172
/gene="ORF08"
/codon_start=1
/product="ORF08"
/protein_id="AAF59985.1"
/db_xref="GI:7329996"
/translation="MAITNRRRLRLAAVVI1AIGAVENYTPKATTTAKPTPGP
STPTPENPRAEAFKERYCASATGELERFNLKCPETEDTKHOEGILMEFKNIV
PHIFVRRYRKATSVTVYRGWTEFAVNGKOBIVIRPVRI1NHMDTYOCSSMNV
VNGIYNTYTRDPTNOTYVLOVYEGITNDIQKIFSPQVLYTTPGMPGILYRRTTYNC
ELVDMARSAEPTSTFVIALGDTVEVSPCHNDSTCSVAEKTENGLGVALNVTYLD
FAYRKPETETRFADSGEYTVSKADEIQSLAVCALMLTSPRAI1OJTHEASVHEVAN
DYATATPTSLSEVANFTGYSC1LDEV1QIOTLADITK1LSDFTVNGSQAQYTEGLEF
LMOPULTPLSLVDENRGLNGTTPAPPATSTSVRSRVSNTNEOAT1NAAFOLQAV
DKLRASINKVLEELSRAMCREQVRDVMYELSK1NPSVMA1AIGRPA5FGDAI
SYTDCVANDQASVSIHKS1RTSTPGMCYSRPVYTRERFLNSTL1FKGOLQPRNEI1LTD
NOVEAKETCEHFTIASNVTYIKDYVEFKK1NTSE1SLGFI1ALNLSFI1NDIEV
1ELYSRAEKRLISGSVFIETMFRXENY1YORLAGRED1DNT1DNR1LSE1NDIEV
AD1GNGVRVNVAVSSVITLFGSIVSGFINFTKSPGGLM1LIV1AVV1IYF1ALNR
TNA1QAP1RBM1YPIIDKMOPSGKVDO1KN1LAGMH1QLQEEBR1RDEQ1RSAPS
LEFRASDGLKRRERGYKPLENEAQEYENSK"
12290..15334
/gene="ORF09"
12290..15334
/gene="ORF09"
/codon_start=1
/product="polymerase"
/protein_id="AAF59986.1"
/db_xref="GI:7329997"
/translation="MDFNPYLGPGRPRSHRGTDAPAPAGAAVOPPPDYCRLLIPA
CLRTPGAGGMIPVTL1PFPYTVENGARGDVL1LANERSMT1ADRRPV1ADPODOSTE
HAYDVETTYADRCAEVSRFOTD1IPSGVILK1LIGRDEGT1SCVNVFROOVYFA
KVPAGIN1YH1LOALKNTAGRAACGFSFRNKR1L1K1YDVAHEHVP1EIT1SSGML
STLSR1VACGEVFPESVND1ARRFVLDHGGFTTTCWY1SCAR1ATP1LAARD1ALEFD
CSMED1SVOADSDMP1RY1VAF1D1ECTGEAGFPCATRGD1V1O1SCVF1RT1REGAP
NPN1L1FSGTCD1P1PD1VLEFPESEYDML1VSF1FAM1R1SVF1E1D1L1G1N1IN1SD1PYL
IT1RASO1VNL1R1NETY1K1IGTS1IFEV1HGRGGGFMFSVSIK1AG1I1GY1PD1MYOVR
EK1LSLDYK1LTVAROC1GKKEKEDVY1CD1PL1P1FSG1GGR1K1VSG1CYMD1VMDL
LK1MEM1H1E1S1I1A1K1G1A1R1V1L1D1G1O1L1B1F1S1C1L1E1A1R1E1M1P1V1P1E1O1G1
YOG1ATV1N1P1R1G1F1D1E1P1V1YD1F1AS1Y1S1I1O1AHN1C1S1TH1G1D1L1H1P1L1T1DDY
E1FV1L1SGG1V1H1K1K1R1E1SL1G1RL1V1W1E1K1R1A11R1L1A1C1D1P1S1L1T1K1D1K1O1LA
1K1VTC1NAV1G1F1G1V1A1S1GL1P1C1N1A1E1TV1L1R1G1R1M1E1MS1K1S1VE1A1L1T1E1D1L1R1G1E1
V1AR1GAR1FR1V1Y1G1D1S1L1F1AC1D1G1S1E1A1V1A1F1C1D1L1A1R1T1A1D1P1P1L1E1K1E1K1
F1C1L1L1K1R1R1I1G1V1L1D1K1M1K1G1V1D1I1R1T1A1C1F1V1O1R1C1A1I1D1V1H1D1E1V1K1A1
R1L1C1K1R1P1H1A1V1E1B1L1P1A1G1F1K1I1V1E1V1A1S1Y1D1L1N1S1V1P1E1Q1L1F1S1E1L1S1P1V1C1D1K1

gene	gene
CDS	CDS
15429..16679	15429..16679
/gene="ORF10"	/gene="ORF10"
15429..16679	15429..16679
/gene="ORF10"	/gene="ORF10"
/codon_start=1	/codon_start=1
/product="ORF10"	/product="ORF10"
/protein_id="AAF59987.1"	/protein_id="AAF59987.1"
/db_xref="GI:7329998"	/db_xref="GI:7329998"
/translation="MLVNELSVVLGDMVEYFHRGRFSEVNLTRLOTFKGGGVARYL PRLDLOLHOHFAFG1VTR1KEL1PDS1CV1AL1I1PLD1SG1D1A1R1A1V1A1F1D1S1R1P L1V1W1V1A1S1G1R1H1R1C1L1E1K1P1D1E1R1AT1V1V1G1E1N1G1A1R1S1G1T1K1P1C1A1T1S1G1P L1V1S1G1R1A1S1O1T1S1H1S1F1V1A1T1P1T1A1N1S1V1A1C1S1L1R1O1V1R1P1S1D1A1H1R1A1R1S1P1R1Y1F1S1N S1G1N1C1K1A1S1V1H1L1S1P1R1C1K1T1A1O1M1E1I1Y1A1G1D1N1A1E1V1L1G1S1P1V1P1T1H1G1V1L1G1V1A D1E1K1I1O1P1O1S1S1E1V1R1O1L1F1O1G1A1A1R1G1D1A1L1V1G1V1A1E1P1E1V1T1P1A1L1S1G1C1T1H1 L1F1E1N1P1G1T1T1K1R1D1L1V1A1A1P1C1P1V1R1S1D1A1P1R1D1V1A1S1P1D1G1A1S1I1N1A1F1T1P1V1G F1G1V1A1S1E1H1S1L1R1D1G1V1H1E1R1N1H1"	TTN1LPH1A1Y1O1K1A1S1C1E1L1P1O1V1H1R1I1P1V1F1D1A1R1S1L1K1S1D1A1E1H1P1D1Y1R1Q1I1P1A1V D1Y1F1D1L1V1H1A1N1I1Q1L1G1N1A1D1T1V1A1L1Y1N1F1N1P1K1F1S1"
16688..17917	16688..17917
/gene="ORF11"	/gene="ORF11"
16688..17917	16688..17917
/gene="ORF11"	/gene="ORF11"
/codon_start=1	/codon_start=1
/product="ORF11"	/product="ORF11"
/protein_id="AAF59988.1"	/protein_id="AAF59988.1"
/db_xref="GI:7329999"	/db_xref="GI:7329999"
/translation="MGTVPFRFRGEMQISS1VNDNGTPRYS1LWMAAT1HDGYLT1LVNR SE1L1C1V1E1R1S1P1C1A1G1S1G1R1L1V1K1R1P1G1A1F1S1A1T1G1D1G1T1F1V1A1F1H1R1N1P1L1D1Y P1A1V1E1R1A1D1R1E1L1V1R1H1A1P1Q1T1R1V1S1R1G1L1F1V1A1I1Y1V1A1R1P1G1V1F1H1F1P1D1R1V1A1L1D1	
Query Match	26.9%; Score 10772; DB 1; Length 130733;
Best Local Similarity	99.4%; Pred. No. 0;
Matches 15792; Conservative	0; Mismatches 98; Indels 1; Gaps 1;
5489 CACAAATCCACCAATAGCACC	5489 CACAAATCCACCAATAGCACC
3658 CACAAATCCACCAATAGCACC	3658 CACAAATCCACCAATAGCACC
5549 TTTTTCGAAGTGCCTGTTAT	5549 TTTTTCGAAGTGCCTGTTAT
3718 TTTTTCGAAGTGCCTGTTAT	3718 TTTTTCGAAGTGCCTGTTAT
5609 AATACTGTTTTGCTCAGAGG	5609 AATACTGTTTTGCTCAGAGG
3778 AATACTGTTTTGCTCAGAGG	3778 AATACTGTTTTGCTCAGAGG
3838 GCCAACCGCGCTTGATTCG	3838 GCCAACCGCGCTTGATTCG
5669 GCCAACCGCGCTTGATTCG	5669 GCCAACCGCGCTTGATTCG
3898 TTTTAAATATTCATATT	3898 TTTTAAATATTCATATT
5789 ACCCTGCGCTACATATTAT	5789 ACCCTGCGCTACATATTAT
3957 ACCCTGCGCTACATATTAT	3957 ACCCTGCGCTACATATTAT
5849 CTCATACGCTTAAGCTACG	5849 CTCATACGCTTAAGCTACG
4017 CTCATACGCTTAAGCTACG	4017 CTCATACGCTTAAGCTACG
5909 GGTACATATTCATTCAGG	5909 GGTACATATTCATTCAGG
4077 GGTACATATTCATTCAGG	4077 GGTACATATTCATTCAGG
5969 GCCAACCAATCACTGTCG	5969 GCCAACCAATCACTGTCG
4137 GCCAACCAATCACTGTCG	4137 GCCAACCAATCACTGTCG
6029 ACTTAATTAACATTAATG	6029 ACTTAATTAACATTAATG
4197 ACTTAATTAACATTAATG	4197 ACTTAATTAACATTAATG

OY	6089	GGGGTCTC	GGCCCGCCAT	TAGGTGGGTG	CGGATAC	GTGTAC	GGCGAT	TTTCA	AAACAAG	CTT	6148						
Dp	4257	GGGGTCTC	GGCCCGCCAT	TAGGTGGGTG	CGGATAC	GTGTAC	GGCGAT	TTTCA	AAACAAG	CTT	4316						
OY	6149	TCCTGTTG	CCGAGGCG	GTCACT	ATCTCG	GGCAAC	AGCAT	CTG	GGCGTTT	CTCGCT	6208						
Dp	4317	TCCTGTTG	CCGAGGCG	GTCACT	ATCTCG	GGCAAC	AGCAT	CTG	GGCGTTT	CTCGCT	4376						
OY	6209	ACCAATC	CTTTAC	GGACTT	ACA	GTGTA	CA	CGAAT	TCCCT	CTCCAC	CGTAAAGCCG	6268					
Dp	4377	ACCAATC	CTTTAC	GGACTT	ACA	GTGTA	CA	CGAAT	TCCCT	CTCCAC	CGTAAAGCCG	4436					
OY	6269	CAAAAAG	GTGAC	CCAC	GAC	AGCGT	CGCGG	CTTAA	GGTAC	GTGCTT	CAC	AGAGGTAT	6328				
Dp	4437	CAAAAAG	GTGAC	CCAC	GAC	AGCGT	CGCGG	CTTAA	GGTAC	GTGCTT	CAC	AGAGGTAT	4496				
OY	6329	TGTGTT	CACA	ATAT	CA	AGTTAT	TAT	CAG	CGCGG	GTGTT	GAC	GGTAC	CGGCTT	6388			
Dp	4497	TGTGTT	CACA	ATAT	CA	AGTTAT	TAT	CAG	CGCGG	GTGTT	GAC	GGTAC	CGGCTT	4556			
OY	6389	ATGCGA	GAAG	AGCC	AGG	CGTCT	CTTT	GGGTAC	AC	GCAG	ATTTAT	ATAG	ACCGGG	CTCAC	TC	6448	
Dp	4557	ATGCGA	GAAG	AGCC	AGG	CGTCT	CTTT	GGGTAC	AC	GCAG	ATTTAT	ATAG	ACCGGG	CTCAC	TC	4616	
OY	6449	CAGCAT	AT	TGGA	AC	CCCT	CT	GGA	AT	CT	CGG	CA	ATTA	CCG	CA	AAAGAT	6508
Dp	4617	CAGCAT	AT	TGGA	AC	CCCT	CT	GGA	AT	CT	CGG	CA	ATTA	CCG	CA	AAAGAT	4676
OY	6509	CGTGTG	TGTTAC	GA	AAAGG	TTTAA	GAA	AAAG	CT	GTGA	GGGG	GTGT	CTG	CTCC	CGCG	6568	
Dp	4677	CGTGTG	TGTTAC	GA	AAAGG	TTTAA	GAA	AAAG	CT	GTGA	GGGG	GTGT	CTG	CTCC	CGCG	4736	
OY	6569	GTTC	CAG	ACC	AG	CAG	GTG	CAG	AT	T	GCC	CGA	CC	AG	CG	6628	
Dp	4737	GTTC	CAG	ACC	AG	CAG	GTG	CAG	AT	T	GCC	CGA	CC	AG	CG	4796	
OY	6629	CGAAG	AC	CTG	TTT	CAC	ACT	CA	CGG	TCAT	PAG	AA	TCC	CA	AAAG	6688	
Dp	4797	CGAAG	AC	CTG	TTT	CAC	ACT	CA	CGG	TCAT	PAG	AA	TCC	CA	AAAG	4856	
OY	6689	CGCGT	AC	CT	CTAC	AG	CT	CCCT	CTTT	TAC	AG	CAT	CG	CC	AG	6748	
Dp	4857	CGCGT	AC	CT	CTAC	AG	CT	CCCT	CTTT	TAC	AG	CAT	CG	CC	AG	4916	
OY	6749	GACG	CGG	GT	CA	T	CAC	GC	CAC	AG	AA	AA	GC	A	A	6808	
Dp	4917	GACG	CGG	GT	CA	T	CAC	GC	CAC	AG	AA	AA	GC	A	A	4976	
OY	6809	GAT	GTG	CA	GA	CC	CA	AA	AG	TTT	TA	AG	AG	CG	TC	6888	
Dp	4977	GAT	GTG	CA	GA	CC	CA	AA	AG	TTT	TA	AG	AG	CG	TC	5036	
OY	6869	CAT	GAT	TG	TG	A	C	AG	CT	CG	CG	CG	AG	CT	CG	6928	
Dp	5037	CAT	GAT	TG	TG	A	C	AG	CT	CG	CG	CG	AG	CT	CG	5096	
OY	6929	GT	GT	CC	CA	GA	GC	GT	CG	CA	GT	T	G	CA	GA	6988	
Dp	5097	GT	GT	CC	CA	GA	GC	GT	CG	CA	GT	T	G	CA	GA	5156	
OY	6989	TG	ACT	CA	CA	GA	GC	GT	AG	GT	TA	AG	CG	GT	TA	7048	
Dp	5157	TG	ACT	CA	CA	GA	GC	GT	AG	GT	TA	AG	CG	GT	TA	5216	
OY	7049	CGT	GG	CG	GG	TC	CA	AT	T	TG	CG	CT	CT	TA	CT	7108	
Dp	5217	CGT	GG	CG	GG	TC	CA	AT	T	TG	CG	CT	CT	TA	CT	5276	
OY	7109	AG	CC	CC	CA	GA	GG	GA	GC	GT	TA	AG	CG	TC	CA	7168	
Dp	5277	AG	CC	CC	CA	GA	GG	GA	GC	GT	TA	AG	CG	TC	CA	5336	

QY	7169	ACTGGGGTTTTTAATNAGAGCCACGATCAAGAAAAAGGACGAGACCTTTAAAGGGCGT	7228
Db	5337	ACTGGGGTTTTTAATNAGAGCCACGATCAAGAAAAAGGACGAGAAAGCCTTTAAAGGGCGT	5396
QY	7229	ACCCCTCAAAAGCCCTCGATGGTGTCTTCGTTTCGTTTCACAGCCGTAACCTGAGCCCTACCCGGGTC	7288
Db	5397	ACCCCTCAAAAGCCCTCGATGGTGTCTTCGTTTCGTTTCACAGCCGTAACCTGAGCCCTACCCGGGTC	5456
QY	7289	TTTTTCGCCCCATCTGCTGGGCGAAGTTATGTTATTTACATGACAGTCTTTCGACACCCAA	7348
Db	5457	TTTTTCGCCCCATCTGCTGGGCGAAGTTATGTTATTTACATGACAGTCTTTCGACACCCAA	5516
QY	7349	AAGCTCCACGAACCAAGGCGCTTTTAACTGGTCCATTATGTCCGAGCCCGGCCCACTCAGA	7408
Db	5517	AAGCTCCACGAACCAAGGCGCTTTTAACTGGTCCATTATGTGTCCGAGCCCGGCCCAACTCAGA	5576
QY	7409	GATGTGCACGCTATGTGCAGGGCAACACGCGCGGCAAGTGTCGCTCAACACGCTGTTCATAG	7468
Db	5577	GATGTGCACGCTATGTGCAGGGCAACACGCGCGGCAAGTGCTCAACACGCTGTTCATAG	5636
QY	7469	ACTGAAGGATAGGTTTCCCGCGTAACACACCCCTCAGCGAGGAGACCCCTACGTGGTGAC	7528
Db	5637	ACTGAAGGATAGGTTTCCCGCGTAACACACCCCTCAGCGAGGAGACCCCTACGTGGTGAC	5696
QY	7529	CGGAACACGCGGGGACCTTTAACGACCTGGAGATCTTGGGCACTTGGCGAGCTTTAGAGA	7588
Db	5697	CGGAACACGCGGGGACCTTTAACGACCTGGAGATCTTGGGCACTTGGCGAGCTTTAGAGA	5756
QY	7589	CCGCGAAGAGGACGGAACCCGGCGCAGCAGCCCAAGTAACGTAACGTAACGGAAGCTATG	7648
Db	5757	CCGCGAAGAGGACGGAACCCGGCGCAGCAGCCCAAGTAACGTAACGTAACGGAAGCTATG	5816
QY	7649	TCAGACCCGTGACAGAAAACTATCCGCGATTGGGAATCACCGAAGACACGATATACAGT	7708
Db	5817	TCAGACCCGTGACAGAAAACTATCCGCGATTGGGAATCACCGAAGACACGATATACAGT	5876
QY	7709	GAACTCATCTACCAACATCCAAAGTTTCTCAGGGGTGTTCAAGGGATGACATCAATTGT	7768
Db	5877	GAACTCATCTACCAACATCCAAAGTTTCTCAGGGGTGTTCAAGGGATGACATCAAAATTGT	5936
QY	7769	GGACGAGAGGTCATCAAGTCGTTAATTCGATGATTTAAATAATACCTTAATTTCGCGGA	7828
Db	5937	GGACGAGAGGTCATCAAGTCGTTAATTCGATGATTTAAATAATACCTTAATTTCGCGGA	5996
QY	7829	GCAGGTCAAATCGGTCATCACATACTCCAGTTCCTCTGCAAGCTGATTATGGACGGGCC	7888
Db	5997	GCAGGTCAAATCGGTCATCACATACTCCAGTTCCTGTCGCAAGCTGATTATGGACGGGCC	6056
QY	7889	GTCGCGGGTTCCTCGAATCTGTACTACAAATCCCTGCTGTGCATCTTACAGATATCTG	7948
Db	6057	GTCGCGGGTTCCTCGAATCTGTACTACAAATCCCTGCTGTGCATCTTACAGATATCTG	6116
QY	7949	CCTGGCGTCTCGATGATACGAACAAGATATCCGGGATATGGGATCCCTCCGCTCGA	8008
Db	6117	CCTGGCGTCTCGATGATACGAACAAGATATCCGGGATATGGGATCCCTCCGCTCGA	6176
QY	8009	GTCGCTAAAGATGCAATTTTCAGACGTTGTGGAGAACTTTAAAGCGGCGCTGTCTCGACCG	8068
Db	6177	GTCGCTAAAGATGCAATTTTCAGACGTTGTGGAGAACTTTAAAGCGGCGGTGTCTCGACCG	6236
QY	8069	CGGGGCTCTCAGCGGGTGGCAACTGAATAATCGTACACCGGACATGTTCTGCGACTTCTT	8128
Db	6237	CGGGGCTCTCAGCGGGTGGCAACTGAATAATCGTACACCGGACATGTTCTGCGCACTTCTT	6296
QY	8129	CGACACCGGACGGGGGTCCAGCGGCTTAATGGCCCTTTAAATACAGGTTTGAATAGC	8188
Db	6297	CGACACCGGACGGGGGTCCAGCGGCTTAATGGCCCTTTAAATACAGGTTTGAATAGC	6356
QY	8189	CCGAGCAGATGATGTCGTTCCGAATAATCAATTAATAATAAATAATGAAATCATTTTTCCTAA	8248
Db	6357	CCGAGCAGATGATGTCGTTCCGAATAATCAATTAATAATAAATAATGAAATCATTTTTCCTAA	6416
QY	8249	CACCCGGGATCCGAGGCGGTGCACTGCGGGGTTCTGTCAAAACGACGGGAACCAAGGACAC	8308

```
|||||
Db 6417 CACCGGGGATCGAGAGCGGTGACGTGGGGTTCTGTAACCGAGCGGAACCGGACAC 6476
OY 8309 TTACGTGTGGCGGACCGTACATGAAGTTTCTCAACTGCTGCATCGCGCTGTTC 8368
Db 6477 TTACGTGTGGCGGACCGTACATGAAGTTTCTCAACTGCTGCATCGCGCTGTTC 6536
OY 8369 CGACACAGACCGCGCGCTGTACTGTGGCACAAGATCTCCAGACCAACAAACCCC 8428
Db 6537 CGACACAGACCGCGCGCTGTACTGTGGCACAAGATCTCCAGACCAACAAACCCC 6596
OY 8429 AGTTCTGAAGAAGCGTCCGAGACGAGGCGGGGAGTGGTGTCTAGTAAAGACAA 8488
Db 6597 AGTTCTGAAGAAGCGTCCGAGACGAGGCGGGGAGTGGTGTCTAGTAAAGACAA 6656
OY 8489 CAGCCTCGGCTTCGAGGAACGACGTGTGACGCTGCTCGGATTCACCTACTGTCTA 8548
Db 6657 CAGCCTCGGCTTCGAGGAACGACGTGTGACGCTGCTCGGATTCACCTACTGTCTA 6716
OY 8549 CCGGAGATCAAACTGAACGGGGCATTTCTAAGGGCATGTGGCAGATTCTACCT 6776
Db 6717 CCGGAGATCAAACTGAACGGGGCATTTCTAAGGGCATGTGGCAGATTCTACCT 6836
OY 8609 CACGACGTCGACGCTCGACGCGGCTGTACAGACGATCGATGGCGAGGAATACCCCA 8668
Db 6777 CACGACGTCGACGCTCGACGCGGCTGTCTACAGACGATCGACGCCGAGGAATACCCCA 6836
OY 8669 CGTGTGGGCTCCGGGGCAATCGCCACACCGGTGGCTTACCTGCGAGAAATACGCGCG 8728
Db 6837 CGTGTGGGCTCCGGGGCAATCGCCACACCGGTGGCTTACCTGCGAGAAATACGCGCG 6896
OY 8729 CACCGCCCTACGCTCCACAGACGCGCGGTGACGCGGCTGCGCCGACAGCGCGCTGG 8788
Db 6897 CACCGCCCTACGCTCCACAGACGCGCGGTGACGCGGCTGCGCCGACAGCGCGCTGG 6956
OY 8789 TCCTCGTAAACCGTTCCATGTAGTCAACAAATACAGGGGGTCAACGGGAACAACA 8848
Db 6957 TCCTCGTAAACCGTTCCATGTAGTCAACAAATACAGGGGGTCAACGGGAACAACA 7016
OY 8849 CGTTTTCCACTGCGGAACCTGGGGTACTTCCGGGGCGCGCGTGGACCGCAACCTGTG 8908
Db 7017 CGTTTTCCACTGCGGAACCTGGGGTACTTCCGGGGCGCGCGTGGACCGCAACCTGTG 7076
OY 8909 GCGGGAACGTCCTTTAAGAAAGCGGCGTCAAGCGCATCTAAGAAAGACACCT 8968
Db 7077 GCGGGAACGTCCTTTAAGAAAGCGGCGTCAAGCGCATCTAAGAAAGACACCT 7136
OY 8969 CATGATGACCCCATTTATGACCGCTAATAAGCAGCGCGGACAGACATCAGCAC 9028
Db 7137 CATGATGACCCCATTTATGACCGCTAATAAGCAGCGCGGACAGACATCAGCAC 7196
OY 9029 GTTCGAGCGGAAGCGTTAAAGAGCGGTGACAGCGCTGTTAGAGATTAAGACACCC 9088
Db 7197 GTTCGAGCGGAAGCGTTAAAGAGCGGTGACAGCGCTGTTAGAGATTAAGACACCC 7256
OY 9089 TAACTATTGAGTGGGTAACTTGTGAGCTTATAGACACCTGGGGAAAGGCTGCCAGA 9148
Db 7257 TAACTATTGAGTGGGTAACTTGTGAGCTTATAGACACCTGGGGAAAGGCTGCCAGA 7316
OY 9149 CTTAAGCTCCGAGAGCTGCATATTACTCGGTGACATATTGTATGTTACGAGCAGGT 9208
Db 7317 CTTAAGCTCCGAGAGCTGCATATTACTCGGTGACATATTGTATGTTACGAGCAGGT 7376
OY 9209 TTTATTTACGTTGATATATATAGACAGTCAAGCGCTGCCGTGACATATCAGAGCGGG 9268
Db 7377 TTTATTTACGTTGATATATATAGACAGTCAAGCGCTGCCGTGACATATCAGAGCGGG 7436
OY 9269 TGCCTTAATAGAGATCCGACAGAGCAGACATCTTCAAGTTCGTAGACAGCAGATAT 9328
Db 7437 TGCCTTAATAGAGATCCGACAGAGCAGACATCTTCAAGTTCGTAGACAGCAGATAT 7496
OY 9329 CGCACCGCTTCTGTCAAGCCCGGAGGAAGCTACGACCCCTAGGCGCGCGCCT 9388
|||||

|||||
Db 7497 CGCACCGCTTCTGTCAAGCCCGGAGGAAGCTACCGACCCCTTAGGCGCGCGCCT 7556
OY 9389 ACTGCCGGGAAGAACGAAAAATTAACGCGCTGTGTAGACGATCTAGACCTTTAGAAAA 9448
Db 7557 ACTGCCGGGAAGAACGAAAAATTAACGCGCTGTGTAGACGATCTAGACCTTTAGAAAA 7616
OY 9449 CCGTGACGGCGGCAACATGGCCAGGAACTCCGAGATTAATACGGCAGCTGTGCGC 9508
Db 7617 CCGTGACGGCGGCAACATGGCCAGGAACTCCGAGATTAATACGGCAGCTGTGCGC 7676
OY 9509 CCTCGCGTGCAGCTTATAGTCTGGTTATCTTTGGGAGCCCGGAGATATGACGGTCCCG 9568
Db 7677 CCTCGCGTGCAGCTTATAGTCTGGTTATCTTTGGGAGCCCGGAGATATGACGGTCCCG 7736
OY 9569 CATTTTAAACAAAAACAGATAGAGAACCTGAACCGGACCTTCTGCGCTGTACG 9628
Db 7737 CATTTTAAACAAAAACAGATAGAGAACCTGAACCGGACCTTCTGCGCTGTACG 7796
OY 9629 CGAGCAAACTCGGTAGACACGTCCAGCCTGTCTCGAAGTGGAGCACCCTGGCAAAA 9688
Db 7797 CGAGCAAACTCGGTAGACACGTCCAGCCTGTCTCGAAGTGGAGCACCCTGGCAAAA 7856
OY 9689 CATCGAGCAAACTCGGAGAGCTGAGCGGACGCTGCGGACAGATATTTCAGACGAGA 9748
Db 7857 CATCGAGCAAACTCGGAGAGCTGAGCGGACGCTGCGGACAGATATTTCAGACGAGA 7916
OY 9749 GCATTTTGAACACTACCTGAGACCCGAAATGTCACTATCACTTACGGTTACTTTTCA 9808
Db 7917 GCATTTTGAACACTACCTGAGACCCGAAATGTCACTATCACTTACGGTTACTTTTCA 7976
OY 9809 GTTTTACGGGGCGGTTATAGATGTAAACATGTCCATTAATAACGATGTGAACGTGT 9868
Db 7977 GTTTTACGGGGCGGTTATAGATGTAAACATGTCCATTAATAACGATGTGAACGTGT 8036
OY 9869 GTGTAAACACTAGGAGTGTGTATTTATGCAATCGGTGCAACGAAGCTCTGTCCGATT 9928
Db 8037 GTGTAAACACTAGGAGTGTGTATTTATGCAATCGGTGCAACGAAGCTCTGTCCGATT 8096
OY 9929 GAACCGGTTCTGACGCTTTCTGTCAACACTGCGGGGTATCTCCCGATCCGACCCAGA 9988
Db 8097 GAACCGGTTCTGACGCTTTCTGTCAACACTGCGGGGTATCTCCCGATCCGACCCAGA 8156
OY 9989 CCTATATGTCACGTGCTGCTGGGTACAGTGGCTGAGGGAATAGAACCTGTACCAA 10048
Db 8157 CCTATATGTCACGTGCTGCTGGGTACAGTGGCTGAGGGAATAGAACCTGTACCAA 8216
OY 10049 TCAGGGGTCAGTTTACTGCGGCTGTGGCAGACCGACACTCGATCACCTCTGTAAAGA 10108
Db 8217 TCAGGGGTCAGTTTACTGCGGCTGTGGCAGACCGACACTCGATCACCTCTGTAAAGA 8276
OY 10109 GGTTAGGGCGGAGCCATACACGCGCTGTTTAGACAGACATGAGCCAGCTGGCTTAAA 10168
Db 8277 GGTTAGGGCGGAGCCATACACGCGCTGTTTAGAGACAGAACGTAGCCACTGGCTTAAA 8336
OY 10169 AGTAACAAAACGTTGGAGCGCACGACGAGAGGGCGTCCGTGCGAGATCAGTTAAG 10228
Db 8337 AGTAACAAAACGTTGGAGCGCACGAGAGCGCGCTCCGTCTGCGAGATCAGTTAAG 8396
OY 10229 GGAGTCGTGCTGGGCGCCATACAGATACAAATATTTCAACGAGGTGTCCGCTCAAT 10288
Db 8397 GGAGTCGTGCTGGGCGCCATACAGATACAAATATTTCAACGAGGTGTCCGCTCAAT 8456
OY 10289 CATGAACTATCCAAATCTAATTTATTTGAGACCGCGGGCAACCGGCTCTCAGACGGGAC 10348
Db 8457 CATGAACTATCCAAATCTAATTTATTTGAGAACCGGGGCAACCGGCTCTCAGACGGGAC 8516
OY 10349 CGAAAAAGAGTGTCTACAAATGGCCAGACTGTCTAACACAGAGGCGGATATCAGAGCA 10408
Db 8517 CGAAAAAGAGTGTCTACAAATGGCCAGACTGTCTAACACAGAGGCGGATATCAGAGCA 8576
OY 10409 CCGTCGCTTAATTAACACCACTAAGCGCGACTACTTCTACGACTGTTTCCGACCGGA 10468
Db 8577 CCGTCGCTTAATTAACACCACTAAGCGCGACTACTTCTACGACTGTTTCCGACCGGA 8636
```


10797 TGTCTATACACTGTGACAAACGGGTGGCGAGTACTACAGAGAAAGGGGGCTGT 10856
12689 TTCTCCTGTGGACGGCTTTAAGCCGCTAAGCTAGCTAGAGATGCGCGAATTTAAAG 12748
10857 TTCTACTGTGGACGGCTTTAAGCCCTTAGCTGCTGTGACGAAATGCCGGGTTAAAG 10916
12749 GCACACGGCCAGACCCCGCCACCAACTCAACCGCCAAACCGCGTTGAGAGAGCGTCG 12808
10917 GCACCGCGCAGACCCCGCCAGCTCAACCGCTCAGCGCGCTTGGTAAAGTGTAA 10976
12809 GTACGAAGAGAGAGGACGAGAGACCTAGTGGCGCCAGCTGAGTTCGGCTAGAGAA 12868
10977 ATACGAACGACAGGACACTGACACCTTGGACGGCCCAAGTTGCAATTCGCTAGACA 11036
12869 AGCTCCGCGAGACATCAACAAAGTGTCTGAGAGAGCTTCAGAGGCGGTGGCCGAGAC 12928
11037 AACTAGCGCGAGACATCAACAAAGTGTCTGAGAGAACTTCAGAGGCGGTGGCCGAGAC 11096
12929 AGGTAGGAGACACTTACATGTGTACGAACCTGACGAATTTAAACCCACAGCTAATGA 12988
11097 AGGTAGGAGACACTTACATGTGTACGAACCTGACGAATTTAAACCCACAGCTAATGA 11156
12989 CGGCGATATACGGGCGCGGCTGTGGCCAAAGTTGTGGGCGACGCGCATCTCGTGACGG 13048
11157 CAGCGATATACGGGCGCGGCTGTGGCCAAAGTTGTGGGCGACGCGCATCTCGTGACAG 11216
13049 ACTGCGTGGCGGTGACACAGGCGTCCGTAGCATCCACAAGACCTCCGACAGTCCACCC 13108
11217 ACTGCGTGGCGGTGACACAGGCGTCCGTAGCATCCACAAGACCTCCGACAGTCCACCC 11276
13109 CGGGGATCTGTACTCTGCGGCGCGCGGTACAGTTCAGGTTCTCTCAACACAGCAGCTGT 13168
11277 CGGGATGTGTACTCTGCGGCGCGCGGTACAGTTCAGGTTCTCTCAACACAGCAGCTGT 11336
13169 TCAGAGGCGCAGCTGGGACCCAGAAACAGAGATCATCTAGCGACAAACAGTGGAGCGT 13228
11337 TCAGAGGCGCAGCTGGGACCCAGAAACAGAGATCATCTAGCGACAAACAGTGGAGCGT 11396
13229 GCAGAGAGAGCTGCGAACCTACTTCATAGCAGAGCAACTAACCTACTACTACAAAGACT 13288
11397 GCAGAGAGAGCTGCGAACCTACTTCATAGCAGAGCAACTAACCTACTACTACAAAGACT 11456
13289 AGCTCTGCTGAAAAAATTAACACTCTCGAGATATCCACCCTCGGTACGTTCAATGCC 13348
11457 AGCTCTGCTGAAAAAATTAACACTCTCGAGATATCCACCCTCGGTACGTTCAATGCC 11516
13349 TGAACCTGTCTTTATAGAGACATAGATTTCAGGGTCAATGAGCTGTACAGCGCGG 13408
11517 TGAACCTGTCTTTATAGAGACATAGATTTCAGGGTCAATGAGCTGTACAGCGCGG 11576
13409 ACAGAAAGCTGTCCGGGAGCGTTTTCGATATAGAAACATGTTCAAGGAAATACACTACT 13468
11577 ACAGAAAGCTGTCCGGGAGCGTTTTCGATATAGAAACATGTTCAAGGAAATACACTACT 11636
13469 ACAGCAAGCGCTGGGGGAGCTCCGGGAGAGACCTGAGACACAGATGCAACCGGAG 13528
11637 ACAGCAAGCGCTGGGGGAGCTCCGGGAGAGACCTGAGACACAGATGCAACCGGAG 11696
13529 ACCGCGTGGCGCGACCTGTCCGAGATAGTGGCGAGCTGGGCAATGTCGCGCGACGG 13588
11697 ACCGCGTGGCGCGACCTGTCCGAGATAGTGGCGAGCTGGGCAATGTCGCGCGACGG 11756
13589 TCGTTAAGCTGGCCAGTAGACGTGATTAACCTGTTTCGATCAATTCGTGAGCGGTTCAATTA 13648
11757 TCGTTAAGCTGGCCAGTAGACGTGATTAACCTGTTTCGATCAATTCGTGAGCGGTTCAATTA 11816
13649 ACTTATAAAGATCCGTTTCGGGGGACATGCTATATCTGATATTTGGGGGCGTCGCC 13708
11817 ACTTATAAAGATCCGTTTCGGGGGACATGCTATATCTGATATTTGGGGGCGTCGCC 11876
13709 TGATCGTGTTCGCTAAACCGCGGACACAAAGCCATCGCCAGGCGCCCATCAGAGATGA 13768
|||||

11877 TGATCGTGTTCGCTAAACCGGCGACCAAGCCATGCGCCCAAGCGCCCATCAGAGATGA 11936
13769 TCTACCCGACATATAGACAAATATGACACCTCTGTGGCGGTAAAGTGCACAGAGACAGATTA 13828
11937 TCTACCCGACATATAGACAAATATGACACCTCTGTGGCGGTAAAGTGCACAGAGACAGATTA 11996
13829 AAAACATTCCTCGCGGATATGACACAGCTTACAGAGACAGAGAGCGGTATGACGAAC 13888
11997 AAAACATTCCTCGCGGATATGACACAGCTTACAGAGACAGAGAGCGGTATGACGAAC 12056
13889 AGCAGAGGTACAGGCGCTGCTTTTCGCGCGCGGCTCAGACGAGACTAAAACGCGCTTAA 13948
12057 AGCAGAGGTACAGGCGCTGCTTTTCGCGCGCGGCTCAGACGAGACTAAAACGCGCTTAA 12116
13949 GGGGATATTAACCGCTGAAAAAGAGAGCTCAAGAGTATGAATGACCAATAATACAC 14008
12117 GGGGATATTAACCGCTGAAAAAGAGAGCTCAAGAGTATGAATGACCAATAATACAC 12176
14009 ACCCAGCGCTGTACTTCCGCGCGGACAGAGCCGCGCGCAATTCGATTCGCGCACCGG 14068
12177 ACCCAGCGCTGTACTTCCGCGCGGACAGAGCCGCGCGCAATTCGATTCGCGCACCGG 12236
14069 GCGGTCGCCGACACCTCTAGCGCCCGCGGCGGCTGCGCGGTGATCAATCATGATTT 14128
12237 GCGGTCGCCGACACCTCTAGCGCCCGCGGCGGCTGCGCGGTGATCAATCATGATTT 12296
14129 TCTTTAACCGCTAGCTGGGCGCTCGCGGACCAAGCCCGCTCTACACAGAGGACACGATG 14188
12297 TCTTTAACCGCTAGCTGGGCGCTCGCGGACCAAGCCCGCTCTACACAGAGGACACGATG 12356
14189 CTCCGCGCGCTGCGCGGCGGAGCGCTTACAGCGCCACCAAGCTTTGCAAGGCTCATCC 14248
12357 CTCCGCGCGCTGCGCGGCGGAGCGCTTACAGCGCCACCAAGCTTTGCAAGGCTCATCC 12416
14249 CCGCGCTGCTCCGAAAGCGCAGGCGGAGGAGGAGGATATCCCGGTCAAGATCCGTTCCGCG 14308
12417 CCGCGCTGCTCCGAAAGCGCAGGCGGAGGAGGAGGATATCCCGGTCAAGATCCGTTCCGCG 12476
14309 CAAAGCTATTGAGAAAGCGTGTCCGCGAGACGTGCTGCTGCCCAACGAACGCTCATGT 14368
12477 CAAAGCTATTGAGAAAGCGTGTCCGCGAGACGTGCTGCTGCCCAACGAACGCTCATGT 12536
14369 GGAAGCGCGGCGAGCGCAAGCGCTGCGCGGAGCGGAGCGGACCGCCAAACATCATCAGGTTTC 14428
12537 GGAAGCGCGGCGAGCGCAAGCGCTGCGCGGAGCGGAGCGGAGCGGACCGCCAAACATCATCAGGTTTC 12596
14429 ACGCGTAGCAGCTGCTTTGAAACAGAGTACGCGCGGAGACAGTGTCCCGAGGTACCTAGGC 14488
12597 ACGCGTAGCAGCTGCTTTGAAACAGAGTACGCGCGGAGACAGTGTCCCGAGGTACCTAGGC 12656
14489 GCTTCCAAAGGACATTTATCCCAAGCGAACCGGTCTCAAGCTCTGGGCGCAACCGAGG 14548
12657 GCTTCCAAAGGACATTTATCCCAAGCGAACCGGTCTCAAGCTCTGGGCGCAACCGAGG 12716
14549 ACGGACACAGCGTGTGCGGTGAACAGTGTTCGCAACAGGTATATTTCTACGGAAGTTTC 14608
12717 ACGGACACAGCGTGTGCGGTGAACAGTGTTCGCAACAGGTATATTTCTACGGAAGTTTC 12776
14609 CAGCGGCAATTAACGTCAACCCACATCTCCACAGAGCCCTCAAGAACACAGCGGCGCTG 14668
12777 CAGCGGCAATTAACGTCAACCCACATCTCCACAGAGCCCTCAAGAACACAGCGGCGCTG 12836
14669 CCGCGTGGCGCTTCTGACAGACAGATGACAAAAAGATTTCTCAAAAGCTACGACGTCCG 14728
12837 CCGCGTGGCGCTTCTGACAGACAGATGACAAAAAGATTTCTCAAAAGCTACGACGTCCG 12896
14729 CCGAGCATCCGCTGACAGGAAATCAAGCATGTCTCGGTTTCAATGCTCGACCCGACGG 14788
12897 CCGAGCATCCGCTGACAGGAAATCAAGCATGTCTCGGTTTCAATGCTCGACCCGACGG 12956
14789 ACCGCTGCTGCGCGGCGGTGCGAGGTGTTGCAATCAAAAGCTGACCGCTTCCGCGGT 14848
12957 ACCGCTGCTGCGCGGCGGTGCGAGGTGTTGCAATCAAAAGCTGACCGCTTCCGCGGT 13016
|||||

OY	14849	TCGTTCTGGAATCAAGGGTTTACCAGCTTGGGGTGTACTGTGTCGGCGCCGACGCCCC	14908
Db	13017	TCGTTCTGGAATCAAGGGTTTACCAGCTTGGGGTGTACTGTGTCGGCGCCGACGCCCC	13076
OY	14909	GCCTGGGGGCGAGGATGCGCAGGACGGCCCTGGAGTTTACGTGACACTGGGAGACCTCA	14968
Db	13077	GCCTGGGGGCGAGGATGCGCAGGACGGCCCTGGAGTTTACGTGACACTGGGAGACCTCA	13136
OY	14969	GCGTTTCAAGCGGAGCCGACGACGACTGGGCCCCCTGACCGCATTCGGGCTTTGATATCGAGT	15028
Db	13137	GCGTTTCAAGCGGAGCCGACGACGACTGGGCCCCCTGACCGCATTCGGGCTTTGATATCGAGT	13196
OY	15029	GCACGTGAGAGCGCGGGATTTCCGTGCGCACGCGCGACGGCGACGCGGTGATCCAGATCT	15088
Db	13197	GCACGTGAGAGCGCGGGATTTCCGTGCGCACGCGCGACGGCGACGCGGTGATCCAGATCT	13256
OY	15089	CCCTGCGCTTCTACAGCACGAGGGAAGCGCGGCCCAATCCGCAACATACGTGTTACAGG	15148
Db	13257	CCCTGCGCTTCTACAGCACGAGGGAAGCGCGGCCCAATCCGCAACATACGTGTTACAGG	13316
OY	15149	TCGGGAGCGTCGACCCCATCCCGGACACGACGCTTTTGGAGTTCCGTGCGAATATGACA	15208
Db	13317	TCGGGAGCGTCGACCCCATCCCGGACACGACGCTTTTGGAGTTCCGTGCGAATATGACA	13376
OY	15209	TGCTGGTGTGCTTCTTCCCATGATCCGACCTTTCGAGTGGACCTTTTAAACCGGCTATA	15268
Db	13377	TGCTGGTGTGCTTCTTCCCATGATCCGACCTTTCGAGTGGACCTTTTAAACCGGCTATA	13436
OY	15269	ACATCTCAAACTTCGATCTCCCGTACCTATATCAGGAGCGTCCCGAGGTGTCACAACTTC	15328
Db	13437	ACATCTCAAACTTCGATCTCCCGTACCTATATCAGGAGCGTCCCGAGGTGTCACAACTTC	13496
OY	15329	GATTAAACGAATACACAAAATAAAAACCGGCTCCATCTTTGAGTTACAGACCCCGTG	15388
Db	13497	GATTAAACGAATACACAAAATAAAAACCGGCTCCATCTTTGAGTTACAGACCCCGTG	13556
OY	15389	GCGGGGGAAGGGGGTTCATGAGTCCGTCTCAAAAATTTAAATAGCGGCGATGTCGCCA	15448
Db	13557	GCGGGGGAAGGGGGTTCATGAGTCCGTCTCAAAAATTTAAATAGCGGCGATGTCGCCA	13616
OY	15449	TAGCATGTTACCAAGGTGTGTCGGGAAAGAGTCAAGCTTCGCCATCAAACTGGAGACGG	15508
Db	13617	TAGCATGTTACCAAGGTGTGTCGGGAAAGAGTCAAGCTTCGCCATCAAACTGGAGACGG	13676
OY	15509	TGGCCAGGACAGTGTCTGTGGTGGGAAAAAAGAGGACGTATCGTACAAGACATTTCCCCCTC	15568
Db	13677	TGGCCAGGACAGTGTCTGTGGTGGGAAAAAAGAGGACGTATCGTACAAGACATTTCCCCCTC	13736
OY	15569	TGTTTCCCTACGTCGCGGGCGGACGGGCTAAAGTGGGACGCTAATCCGTGATGGACTCGG	15628
Db	13737	TGTTTCCCTACGTCGCGGGCGGACGGGCTAAAGTGGGACGCTAATCCGTGATGGACTCGG	13796
OY	15629	TCCGTGGTATGGACCTCTTAAAAATGTTTATGATATACGTGGAGATTTGCGGATATGCCA	15688
Db	13797	TCCGTGGTATGGACCTCTTAAAAATGTTTATGATATACGTGGAGATTTGCGGATATGCCA	13856
OY	15689	AGCTGGCCAAAGATTACAGGCCAGGCGCGTCTGTGACGAGCGGCAACAGCTCCGCGATTCT	15748
Db	13857	AGCTGGCCAAAGATTACAGGCCAGGCGCGTCTGTGACGAGCGGCAACAGCTCCGCGATTCT	13916
OY	15749	CCCTGCTGTGAGAGCGCCGCGCCCAAGGAGAACTTATCCTCCGGTTTCCACGCCCAGAG	15808
Db	13917	CCCTGCTGTGAGAGCGCCGCGCCCAAGGAGAACTTATCCTCCGGTTTCCACGCCCAGAG	13976
OY	15809	GACAGGGGGCTATACAGAGGGCGACAGGTGATCAACCCCAATCCCGGGGTTTACAGACGAC	15868
Db	13977	GACAGGGGGCTATACAGAGGGCGACAGGTGATCAACCCCAATCCCGGGGTTTACAGACGAC	14036
OY	15869	CGGTCCTGTGTGATATTTTGCACAGCCTGTACCGAGCAATCATCAGGCGCACAACTGT	15928
Db	14037	CGGTCCTGTGTGATATTTTGCACAGCCTGTACCGAGCAATCATCAGGCGCACAACTGT	14096

QY	15929	GCTACTCCACCTGATATACACGGACGACGACCTGACCTGACACCCCAACTGACGGCGGACG	15988
Db	14097	GCTACTCCACCAATGATATACACGGACGACGACCTGACCTGACACCCCAACTGACGGCGGACG	14156
QY	15989	ACTACGAGACGTTTCGTGCTGACGGGGGACCGGCTACATTTTGTAAAAAACAACAGCGGG	16048
Db	14157	ACTACGAGACGTTTCGTGCTGACGGGGGACCGGCTACATTTTGTAAAAAACAACAGCGGG	14216
QY	16049	AGTCTCTGCTGGGAAGACTGCTTAACCGTGTGGTTAGAAAAAGCAAGGGCGATCCGGCGCA	16108
Db	14217	AGTCTCTGCTGGGAAGACTGCTTAACCGTGTGGTTAGAAAAAGCAAGGGCGATCCGGCGCA	14276
QY	16109	CCCTGGCGCGTGGCATGACCCGCTGCTAAAAACCATCTTAGATTAACAACAGCTGGCCA	16168
Db	14277	CCCTGGCGCGTGGCATGACCCGCTGCTAAAAACCATCTTAGATTAACAACAGCTGGCCA	14336
QY	16169	TCAAGGTGCATGTAAACGGGGTTACGGGGTTACCGGGGTGGCCACGGGCTCTCCCAAT	16228
Db	14337	TCAAGGTGCATGTAAACGGGGTTACGGGGTTACCGGGGTGGCCACGGGCTCTCCCAAT	14396
QY	16229	GCATTTAACATAGCGGAAAAACCGTGACGCTCCGGGGGCGACAGATGCTGAGATGTCAAGT	16288
Db	14397	GCATTTAACATAGCGGAAAAACCGTGACGCTCCGGGGGCGACAGATGCTGAGATGTCAAGT	14456
QY	16289	CTTACGTGGAGGCGCTGACGACGAGAAAGACCTGCAACGCGTCTGGTGGCGAGGTGACCG	16348
Db	14457	CTTACGTGGAGGCGCTGACGACGAGAAAGACCTGCAACGCGTCTGGTGGCGAGGTGACCG	14516
QY	16349	CCCCGTACAGGCGCGGGGTTTCGGCTGCTACGGGTGACACCGCATCTCCCTTTATCGCGT	16408
Db	14517	CCCCGTACAGGCGCGGGGTTTCGGCTGCTACGGGTGACACCGCATCTCCCTTTATCGCGT	14576
QY	16409	GGCAGGTGTTATTCGCGGGAAGCGGTTCCGCTTTCGTAGCATCTGGCGCGCAGATGCA	16468
Db	14577	GGCAGGTGTTATTCGCGGGAAGCGGTTCCGCTTTCGTAGCATCTGGCGCGCAGATGCA	14636
QY	16469	CTGGCGGACCTGTTCGCCCCACCCATTAAAGCTAGAGCGGAGAAAAAGAGCTTCAAGTGTCTGC	16528
Db	14637	CTGGCGGACCTGTTCGCCCCACCCATTAAAGCTAGAGCGGAGAAAAAGAGCTTCAAGTGTCTGC	14696
QY	16529	TGCTCTGACGAAAAAGCGCTACATCGGGGTCTCTATTGAACGACAAATGTCATGTAAG	16588
Db	14697	TGCTCTGACGAAAAAGCGCTACATCGGGGTCTCTATTGAACGACAAATGTCATGTAAG	14756
QY	16589	GGGTGACCTCTATTGCGCAAAAGCGGCTGCAAAATTTTGCAGAGACGATCCGCGCCATCC	16648
Db	14757	GGGTGACCTCTATTGCGCAAAAGCGGCTGCAAAATTTTGCAGAGACGATCCGCGCCATCC	14816
QY	16649	TGGACCTGCTGCTCCACGATCCGAGGTCCAGGTCCAGGCTGCGGCGGCTGTTGTGCAGACGGC	16708
Db	14817	TGGACCTGCTGCTCCACGATCCGAGGTCCAGGTCCAGGCTGCGGCGGCTGTTGTGCAGACGGC	14876
QY	16709	CGCCGACCGGCTATACGAGGAGGGGGCTGCGGGTGTCTTTATAAAAATCTGTAGAGTCC	16768
Db	14877	CGCCGACCGGCTATACGAGGAGGGGGCTGCGGGTGTCTTTATAAAAATCTGTAGAGTCC	14936
QY	16769	TCAAGCGAGCTATCTGACACTCCGCAAAACAGGCTGTGGCCATCGACAGTTAACTTCT	16828
Db	14937	TCAAGCGAGCTATCTGACACTCCGCAAAACAGGCTGTGGCCATCGACAGTTAACTTCT	14996
QY	16829	CCACGAGACTGACCGCCCGCTGTGCGATTACAAAGCCACCAACTGCCCCACCTGGCGG	16888
Db	14997	CCACGAGACTGACCGCCCGCTGTGCGATTACAAAGCCACCAACTGCCCCACCTGGCGG	15056
QY	16889	TGTACCAAAAGCTGGCGGACGAGAGTGTGCGAGAGACTGCCCCAGGTGCACGATTAGATCCCT	16948
Db	15057	TGTACCAAAAGCTGGCGGACGAGAGTGTGCGAGAGACTGCCCCAGGTGCACGATTAGATCCCT	15116
QY	16949	ACGTTTGTGTTGACCGCGCGGGGTCCTTAAATCTGCAGCTTGCGCGCAACCGGATTTAG	17008
Db	15117	ACGTTTGTGTTGACCGCGCGGGGTCCTTAAATCTGCAGCTTGCGCGCAACCGGATTTAG	15176
QY	17009	TCAGCAGACCAAGTATCCCGTCCGGTCCGACTATATTTTGACAAATGTTGTGCACGGCG	17068

Db	15177	TCACAGACGACAGATTC	CCGCGTGCAGCTATATTTTCGACAACTGTGCAGCGG	15236
Qy	17069	CGGCCAACATCTCTCAGATGTC	GTGTGGCAACAACGCGGACACACGATGGCCATCTCT	17128
Db	15237	CGGCAACATCTCTCAGATGTC	GTGTGGCAACAACGCGGACACACGATGGCCATCTCT	15296
Qy	17129	ACATTTTTCACAGCTCCGCTAT	AGCTGTCTCGTAACGCCAATTTGGAAAGCGCAC	17188
Db	15297	ACATTTTTCACAGCTCCGCTAT	AGCTGTCTCGTAACGCCAATTTGGAAAGCGCAC	15356
Qy	17189	ATAAGACGCGCGCGCACGAG	AGTCCGAGAGAGCTCGAGCGCGCAGAGAGCGACACG	17248
Db	15357	ATAAGACGCGCGCGCACGAG	AGTCCGAGAGAGCTCGAGCGCGCAGAGAGCGACACG	15416
Qy	17249	GAGACCGCCACACATGCTG	GTTAACGAACCTGCGGTGTCTCTGGCGACCTGGAGAGT	17308
Db	15417	GAGACCGCCACACATGCTG	GTTAACGAACCTGCGGTGTCTCTGGCGACCTGGAGAGT	15476
Qy	17309	TTTTCACGCGGGGTAGATT	CACCTTCGTCACACCTCACCGCGCTGCAAAAGCTTCAAGGGCAC	17368
Db	15477	TTTTCACGCGGGGTAGATT	CACCTTCGTCACACCTCACCGCGCTGCAAAAGCTTCAAGGGCAC	15536
Qy	17369	GGGGGCTACGCGCAGAGT	CCGACTCTCTGCTGACACAGTTACTCCACCAACATTTTC	17428
Db	15537	GGGGGCTACGCGCAGAGT	CCGACTCTCTGCTGACACAGTTACTCCACCAACATTTTC	15596
Qy	17429	GCGTTTCGAGTCTGAGACG	CGTCTCTCAAGAACCTGCCCGCTTCTCCACAGTGGCGGCTT	17488
Db	15597	GCGTTTCGAGTCTGAGACG	CGTCTCTCTCAAGAACCTGCCCGCTTCTCCACAGTGGCGGCTT	15656
Qy	17489	ATGCGCCCGTTGGATTCCG	CGGCGCAGCGGACGCGCGCGCGCGTGGCCCGCGGTTCTGTG	17548
Db	15657	ATGCGCCCGTTGGATTCCG	CGGCGCAGCGGACGCGCGCGCGCGCGTGGCCCGCGGTTCTGTG	15716
Qy	17549	CTGGACCTCTCTGCGCCG	CGTGCAGCGGTGGGTAAAGCGACGCGGGGGGAGCAACGATCCGG	17608
Db	15717	CTGGACCTCTCTGCGCCG	CGTGCAGCGGTGGGTAAAGCGACGCGGGGGGAGCAACGATCCGG	15776
Qy	17609	TTTCTGCTCTCTTCTTAA	AGCGATGACCTTGAGCGCGCGGTCTACGTACTCTTCTGCGC	17668
Db	15777	TTTCTGCTCTCTTCTTAA	AGCGATGACCTTGAGCGCGCGGTCTACGTACTCTTCTGCGC	15836
Qy	17669	GAGAACGCGCGCGCGCGCT	TCGGAAGGACCCCAACCCACTGCGCGACCGAAAGCTTG	17728
Db	15837	GAGAACGCGCGCGCGCGCT	TCGGAAGGACCCCAACCCACTGCGCGACCGAAAGCTTG	15896
Qy	17729	CCCGGTGAGACCTCTGCG	CGTCTCCGGGAGCGCTCTACAGCGTCCGCCATTTCTTCTGCT	17788
Db	15897	CCCGGTGAGACCTCTGCG	CGTCTCCGGGAGCGCTCTACAGCGTCCGCCATTTCTTCTGCT	15956
Qy	17789	GCGTATTTTCCCAAGCG	CAACTCGGTGGCTTGAAGCGCTGTTGGCGGTTACAGGTGAGG	17848
Db	15957	GCGTATTTTCCCAAGCG	CAACTCGGTGGCTTGAAGCGCTGTTGGCGGTTACAGGTGAGG	16016
Qy	17849	CCGTTTTCGATACGCGG	CGCACAGGACGCGCGGATCTCCCGGAAATACGTCAGTGT	17908
Db	16017	CCGTTTTCGATACGCGG	CGCACAGGACGCGCGGATCTCCCGGAAATACGTCAGTGT	16076
Qy	17909	AGTAACTCCGCGGGGT	AAAGCTCTGCAAGCGCTCGTTTACACAGCTGTCCCGTGGCGGT	17968
Db	16077	AGTAACTCCGCGGGGT	AAAGCTCTGCAAGCGCTCGTTTACACAGCTGTCCCGTGGCGGT	16136
Qy	17969	AAAAAGCGCGCAAT	TGAAATCATCTACGCTCCCGGGGACCCCAACGCGAGATATCTG	18028
Db	16137	AAAAAGCGCGCAAT	TGAAATCATCTACGCTCCCGGGGACCCCAACGCGAGATATCTG	16196
Qy	18029	GCGCAGTCCGAGCCGCT	GTGCGCACACACGCGCGGCTATTTGGGGGCTACGCGC	18088
Db	16197	GCGCAGTCCGAGCCGCT	GTGCGCACACACGCGCGGCTATTTGGGGGCTACGCGC	16256
Qy	18089	GACGCGAAAAAACAT	CTCAACCTGAGACTCCGCGGAAGTCCGGGTTTCACTTAATCTTTC	18148
Db	16257	GACGCGAAAAAACAT	CTCAACCTGAGAGCTCCGCGGAAGTCCGGGTTTCACTTAATCTTTC	16316
Qy	18149	CACACGAGAGCGCCCGCT	CGGGGAGATCTGGCGTTTGTGTACAGGGCGTGGCACCGGAG	18208
Db	16317	CACACGAGAGCGCCCGCT	CGGGGAGATCTGGCGTTTGTGTACAGGGCGTGGCACCGGAG	16376
Qy	18209	CCCGATTCTGCTACCGCG	CGCACTCTGTTTCCGTTTTCGTTTGCACAAACCCACCTCGCCCTA	18268
Db	16377	CCCGATTCTGCTACCGCG	CGCACTCTGTTTCCGTTTTCGTTTGCACAAACCCACCTCGCCCTA	16436
Qy	18269	TTCAACCCCAACGCTAC	CCCCACAGTATATAAAGACACCTTGTGGCCGCGCGCG	18328
Db	16437	TTCAACCCCAACGCTAC	CCCCACAGTATATAAAGACACCTTGTGGCCGCGCGCG	16496
Qy	18329	CCCTGCCCCGTTGGCAT	TAAAGTTCGCGCGACGACGCGCGGAGACCTCGTGGGTCA	18388
Db	16497	CCCTGCCCCGTTGGCAT	TAAAGTTCGCGCGACGACGCGCGGAGACCTCGTGGGTCA	16556
Qy	18389	CCAGACACCGGGGCGCT	CTCATTAACGCTTCAACATCCCGGTCCGTTTCCAGGGGTTG	18448
Db	16557	CCAGACACCGGGGCGCT	CTCATTAACGCTTCAACATCCCGGTCCGTTTCCAGGGGTTG	16616
Qy	18449	GTCTTCGGGAGTGTACAG	TGTCTCTTACGGGACAAAGGGGTCCACGACGATGAACCAAT	18508
Db	16617	GTCTTCGGGAGTGTACAG	TGTCTCTTACGGGAGCAACGGGGTCCACGACGATGAACCAAT	16676
Qy	18509	TGACGGCACAGTGGGAAC	ACCGGTGCTTCTTTCGCGCGAGTGGGACGACTCCGAGTC	18568
Db	16677	TGACGGCACAGTGGGAAC	ACCGGTGCTTCTTTCGCGCGAGTGGGACGACTCCGAGTC	16736
Qy	18569	TAGTGGACACGCGCACG	CGATACAGCTTCTGTGTGGCGCCCACTATTCACAGAG	18628
Db	16737	TAGTGGACACGCGCACG	CGATACAGCTTCTGTGTGGCGCCCACTATTCACAGAG	16796
Qy	18629	GCTACCTGACACTGTGTA	ACAGGTCAGAGCTGTGCGTCAAGGAGAGTCTCCGTGTCTGC	18688
Db	16797	GCTACCTGACACTGTGTA	ACAGGTCAGAGCTGTGCGTCAAGGAGAGTCTCCGTGTCTGC	16856
Qy	18689	CGGATGCCCCAGCATG	CGGAGACTGTGGGAAAGAGTTTCCCGGCTTCCGCTTTCGA	18748
Db	16857	CGGATGCCCCAGCATG	CGGAGACTGTGGGAAAGAGTTTCCCGGCTTCCGCTTTCGA	16916

QY 19229 CGGAACAATGCTCACCAGGCCCCGTGACGGCGACCTGTCCCTCACCGGTATGCGC 19288
| | | | |
Db 17397 CGGAACAATGCTCACCAGGCCCCGTGACGGCGACCTGTCCCTCACCGGTATGCGC 17456
QY 19289 CAATGCGCTTTGGCCACACCCCATACTTTGAATCTCCGTGGTCTGCACAAAGCGGATAT 19348
| | | | |
Db 17457 CAATGCGCTTTGGCCACACCCCATACTTTGAATCTCCGTGGTCTGCACAAAGCGGATAT 17516
QY 19349 TCACGCGCGGTGTAGTGGGGCTGAACCGGTGCAATCCCACTGTATGCAAAATTCG 19408
| | | | |
Db 17317 TCACGCGCGGTGTAGTGGGGCTGAACCGGTGCAATCCCACTGTATGCAAAATTCG 17576
QY 19409 TAAAGTACGGTAAACCTTACGCTTCGACATTTAAACCGCAAGCTAGCGGATTTATGACA 19468
| | | | |
Db 17577 TAAAGTACGGTAAACCTTACGCTTCGACATTTAAACCGCAAGCTAGCGGATTTATGACA 17636
QY 19469 ATCAGCGCCACACAGCGCGGGTTCGGATTCAAGACTCGAGTGGCCACCGAAGCGGAGA 19528
| | | | |
Db 17637 ATCAGCGCCACACAGCGCGGGTTCGGATTCAAGACTCGAGTGGCCACCGAAGCGGAGA 17696
QY 19529 TAGAGATTTGTGTACCAAGCTGTCCAGCGCCCGGTGTACATAGACAGCGGAGCGAGC 19588
| | | | |
Db 17697 TAGAGATTTGTGTACCAAGCTGTCCAGCGCCCGGTGTACATAGACAGCGGAGCGAGC 17756
QY 19589 TGGGGCAAGCCATCTTGTGTTCGCGCGCGGTTCCGTTGGCCCGGCAAACTGGCGAGC 19648
| | | | |
Db 17757 TGGGGCAAGCCATCTTGTGTTCGCGCGCGGTTCCGTTGGCCCGGCAAACTGGCGAGC 17816
QY 19649 TCTCGGCGCACCGATTCGCGCGCGCTGGAGCTGCCGGCGGGGTGACAGTGGACAGCCAA 19708
| | | | |
Db 17817 TCTCGGCGCACCGATTCGCGCGCGCTGGAGCTGCCGGCGGGGTGACAGTGGACAGCCAA 17876
QY 19709 AACGTGTAGGTGTGACACATGTACGTTTTCAGTAAATTAACCGTTTG 19768
| | | | |
Db 17877 AACGTGTAGGTGTGACACATGTACGTTTTCAGTAAATTAACCGTTTG 17936
QY 19769 CTCGTATGCTCACACAAAGCCAAACGCTCTCTCATTTCTCGGGTCCGCGCTCGGAA 19828
| | | | |
Db 17937 CTCGTATGCTCACACAAAGCCAAACGCTCTCTCATTTCTCGGGTCCGCGCTCGGAA 17996
QY 19829 CACCAAGGTGGCTCAAAACACCCCTCCGCGACCTCGCCACCAAAACAGTTAAAGC 19888
| | | | |
Db 17997 CACCAAGGTGGCTCAAAACACCCCTCCGCGACCTCGCCACCAAAACAGTTAAAGC 18056
QY 19889 CTTCCGTAGATGAGTTTATTTATTTATTTATTTACATAGTATTTGGCGGGCGCGC 19948
| | | | |
Db 18057 CTTCCGTAGATGAGTTTATTTATTTATTTATTTACATAGTATTTGGCGGGCGCGC 18116
QY 19949 TCCCGCAAAAACATCTGTAGATTTTCAGTATGCAAAAGCGCTGAGAAACAGCTCCCG 20008
| | | | |
Db 18117 TCCCGCAAAAACATCTGTAGATTTTCAGTATGCAAAAGCGCTGAGAAACAGCTCCCG 18176
QY 20009 GGGCTGTGCGCTCCCAACGCGACGAGGTTTTTTCATTAGACTCCGGCCACCTATCTTG 20068
| | | | |
Db 18177 GGGCTGTGCGCTCCCAACGCGACGAGGTTTTTTCATTAGACTCCGGCCACCTATCTTG 18236
QY 20069 TTATTTAGGGAAGCTCCTCAATTAGAGAGTGAAGGGGAGACAGACAGGTACCGCG 20128
| | | | |
Db 18237 TTATTTAGGGAAGCTCCTCAATTAGAGAGTGAAGGGGAGACAGACAGGTACCGCG 18296
QY 20129 GAGCAATGCGCGCGGGTCCGCTCCCGGGCGCGTGTGACAGAGCATCTCACTGCGC 20188
| | | | |
Db 18297 GAGCAATGCGCGCGGGTCCGCTCCCGGGCGCGTGTGACAGAGCATCTCACTGCGC 18356
QY 20189 GTCAAGTAACTCTGTAGGGCCGAGCGCCGGAACCATGGCTTCATACACTCGGCCCCG 20248
| | | | |
Db 18357 GTCAAGTAACTCTGTAGGGCCGAGCGCCGGAACCATGGCTTCATACACTCGGCCCCG 18416
QY 20249 CGAAACTCGGCGGCTGGCACTCAAGGTTAGACATCAATATAGGAAGTGAACAAAGCAGC 20308
| | | | |
Db 18417 CGAAACTCGGCGGCTGGCACTCAAGGTTAGACATCAATATAGGAAGTGAACAAAGCAGC 18476

QY 20309 ATGATGCGCGGGTACTCAACGACCCGACAGAGAGTGAAGTGTGGACAGGTAAACGAMC 20368
| | | | |
Db 18477 ATGATGCGCGGGTACTCAACGACCCGACAGAGAGTGAAGTGTGGACAGGTAAACGAMC 18536
QY 20369 CAGCGCTGTATGTTTAAACCCACATTCAAGACAGGCGCCCTGTGTCTGTCAAGAGAGCG 20428
| | | | |
Db 18537 CAGCGCTGTATGTTTAAACCCACATTCAAGACAGGCGCCCTGTGTCTGTCAAGAGAGCG 18596
QY 20429 CGGTTGGCGGCGCACTGGGGGAGAACGTTAATTCAGCGGCGAGTCGGGGGAGGCGCAGC 20488
| | | | |
Db 18597 CGGTTGGCGGCGCACTGGGGGAGAACGTTAATTCAGCGGCGAGTCGGGGGAGGCGCAGC 18656
QY 20489 GTAAGCTGTGGCGCCCAACACAGACAGGTAAACAAAGAACGAAACAGACAGGGAATGACC 20548
| | | | |
Db 18657 GTAAGCTGTGGCGCCCAACACAGACAGGTAAACAAAGAACGAAACAGACAGGGAATGACC 18716
QY 20549 GGTAAATTTACTCGCTTAAATCGCGGGCGGGCGGCTCAACGCCAGTTCATTAAAA 20608
| | | | |
Db 18717 GGTAAATTTACTCGCTTAAATCGCGGGCGGGCGGCTCAACGCCAGTTCATTAAAA 18776
QY 20609 CACACGGCGCGCAACCCCGCAAGCGGGGCGCGCGCTGGAAGCGGGTTCCTTCCAAATCG 20668
| | | | |
Db 18777 CACACGGCGCGCAACCCCGCAAGCGGGGCGCGCGCTGGAAGCGGGTTCCTTCCAAATCG 18836
QY 20669 CAAGAACCGCGCTCAAAAAAGGCTGTGTTGAACCATTTTGTGCATCGGGTTTCGT 20728
| | | | |
Db 18837 CAAGAACCGCGCTCAAAAAAGGCTGTGTTGAACCATTTTGTGCATCGGGTTTCGT 18896
QY 20729 TTTTCAATACGGAACAGGCTGTCTCAAAACACCCAAAGGGGTGTGCTCAACGGCCAT 20788
| | | | |
Db 18897 TTTTCAATACGGAACAGGCTGTCTCAAAACACCCAAAGGGGTGTGCTCAACGGCCAT 18956
QY 20789 CTTCCATCTATGTGGGGATGGGGTGTGTACCCCTGAGATCTAGATCCGGCGCGTAAA 20848
| | | | |
Db 18957 CTTCCATCTATGTGGGGATGGGGTGTGTACCCCTGAGATCTAGATCCGGCGCGTAAA 19016
QY 20849 GTCTCCAGAGCGCCCAACCTTTCAAAAATTTTCAGCGCGGAAACGAGACGCGGGTCT 20908
| | | | |
Db 19017 GTCTCCAGAGCGCCCAACCTTTCAAAAATTTTCAGCGCGGAAACGAGACGCGGGTCT 19076
QY 20909 CCGCAGCTGAAGCAGAGGGGATCAAGCTGTGTGTTGTTAAACGTGGGCGTCAACCAAGT 20968
| | | | |
Db 19077 CCGCAGCTGAAGCAGAGGGGATCAAGCTGTGTGTTGTTAAACGTGGGCGTCAACCAAGT 19136
QY 20969 GTGCACAAAGTCTCCCGGGGTCAGAGCCGTTGACGTGAGAGCATCAATCAAGTACAGAGGC 21028
| | | | |
Db 19137 GTGCACAAAGTCTCCCGGGGTCAGAGCCGTTGACGTGAGAGCATCAATCAAGTACAGAGGC 19196
QY 21029 GTAGCTGGCGATGTTAAACGGGACCCGAGGCCCATGTGCGCGGACCTTGTGTACAGTGT 21088
| | | | |
Db 19197 GTAGCTGGCGATGTTAAACGGGACCCGAGGCCCATGTGCGCGGACCTTGTGTACAGTGT 19256
QY 21089 GCAGGACAGCTCCCGCCGAGCGACAGTAAACGTGACAAAAAGTGAAGAGGAGAGC 21148
| | | | |
Db 19357 GCAGGACAGCTCCCGCCGAGCGACAGTAAACGTGACAAAAAGTGAAGAGGAGAGC 19316
QY 21149 CATCCGCGAGAGTCCCGGGGTTCCAGCGCCACATFACATGAGATGAGGCGATGTGGGCGC 21208
| | | | |
Db 19317 CATCCGCGAGAGTCCCGGGGTTCCAGCGCCACATGAGATGAGGCGATGTGGGCGC 19376
QY 21209 CCTGTTAATTTAGATCCACACAGTAAAGCAGTGTGACACCCCTGACCCCTGTGTGTGTC 21268
| | | | |
Db 19377 CCTGTTAATTTAGATCCACACAGTAAAGCAGTGTGTCACCCCTGACCCCTGTGTGTGTC 19436
QY 21269 GTGGGGCCCTGTATCTCCGCGCCCAAAATGTCTCACTGTGAACCCGATACACGGCCCGCAG 21328
| | | | |
Db 19437 GTGGGGCCCTGTATCTCCGCGCCCAAAATGTCTCACTGTGAACCCGATACACGGCCCGCAG 19496
QY 21329 ATCGCCTCTGGCGGGGTCCCGAAGCCCTGGCGCCCAAAAGGCGGGGA 21379
| | | | |
Db 19497 ATCGCCTCTGGCGGGGTCCCGAAGCCCTGGCGCCCAAAAGGCGGGGA 19547

[illegible]

QY 15217 TCGTCTTCGCGATGATCCGCGACTTCGAGGTGAGACTTTTAAACGGGCTATATACTCTA 15276
|||||
Db 4187 TCGTCTTCGCGATGATCCGCGACTTCGAGGTGAGACTTTTAAACGGGCTATATACTCTA 4246
QY 15277 AACTTCGATCTCCCGTACCTAATACGAGCGGTCCAGGTGTACAACTTGATTAAC 15336
|||||
Db 4247 AACTTCGATCTCCCGTACCTAATACGAGCGGTCCAGGTGTACAACTTGATTAAC 4306
QY 15337 GAATACACAAAAATAAAAAACGGGCTCCATCTTTGAAGTTCACGAGCCCGTGGCGGGGA 15396
|||||
Db 4307 GAATACACAAAAATAAAAAACGGGCTCCATCTTTGAAGTTCACGAGCCCGTGGCGGGGA 4366
QY 15397 GGGGGGTTTCATAGAGTCCGCTCCAAAAATTAATATAGCGGATCGTCCCATAGCATAG 15456
|||||
Db 4367 GGGGGGTTTCATAGAGTCCGCTCCAAAAATTAATATAGCGGATCGTCCCATAGCATAG 4426
QY 15457 TACCAAGTGTGTGCGGAAAAAGCTCAGCCCTCTCCGACTACAACTGGACAGCGGGCAGG 15516
|||||
Db 4427 TACCAAGTGTGTGCGGAAAAAGCTCAGCCCTCTCCGACTACAACTGGACAGCGGGCAGG 4486
QY 15517 CAGTGTCTGGGTGGGAAAAAGAGAGAGATGCTACAAAGACATTCGCCCTCGTTTCCG 15576
|||||
Db 4487 CAGTGTCTGGGTGGGAAAAAGAGAGAGATGCTACAAAGACATTCGCCCTCGTTTCCG 4546
QY 15577 TTAGGTCCGGGGGCGAGGGCTAAGGTGGGCACTATGTGGTATGAGACTCGGCTCGTG 15636
|||||
Db 4547 TTAGGTCCGGGGGCGAGGGCTAAGGTGGGCACTATGTGGTATGAGACTCGGCTCGTG 4606
QY 15637 ATGACACTCTTAAAAATGTTTATGATACACGTGAGATTCGGAGATAGCAAGCTGAGCC 15696
|||||
Db 4607 ATGACACTCTTAAAAATGTTTATGATACACGTGAGATTCGGAGATAGCAAGCTGAGCC 4666
QY 15697 AAGATTCAAGGCCAGCGCGCTCTGAACGAGCGGCCAAGACCTCCGCTGTTCTCTGCTCG 15756
|||||
Db 4667 AAGATTCAAGGCCAGCGCGCTCTGAACGAGCGGCCAAGACCTCCGCTGTTCTCTGCTCG 4726
QY 15757 CTGGAGGCGCGGGGCGAGGAGAACTTTATCTCCGGGTTCCAAACGCCGAGGAGACAGGG 15816
|||||
Db 4727 CTGGAGGCGCGGGGCGAGGAGAACTTTATCTCCGGGTTCCAAACGCCGAGGAGACAGGG 4786
QY 15817 GGCATACAGGGGCGAGCGGTGATCAACCCATTCCGGGGTTTAAAGAGCGCGGTCTCG 15876
|||||
Db 4787 GGCATACAGGGGCGAGCGGTGATCAACCCATTCCGGGGTTTAAAGAGCGCGGTCTCG 4846
QY 15877 GTGTGCAATTTTCCAGCCTGTATCCGAGACATATCAAGCGGCACAACTGTGTACTCC 15936
|||||
Db 4847 GTGTGCAATTTTCCAGCCTGTATCCGAGACATATCAAGCGGCACAACTGTGTACTCC 4906
QY 15937 ACCATGATACAGGAGAGACTGACCTGACCTGACCCCAACCTGAGCGCGGAGCATACAG 15996
|||||
Db 4907 ACCATGATACAGGAGAGACTGACCTGACCTGACCCCAACCTGAGCGCGGAGCATACAG 4966
QY 15997 ACGTTTGTGTGAGGCGGCGAGCGGTATATTTTGTAAAAAACAAGCGGGAGTCTCG 16056
|||||
Db 4967 ACGTTTGTGTGAGGCGGCGAGCGGTATATTTTGTAAAAAACAAGCGGGAGTCTCG 5026
QY 16057 CTGGGAAAGACTGTAACTGTGTGTAGAAAAAGCAAGGGGATCCGGCGCACTCGTGGCG 16116
|||||
Db 5027 CTGGGAAAGACTGTAACTGTGTGTAGAAAAAGCAAGGGGATCCGGCGCACTCGTGGCG 5086
QY 16117 GCGTCGATGACCCCTGCTAAAAACATCTTAAATTAACAACACACTGGGCTCAAGGTG 16176
|||||
Db 5087 GCGTCGATGACCCCTGCTAAAAACATCTTAAATTAACAACACACTGGGCTCAAGGTG 5146
QY 16177 ACATGTAACGCGGTTTACGGGTTTACCGGGGTGGCCAGGGGCTCTCCCATGCAATTAA 16236
|||||
Db 5147 ACATGTAACGCGGTTTACGGGTTTACCGGGGTGGCCAGGGGCTCTCCCATGCAATTAA 5206
QY 16237 ATAGGGAACCCGTACCGTCCGGGGGCGACAGATGTGAGATGTCAAAGTCTTAACGTG 16296
|||||
Db 5207 ATAGGGAACCCGTACCGTCCGGGGGCGACAGATGTGAGATGTCAAAGTCTTAACGTG 5266
QY 16297 GAGGCGCTGAGAGAGAAAGACTGTGGAACGGGTCTCGGTCGGAGAGTGAACCCCGCTAC 16356

Db 5267 GAGGCGCTGAGAGAGAAAGACCTGGAACGGCTCTCGGCGAGGTGACCCCGCTCAC 5326
|||||
QY 16357 GCGCGCGGTTTTCGGGCTGCTACGGTACACGACCTCCCTTTATCGCGTGCAGGTT 16416
|||||
Db 5327 GCGCGCGGTTTTCGGGCTGCTACGGTACACGACCTCCCTTTATCGCGTGCAGGTT 5386
QY 16417 TATTCGGGGAAGCCGTTTCCGCTTCTGTGACAGATCTGGCCGACAGATCACTGGGAC 16476
|||||
Db 5387 TATTCGGGGAAGCCGTTTCCGCTTCTGTGACAGATCTGGCCGACAGATCACTGGGAC 5446
QY 16477 CTGTTCGCCCCCACTTAAGTATAGAGCGGAAAGAGCTCAAGTCTGCTGCTCG 16536
|||||
Db 5447 CTGTTCGCCCCCACTTAAGTATAGAGCGGAAAGAGCTCAAGTCTGCTGCTCG 5506
QY 16537 ACGAAAAACGCTTACATCGGGGTCTTATTAAGACGACAAATATGCTATGAAGGGTGCAC 16596
|||||
Db 5507 ACGAAAAACGCTTACATCGGGGTCTTATTAAGACGACAAATATGCTATGAAGGGTGCAC 5566
QY 16597 CTATTCGCAAAACGGCTGCAAGTTCCTCAGAGAGCATGCGCGCCATCTGACCTG 16656
|||||
Db 5567 CTATTCGCAAAACGGCTGCAAGTTCCTCAGAGAGCATGCGCGCCATCTGACCTG 5626
QY 16657 GTGCTCCAGATCCCGAGGTCAAGGCTGGGGGCGGCTGTGGAAGCGGCGCGCAC 16716
|||||
Db 5627 GTGCTCCAGATCCCGAGGTCAAGGCTGGGGGCGGCTGTGGAAGCGGCGCGCAC 5686
QY 16717 GCGGTATACGAGAGGGGCTGCGGCTGCTTATTAATGATAGAGTCTCTCAACGCG 16776
|||||
Db 5687 GCGGTATACGAGAGGGGCTGCGGCTGCTTATTAATGATAGAGTCTCTCAACGCG 5746
QY 16777 AACTATCTGAGCTCCGAAACAGCTGTGCGCCATCGAGCACTTAAGCTTCTCCACCGAG 16836
|||||
Db 5747 AACTATCTGAGCTCCGAAACAGCTGTGCGCCATCGAGCACTTAAGCTTCTCCACCGAG 5806
QY 16837 CTACAGCGCGCCGCTCGGAGTTTACAAGACCAACAACCTGCGCCACTGGCGGTGTAACCA 16896
|||||
Db 5807 CTACAGCGCGCCGCTCGGAGTTTACAAGACCAACAACCTGCGCCACTGGCGGTGTAACCA 5866
QY 16897 AAGCTGCGAGCAGAGTGCAGAGAGCTGCCCAAGGTGCAAGATAGATCCCTTACGTGTT 16956
|||||
Db 5867 AAGCTGCGAGCAGAGTGCAGAGAGCTGCCCAAGGTGCAAGATAGATCCCTTACGTGTT 5926
QY 16957 GTTGAAGCGCCCGGGTCCCTAAAGTGCAGACTGCGCCGAAACACCGGGATTACGTACA 17016
|||||
Db 5927 GTTGAAGCGCCCGGGTCCCTAAAGTGCAGACTGCGCCGAAACACCGGGATTACGTACA 5986
QY 17017 CACCAAGATTCCTGTCGCGGTGACCTATATTTGCAACAACTGTGTCACGCGCGGCCAAC 17076
|||||
Db 5987 CACCAAGATTCCTGTCGCGGTGACCTATATTTGCAACAACTGTGTCACGCGCGGCCAAC 6046
QY 17077 ATCTTCAGTGTCTGTTCGGCAACAACGCGGACACACAGGTGGCCATCTCTTACAATTT 17136
|||||
Db 6047 ATCTTCAGTGTCTGTTCGGCAACAACGCGGACACACAGGTGGCCATCTCTTACAATTT 6106
QY 17137 CTCAACGTCCTGTATTAAGCTGTCTGTGTAAGCCCAATTTGGAAGCCCAATTAAGCG 17196
|||||
Db 6107 CTCAACGTCCTGTATTAAGCTGTCTGTGTAAGCCCAATTTGGAAGCCCAATTAAGCG 6166
QY 17197 CCGGCGCAGCGGAGTCCGAGGAGAGCTGCAAGCGGCGAGAGCAACCAAGAGACCGC 17256
|||||
Db 6167 CCGGCGCAGCGGAGTCCGAGGAGAGCTGCAAGCGGCGAGAGCAACCAAGAGACCGC 6226
QY 17257 CACCATGCTGTGTTAAAGAACTGTGCTGCTGCGGCACTGGAAGGTGACTTTTCACCG 17316
|||||
Db 6227 CACCATGCTGTGTTAAAGAACTGTGCTGCTGCGGCACTGGAAGGTGACTTTTCACCG 6286
QY 17317 GGGTAGATTACGCTTCGTCAACCTCAACCCGCTGGAACGTTCAAGGGGCGACAGGGGCTA 17376
|||||
Db 6287 GGGTAGATTACGCTTCGTCAACCTCAACCCGCTGGAACGTTCAAGGGGCGACAGGGGCTA 6346
QY 17377 GCGCAGGGTGCAGACTCCCTTCTGCTGACAGATTACTCCACAACATTTTCGCTTCGG 17436
|||||

Db	6347	CGCCAGGGTCCGACATCCCCCTTCCTCGCTCCAGCACAGTTATCTCACAAACATTGGCGTTCCG	6406
Oy	17437	ACTCGTAGCGCGTCTCAAGGAACATGCCCCCTTCCTCCGACTGCGTGCCCTTATCGCCCC	17438
Db	6407	ACTCGTAGCGCGTCTCAAGGAACATGCCCCCTTCCTCCGACTGCGTGCCCTTATCGCCCC	6466
Oy	17497	GTTTGGAATCCGGCGGCGACCGGACGGGCGCGCTGGGCCCTCGGTGCTGTGATCTC	17556
Db	6467	GTTTGGAATCCGGCGGCGACCGGACGGGCGCGCGCTGGGCCCTCGGTGCTGTGATCTC	6526
Oy	17557	CTCTCGGCGCGCTGACCGGTGGGGTAAACGGGACCGGGGGGACACAGATCGGGTTCGGCT	17616
Db	6527	CTCTCGGCGCGCTGACCGGTGGGGTAAACGGGACCGGGGGGACACAGATCGGGTTCGGCT	6586
Oy	17617	CTCTTTCTTAAGCCGATACCTGTGAGCCGCGCGGTACAGTGTTCGGGAGAACGG	17678
Db	6587	CTCTTTCTTAAGCCGATACCTGTGAGCGCGCGGTACAGTGTTCGGGAGAACGG	6646
Oy	17677	CGGCGCGCGCTCGGAGGGGACCCCAAGGCCACCTGCGGACCGAAAGCTGCGCGGTG	17738
Db	6647	CGGCGCGCGCTCGGAGGGGACCCCAAGGCCACCTGCGGACCGAAAGCTGCGCGGTG	6706
Oy	17737	ACCCCTGCGGCTGCCGGGAGGCGGTCTGAGAGTGGGCCCATTTCTTGTTGGCGATTT	17798
Db	6707	ACCCCTGCGGCTGCCGGGAGGCGGTCTGAGAGTGGGCCCATTTCTTGTTGGCGATTT	6766
Oy	17797	TCCACAGCGCACTCGGTGGCTGCGCTTAAGCTGTGGTTCAGAGTAGAGCGCTTTTC	17858
Db	6767	TCCACAGCGCACTCGGTGGCTGCGCTTAAGCTGTGGTTCAGAGTAGAGCGCGTTTC	6826
Oy	17857	GGATGACGGGCGCACAGGAGCGGCGGATCTCCCGGAATACGTACGTTTAGTATCTC	17918
Db	6827	GGATGACGGGCGCACAGGAGCGGCGGATCTCCCGGAATACGTACGTTTAGTATCTC	6886
Oy	17917	CGGGGGTAAAGTCTGCGAAGGCGGTCCGTTCAACAGGCTGCCGCTCGCGGTAAAGGCG	17978
Db	6887	CGGGGGTAAAGTCTGCGAAGGCGGTCCGTTCAACAGGCTGCCGCTCGCGGTAAAGGCG	6946
Oy	17977	GCAAAATGGAATCATCTACGCTCCCGGGGAGCCCAACGCGGAGATAGTCTCGGCGCACTC	18038
Db	6947	GCAAAATGGAATCATCTACGCTCCCGGGGAGCCCAACGCGGAGATAGTCTCGGCGCACTC	7006
Oy	18037	CGGACCCGCTCTGCGCACCCACACCGGCGGCGCGATTTGGGGGTCTACGCCGACGCCGA	18096
Db	7007	CGGACCCGCTCTGCGCACCCACACCGGCGGCGCGATTTGGGGGTCTACGCCGACGCCGA	7066
Oy	18097	AAAAACCATCACTCAACTGGAAGCTCCGGGAAATCCGGGTTCACTTAATCTTCCAAACAGG	18158
Db	7067	AAAAACCATCACTCAACTGGAAGCTCCGGGAAATCCGGGTTCACTTAATCTTCCAAACAGG	7126
Oy	18157	AGCGGCGGCTCGGGGCGCATCTGGGGTTTCGGTACAGGGGAGTGGACCGGAGCGCCCTATT	18218
Db	7127	AGCGGCGGCTCGGGGCGCATCTGGGGTTTCGGTACAGGGGAGTGGACCGGAGCGCCCTATT	7186
Oy	18217	CGTGTGACCCCGGCACTCTTGTTCGGGTTGCACAAACCACTGCGGCTATTTCACACC	18278
Db	7187	CGTGTGACCCCGGCACTCTTGTTCGGGTTGCACAAACCACTGCGGCTATTTCACACC	7246
Oy	18277	CAACGGTAAACCCCAACGACTATAAAAAAGACACACCTTTGAGCGCGCGCGCTCGCC	18338
Db	7247	CAACGGTAAACCCCAACGACTATAAAAAAGACACACCTTTGAGCGCGCGCGCTCGCC	7306
Oy	18337	CGTGTGCGATTAAGTCTCGCGCGACGAGCGGCGCGGACACTGTGCGCGTACACAGACG	18398
Db	7307	CGTGTGCGATTAAGTCTCGCGCGACGAGCGGCGCGGACACTGTGCGCGTACACAGACG	7366
Oy	18397	CGGGGCGCTCTCATTAACGCGTTACAAATCCGCGTGGTTTTCCAGGGGTGGTCTCGCG	18458
Db	7367	CGGGGCGCTCTCATTAACGCGTTACAAATCCGCGTGGTTTTCCAGGGGTGGTCTCGCG	7426
Oy	18457	GGAGTGTACGTGTCTTACAGCGACAAACGGGGTTCACGAAACGATGACATTATGACGGA	18518
Db	7427	GGAGTGTACGTGTCTTACAGCGACAAACGGGGTTCACGAAACGATGACATTATGACGGA	7486

QY	18517	ACGATGGGAACACCGGTGCGTTTCTTTCGCGCGAGTGGCAGACCTCCAGTCTAGTGGAC	18576
Db	7487	ACGATGGGAACACCGGTGCGTTTCTTTCGCGCGAGTGGCAGACCTCCAGTCTAGTGGAC	7546
QY	18577	AACGGCAGCCACCGGTACAGCTCCCGGTGTGGGCGCCAGTATTACAGACGGCTACGAG	18636
Db	7547	AACGGCAGCCACCGGTACAGCTCCCGGTGTGGGCGCCAGTATTACAGACGGCTACCTG	7606
QY	18637	ACACTGTGTAACAGGTTCAGAGCTGTGCGCTACAGGAGAGGTCTCCGTCTGCGCGCATGC	18696
Db	7607	ACACTGTGTAACAGGTTCAGAGCTGTGCGCTACAGGAGAGGTCTCCGTCTGCGCGCATGC	7666
QY	18697	CCCACATCAGGAGACAGTGTGGGGAAGAGTTCGCCGCTCGCCCTTTCGCCACGGCCACT	18756
Db	7667	CCCACATCAGGAGACAGTGTGGGGAAGAGTTCGCCGCTCGCCCTTTCGCCACGGCCACT	7726
QY	18757	CTGGCGCATCGGGGGAACACGACACCGGTCTACAGCGCTTGAGTCCAGCGCAACACCCACTG	18816
Db	7727	CTGGCGCATCGGGGGAACACGACACCGGTCTACAGCGCTTGAGTCCAGCGCAACACCCACTG	7786
QY	18817	GACATATGTAACCCGCGGTGTCGAGCGCGCGGATCCGGAAGTGGTGGGGTTTCAAGCT	18876
Db	7787	GACATATGTAACCCGCGGTGTCGAGCGCGCGGATCCGGAAGTGGTGGGGTTTCAAGCT	7846
QY	18877	CCGCAACACACCGCGGTGTGCGGATACGAGACTTAAAGTATTGCTGTCGATCTGTACGGTG	18936
Db	7847	CCGCAACACACCGCGGTGTGCGGATACGAGACTTAAAGTATTGCTGTCGATCTGTACGGTG	7906
QY	18937	GTCGCGCGCGCGCGGGGTGTTCTCTACACTTTCACACAAGCCGCTCCGATCCGCGTGACA	18996
Db	7907	GTCGCGCGCGCGCGGGGTGTTCTCTACACTTTCACACAAGCCGCTCCGATCCGCGTGACA	7966
QY	18997	GACGGGTGAGGACAGAGGGGTCCAGGCTAACCTCTGAAGAGCGCGTGAATTAATAATTCAA	19056
Db	7967	GACGGGTGAGGACAGAGGGGTCCAGGCTAACCTCTGAAGAGCGCGTGAATTAATAATTCAA	8026
QY	19057	GGCTTTCCCGCTCTATCTGACGAGACCGGCAACCCATTCTCTTAAACCCAGGAAGACCAAG	19116
Db	8027	GGCTTTCCCGCTCTATCTGACGAGACCGGCAACCCATTCTCTTAAACCCAGGAAGACCAAG	8086
QY	19117	CCCTTTACCGAGACGAAGTTTTCGCGCGTATCATGGACACAGCACGACGCGCGTTC	19176
Db	8087	CCCTTTACCGAGACGAAGTTTTCGCGCGTATCATGGACACAGCACGACGCGCGTTC	8146
QY	19177	AACACCGTCTACTCTGGGAAGACGACAGTGAAGGTTACCGTGAACCCGCCCGCCGGAACA	19236
Db	8147	AACACCGTCTACTCTGGGAAGACGACAGTGAAGGTTACCGTGAACCCGCCCGCCGGAACA	8206
QY	19237	ATCGTACCCGAGCGGCCCGGTGAAGGCGTGTCCCTCAACCGGTAAATGCGCAATGCGC	19296
Db	8207	ATCGTACCCGAGCGGCCCGGTGAAGGCGTGTCCCTCAACCGGTAAATGCGCAATGCGC	8266
QY	19297	TTTTCGCAACACCCATCTTTGAACATCCCGGTGCTCTCCCAACGGCGGATATTACAGCCC	19356
Db	8267	TTTTCGCAACACCCATCTTTGAACATCCCGGTGCTCTCCCAACGGCGGATATTACAGCCC	8326
QY	19357	GTCGTGTACGTGGGCGCTGACCGGTGTGATCCACCCCACTGTAGCAAAATTCTGAAGGTAC	19416
Db	8327	GTCGTGTGTACGTGGGCGCTGACCGGTGTGATCCACCCCACTGTGTAGCAAAATTCTGAAGGTAC	8386
QY	19417	GGTAAACACTAGCTGTGCGCATTTTAAACCGCAAGCTACGGCGTATTATTAGCATTCAGGCC	19476
Db	8387	GGTAAACACTAGCTGTGCGCATTTTAAACCGCAAGCTACGGCGTATTATTAGCATTCAGGCC	8446
QY	19477	CACAACGGGCGGTCTCCGATTCAGAGCTCGAGTGGCCACCCGAACCGGAGATAGAGATT	19536
Db	8447	CACAACGGGCGGTCTCCGATTCAGAGCTCGAGTGGCCACCCGAACCGGAGATAGAGATT	8506
QY	19537	TTGTGTAAACCAAGCTGTCCAGGCGCCCGGTGTACATACAGACGGGACGCACTGGGGCAA	19596
Db	8507	TTGTGTAAACCAAGCTGTCCAGGCGCCCGGTGTACATACAGACGGGACGCACTGGGGCAA	8566

OY	19597	GCATCTTTCGTTTCGGCCGGGTTTCGGTGGCCGGCAAACTGGGCGACGTCCTCGGC	19596
Db	8567	GCATCTTCGTTTCGGCCGGGTTTCGGTGGCCGGCAAACTGGGCGACGTCCTCGGC	8626
OY	19657	CACCATCGGGCCCTCGAGAGCTCCGGGGGGGGGTACAGTGGACAGCCAAAACGTTGT	19716
Db	8627	CACGATCGGGGGCCCTGGAGCTACCGGGGGGGGTGACAGTGGACAGCCAAAACGTTGT	8686
OY	19717	AGTTTAGACATGTACCTGTTTCCAGCTAAATTACTAATAACCGTTGCTCGTATC	19776
Db	8687	AGGTTTAGACATGTACCTGTTTCCACGTAATTACTAATAACCGTTGCTCGTATC	8746
OY	19777	GCTACACAAGGCCAAACGGTCTCAATTCGGGGGGGGGGGGCCCGGGAACACACAAG	19836
Db	8747	GCTACACAAGGCCAAACGGTCTCAATTCGGGGGGGGGGGGCCCGGGAACACACAAG	8806
OY	19837	GTGGCTCAAAACACCCCTCCCGACCCCTCGCACAAAACAGTAACGGCTTCCTGT	19896
Db	8807	GTGGCTCAAAACACCCCTCCCGACCCCTCGCACAAAACAGTAACGGCTTCCTGT	8866
OY	19897	AGATGCAGTTTATTTATTTATTTATTAATCATAGCTATTGCGGGGCCCGTCCGC	19956
Db	8867	AGATGCAGTTTATTTATTTATTTATTTATTAATCATAGCTATTGCGGGGCCCGTCCGC	8926
OY	19957	AAATATGTGAGATTTCCAGTATGCGAAACGGGCGTGAACAACAGTCCCGGGGCTCTG	20016
Db	8927	AAATATGTGAGATTTCCAGTATGCGAAACGGGCGTGAACAACAGTCCCGGGGCTCTG	8986
OY	20017	CCCTCCCAACGACAGCACGGTTTTCATATAGACTCCGGCCACCTATCTTGTTATTTAC	20076
Db	8987	CCCTCCCAACGACAGCACGGTTTTCATATAGACTCCGGCCACCTATCTTGTTATTTAC	9046
OY	20077	GGGAAGCTCTCTCAATTAGAGAGTGAAGGCGGACAGCACAGGTCACCGGAGACCAAT	20136
Db	9047	GGGAAGCTCTCTCAATTAGAGAGTGAAGGCGGACAGCACAGGTCACCGGAGACCAAT	9106
OY	20137	GGCGGGGGGCTCCGGCGTCCCGGGGGGGGCGTGCACAGACATCCTACGCGGTCAAGTA	20196
Db	9107	GGCGGGGGGCTCCGGCGTCCCGGGGGGGGCGTGCACAGACATCCTACGCGGTCAAGTA	9166
OY	20197	ACTCTCTAGAGCCCGGAGGCCCGGGAACCATGGCGTTCATACACTCGGCCCGCGAAACTC	20256
Db	9167	ACTCTCTAGAGCCCGGAGGCCCGGGAACCATGGCGTTCATACACTCGGCCCGCGAAACTC	9226
OY	20257	GGCGGCTGGCACTCAACGTTAGACATCAATATAGGAAAGTGAACAAACAGCATGTATCG	20316
Db	9227	GGCGGCTGGCACTCAACGTTAGACATCAATATAGGAAAGTGAACAAACAGCATGTATCG	9286
OY	20317	CGGGTACTCAACGACCCGAGAGAGAGTGTGTGGCACAGGTAAACGACACAGCGCTG	20376
Db	9287	CGGGTACTCAACGACCCGAGAGAGAGTGTGTGGCACAGGTAAACGACACAGCGCTG	9346
OY	20377	TATGTTTAAACCCCACTTCAGACAGGGCCCGCTGCTCAGTCAAGAGAGCGCGGTGGCC	20436
Db	9347	TATGTTTAAACCCCACTTCAGACAGGGCCCGCTGCTGCTCAGAGAGAGCGCGGTGGCC	9406
OY	20437	GGCCCACTGGGGGAGAACGTTAATTCAGGCGCAGTCGGGGGAGGCCAGCGTAGGGCT	20496
Db	9407	GGCCCACTGGGGGAGAACGTTAATTCAGGCGCAGTCTGGGGGAGGCCAGCGTAGGGCT	9466
OY	20497	GGCGGCCCAACAGACAGGTAAAAACAAGACGAACAGACAGGAGACATGACCGGTTAAAT	20556
Db	9467	GGCGGCCCAACAGACAGGTAAAAACAAGACGAACAGACAGGAGACATGACCGGTTAAAT	9526
OY	20557	TACTCGGTTCAATTCGGGGGGGGGGCGGCTCAACGCCAGAGTCCNTTAAAAACACACGG	20616
Db	9527	TACTCGGTTCAATTCGGGGGGGGGGCGGCTCAACGCCAGGTCCATTTAAAAACACACGG	9586
OY	20617	CCGCGCAACCCCAACGAGGGGGCGCGCCCTCGGAACCGGTTCCTTCCTCAATCGCAAGAAC	20676
Db	9587	CCGCGCAACCCCAACGAGGGGGCGCGCCCTCGGAACCGGTTCCTTCCTCAATCGCAAGAAC	9646
OY	20677	CGCGTCAAAAAAGGCTCGTTTGAACCATTTGTGTCATCGGGTTTCGTTTCAGAT	20736

[illegible]

QY	20903	16TCTCCCGACGCTGGAAGCAGACAGGAGATCAACGTGTGTTTAAACGTGGGCGTCACC	20902
Db	1501	GGCTCCCTCGACGCTGAAGCAGACAGGGGATCAACGTGGTGTGTTAAACGTGGGCGTCACC	1560
QY	20963	CAAGGTGACCAAAAGTCTCCCGGGGTCAGAGCCGTGACGTGAGCATAGATACGTCAAG	21022
Db	1561	CAAGGTGACCAAAAGTCTCCCGGGGTCAGAGCCGTGACGTGAGCATAGATACGTCAAG	1620
QY	21023	GAGGCGGTAGCTGGCGATGTTTAAACGGGACCCCGAGGCCCCATGTGCGGCGGACCTGTGATA	21082
Db	1621	GAGGCGGTAGCTGGCGATGTTTAAACGGGACCCCGAGGCCCCATGTGCGGCGGACCTGTGATA	1680
QY	21083	CAGCTGGCAGACAGCTCTCCCCCGAGCCAGCTAAACTGACACAAAAGTGAACAGAGAG	21142
Db	1681	CAGCTGGCAGACAGCTCTCCCCCGAGCCAGCTAAACTGACACAAAAGTGAACAGAGAG	1740
QY	21143	GAGAGCCATCCCGCCGAGAGTCCGGGGGTTCCACGGGCAATPAGCATGGCGGATCGAG	21202
Db	1741	GAGAGCCATCCCGCCGAGAGTCCGGGGGTTCCACGGGCAATPAGCATGGCGGATCGAG	1800
QY	21203	GGGCGGCCGTGTTAAFTAGATCCACACAGTAACGACAGTGGTCTCCACCCTCGACCCCTGATA	21262
Db	1801	GGGCGGCCGTGTTAAFTAGATCCACACAGTAACGAGTGGTCTCCACCCTCGACCCCTGATA	1860
QY	21263	GTTGGCGCTGGCCCCCTGTGATCTCCGCCCCCAAAATGTCTCTCACTGAAACCGCTGACCGG	21322
Db	1861	GTTGGCGCTGGCCCCCTGTGATCTCCGCCCCCAAAATGTCTCTCACTGAAACCGCTGACCGG	1920
QY	21323	CCCCAGATTCGCGCTCGGCGGGGAGTCCCGCCAGAGCCCTGGCGCCGCAAAAAGGCGGGGACCG	21382
Db	1921	CCCCAGATTCGCGCTCGGCGGGGAGTCCCGCCAGAGCCCTGGCGCCGCAAAAAGGCGGGACCG	1980
QY	21383	GTGCGCGTCCCAAAFTTTTAAAGCGCGCGCGAGCACTGTGGTGAAGTGGAGGCCCT	21442
Db	1981	GTGCGCGTCCCAAAFTTTTAAAGCGCGCGCGAGCACTGTGGTGAAGTGGAGGCCCT	2040
QY	21443	GATTAACCAACAGCAACTCTCCACAGAGCCCCCTCCAAAACACCTTTTGGTGTATACAG	21502
Db	2041	GATTAACCAACAGCAACTCTCCACAGAGCCCCCTCCAAAACACCTTTTGGTGTATACAG	2100
QY	21503	AGGAACATCTGCGCTCGTAGGTTTATATCGGGGCTTAAGCCCGACACGAGCACTGGTGGCCAC	21562
Db	2101	AGGAACATCTGCGCTCGTAGGTTTATATCGGGGCTTAAGCCCGACACGAGCACTGGTGGCCAC	2160
QY	21563	GCCGCTCCTGTCTCTCCCTCTGACAGCGCCGTGTTTAAFTAAATTCAGGTGCGCCAAAGTA	21622
Db	2161	GCCGCTCCTGTCTCTCCCTCTGACAGCGCCGTGTTTAAFTAAATTCAGGTGCGCCAAAGTA	2220
QY	21623	CTGCAAGCTCGCGCTGTGCTCGCCGGGACAGCGCAGCGAGCGCGCGGCACTTCCGGGTGC	21682
Db	2221	CTGCAAGCTCGCGCGCTGTGCTCGCCGGGACAGCGCAGCGAGCGCGCGGCACTTCCGGGTGC	2280
QY	21683	GGAAGAAAAACCGGAGTGTGTGCGGGCGGAGTTTCCAGCGACGCAAAAGGGATATATTTT	21742
Db	2281	GGAAGAAAAACCGGAGTGTGTGCGGGCGGAGTTTCCAGCGACGCAAAAGGGATATATTTT	2340
QY	21743	AACGTAGACATACCGAGATGACACACAGACATCATATTTACAAACGAGAGCTCTTACAA	21802
Db	2341	AACGTAGACATACCGAGATGACACACAGACATCATATTTACAAACGAGAGCTCTTACAA	2400
QY	21803	CTATTAACCGTTAAACGGCTGAAGACGAACCTTATTTTAAAGGCAAGTGTGGGCGGGCGCAC	21862
Db	2401	CTATTAACCGTTAAACGGCTGAAGACGAACCTTATTTTAAAGGCAAGTGTGGGCGGGCGCAC	2460
QY	21863	CACAGGGGGGCGCGCGCTGTACCGAGTAAACCCAGCTGTCTCCCAAGCGCTTCC	21922
Db	2461	CACAGGGGGGCGCGCGCTGTGTACCGAGTAAACCCAGCTGTCTCCCAAGCGCTTCC	2520
QY	21923	CCGAGCGCTGAGCGTCTCCCAAAAGCCAAAACAACACAGATATATTAATTAATTAACATG	21982
Db	2521	CCGAGCGCTGAGCGTCTCCCAAAAGCCAAAACAACACAGATATATTAATTAATTAACATG	2580
QY	21983	TTTAAFTTTTATAAACTTAAACGGCGATTAATGCTTCTTAAACAGGGGCCAATGAAGCAAC	22042

Db	2581	TTTATTTTTTTAAACCTTAACGGCGATTAAGCTTCTTAACAGGGGCAATTAGAACAAAC	2640
QY	22043	GTGGCAGCGGCATCTCGCGCGCTCAAAAGGCAACCGCAACCGCGCGCTGTAAACAGCTA	22102
Db	2641	GTGGCAGGGCGGCATTTGGGGGCTCAAAAGGCAACCGCAACCGGGGCTGTAAACAGCTA	2700
QY	22103	AACAACAACTAATTAGCCATTCTGTAAACCGTAAATCCAACCCCTGTGCTCCGAGCCATT	22162
Db	2701	AACAACAACATTAATAGCCATTCTGTAAACCGTAAATCCAACCCCTGTGCTCCGAGCCATT	2760
QY	22163	CGCCGAGTGGCTGTACGTGCAAGGGGTGTTTCTAAGTGTGCAATTTGAGCCCTTGCGACGGC	22222
Db	2761	CGCCGAGTGGCTGTACGTGCAAGGGGTGTTTCTAAGTGTGCAATTTGAGCCCTTGCGACGGC	2820
QY	22223	CGCGCTCTGTAAATGCTTTCTAAATTCGCCGTCCAGCAAGCCCTTGTGGAATCGTCAA	22282
Db	2821	CGCGCTCTGTAAATGCTTTCTAAATTCGCCGTCCAGCAAGCCCTTGTGGAATCGTCAA	2880
QY	22283	TCAGGCTCGCGGGGTCTCTGCGCTTTTGGGAGCGTGTCCACCGGCTGAGCAGATT	22342
Db	2881	TCAGGCTCGCGGGGTCTCTGCGCTTTTGGGAGCGTGTCTACCGGCTGAGCAGATT	2940
QY	22343	TCTTACGCGCTGCCCCGGGATTTGGCACAACCTTTACGGCGGCAAGTGTTAATA	22402
Db	2941	TCTTACGCGCTGCCCCGGGATTTGGCACAACCTTTTACCGCGGCAAGTGTTAATA	3000
QY	22403	TCACGGCGCTCCACGAGACATGCGACAGAGGTGTGTGAGTAAGACACTAAACCGGCTG	22462
Db	3001	TCACGGCGCTCCACGAGACATGCGACAGAGGTGTGTGAGTAAGACACTAAACCGGCTG	3060
QY	22463	GGCGGAGATGAGTTACATACCCCAACAGCAGAGTTGGCGCGGCTCGGCTATGTGAGC	22522
Db	3061	GGCGGAGATGAGTTACATACCCCAACAGCAGAGTTGGCGCGGCTCGGCTATGTGAGC	3120
QY	22523	CCATGAGAAAGGCAATACACTACACGCGGAACCGCAAAAAAGGCAACAGCAAGAAA	22582
Db	3121	CCATGAGAAAGGCAATACACTACACGCGGAACCGCAAAAAAGGCAACAGCAAGAAA	3180
QY	22583	GGCCCGCTATGCTGACAAAACACAAAACAAAGACGGGCTCGCTGCTGGCTTGCACACAG	22642
Db	3181	GGCCCGCTATGCTGACAAAACACAAAACAAAGACGGGCTCGCTGCTGGCTTGCACACAG	3240
QY	22643	CGCCACGCTCGCCGCTGCTCGGCGCACGGTGTGACGGGCTCATTAATACCGCGGCCGGGC	22702
Db	3241	CGCCACGCTCGCCGCTGCTCGGCGCACGGTGTGACGGGCTCATTAATACCGCGGCCGGGC	3300
QY	22703	CCGCTCGACAGGAAACCAAGGCTGTGAGCCACTGACGACGCTGCCCTCCGTCAGATG	22762
Db	3301	CCGCTCGACAGGAAACCAAGGCTGTGAGCCACTGACGACGCTGCCCTCCGTCAGATG	3360
QY	22763	TGGCATTCGAGTCCCAAAAAGGGCGTGTAACTACAGCTCGCGCCGGGGTTCAAAAGATC	22822
Db	3361	TGGCATTCGAGTCCCAAAAAGGGCGTGTAACTACAGCTCGCGCCGGGGTTCAAAAGATC	3420
QY	22823	GGGATGCCCAACAGGTAATAAAGCTTTTGTCCAAACGAAAGCCAACAGCACCGAA	22882
Db	3421	GGGATGCCCAACAGGTAATAAAGCTTTTGTCCAAACGAAAGCCAACAGCACCGAA	3480
QY	22883	AGGAATCTCCAAAACAGCAAGGTCCTCCGTCGGGGCATTAAGGAAATTTTCCCTCACAC	22942
Db	3481	AGGAATCTCCAAAACAGCAAGGTCCTCCGTCGGGGCATTAAGGAAATTTTCCCTCACAC	3540
QY	22943	TAAACACACGGCGCGGTAACCTGTTAAACACGCAATACTTCCTAGGCGCTGTATTAT	23002
Db	3541	TAAACACACGGCGCGGCTTAACCTGTTAAACACGCAATACTTCTTAGGCGCTGTATTAT	3600
QY	23003	AAAACACAAAGGGTGTAAATTTTCGCGGGGCTTTTGCGCCCGCGCGCTGTGAGGGTGGC	23062
Db	3601	AAAACACAAAGGGTGTAAATTTTCGCGGGGCTTTTGCGGGGCTTTTGCGGGTGGGCTGGC	3660
QY	23063	TTGTCTGTTGTGTGCAATACCAACCCCGCTGCGGAAACAGGCAACACCCCT	23122

Db 3661 TTGTCGTGTTGTTGCGAATGACACACCCGCCCTGCCGAAAAACAGGGCAACACCCCC 3720
QY 23123 TGCCCTAGTTTTTTAAACTTAACACGGGCAAGGGAGAGAGAGAGGGGTGCGCTAA 23182
Db 3721 TGCCCTAGTTTTTTAAACTTAACACGGGCAAGGGAGAGAGAGAGGGGTGCGCTAA 3780
QY 23183 ATGGGCTGTATGACGACCCACCGCA 23206
Db 3781 ATGGGCTGTATGACGACCCACCGCA 3804

RESULT 5
AF159033 475 bp DNA linear VRL 28-Apr-2000
LOCUS Macaque gamma virus strain Macaca mulatta gamma virus DNA
DEFINITION polymerase (pol) gene, partial cds.
ACCESSION AF159033
VERSION AF159033.1 GI:6671074
KEYWORDS
SOURCE Macaque gamma virus
ORGANISM Macaque gamma virus
VIRUSES: dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Rhadinovirus.

REFERENCE 1 (bases 1 to 475)
AUTHORS Strand,K., Harper,E., Thormahlen,S., Thoulless,M.E., Tsai,C.,
Rose,T. and Bosch,M.L.
TITLE Two distinct lineages of macaque gamma herpesviruses related to the
Kaposi's sarcoma associated herpesvirus
JOURNAL J. Clin. Virol. 16 (3), 253-269 (2000)
MEDLINE 20204465
PUBMED 10738144

REFERENCE 2 (bases 1 to 475)
AUTHORS Strand,K.B. and Bosch,M.L.
TITLE Direct Submission
JOURNAL Submitted (14-JUN-1999) Pathobiology, University of Washington, Box
357238, Seattle, WA 98125, USA
location/Qualifiers
1. 475
/organism="Macaque gamma virus"
/mol_type="genomic DNA"
/strain="Macaque mulatta gamma virus"
/db_xref="taxon:111468"
/gene="pol"
/gene="pol"
/gene="pol"
/codon_start=2
/product="DNA polymerase"
/protein_id="AAE23083.1"
/db_xref="GI:6671075"
/translation="SIIOAHNLCTSPMIGHRDHLHPNLTTPDDYEFVLSGGPVHEVK
KHRESLIGRLTVLEKRRIRRTLAACDDPSLKTLDKQOLAIVKTCNAVVGFTV
ASGLPCINAEIVTIRGRITMLEMSKSYVALTTEDLRTRIGREVTARHARRRVV"

BASE COUNT 110 a 141 c 143 g 81 t
ORIGIN

Query Match 1.2%; Score 475; DB 1; Length 475;
Best Local Similarity 100.0%; Pred. No. 4,8e-268;
Matches 475; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 181 AGAAAAAGGAGGCGATCCGCGCACCCCTGGCGCGCTGGGATGACCCGTGCTAAAAAC 240
QY 16143 CATCTTAGATAAACAAACAGCTGGCCATCAAGTGCATCACTGTAACCCGTTACGGCTCAC 16202
Db 241 CATCTTAGATAAACAAACAGCTGGCCATCAAGTGCATCACTGTAACCCGTTACGGCTCAC 300
QY 16203 CGGGGTGGCAGCGGCTCCCTCCATGATTAACATAGCGGAACCGCTGACGCTCGGGG 16262
Db 301 CGGGGTGGCAGCGGCTCCCTCCATGATTAACATAGCGGAACCGCTGACGCTCGGGG 360

QY 16263 GCGCAGATGCTGAGATGTCAAAGTCTACGTGAGAGCCCTGACGACGGAAGACCTGCG 16322
Db 361 GCGCAGATGCTGAGATGTCAAAGTCTACGTGAGAGCCCTGACGACGGAAGACCTGCG 420

QY 16323 AACGCTCTGCTGCTGCGCAGAGTGAACCGGCGCTGACGAGCGGCTTGGCGCTGTC 16377
Db 421 AACGCTCTGCTGCTGCGCAGAGTGAACCGGCGCTGACGAGCGGCTTGGCGCTGTC 475

RESULT 6
AF159041 395 bp DNA linear VRL 28-Apr-2000
LOCUS Macaque gamma virus strain Macaca mulatta gamma virus glycoprotein
DEFINITION B (gB) gene, partial cds.
ACCESSION AF159041
VERSION AF159041.1 GI:6671090
KEYWORDS
SOURCE Macaque gamma virus
ORGANISM Macaque gamma virus
VIRUSES: dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Rhadinovirus.

REFERENCE 1 (bases 1 to 395)
AUTHORS Strand,K., Harper,E., Thormahlen,S., Thoulless,M.E., Tsai,C.,
Rose,T. and Bosch,M.L.
TITLE Two distinct lineages of macaque gamma herpesviruses related to the
Kaposi's sarcoma associated herpesvirus
JOURNAL J. Clin. Virol. 16 (3), 253-269 (2000)
MEDLINE 20204465
PUBMED 10738144

REFERENCE 2 (bases 1 to 395)
AUTHORS Strand,K.B. and Bosch,M.L.
TITLE Direct Submission
JOURNAL Submitted (14-JUN-1999) Pathobiology, University of Washington, Box
357238, Seattle, WA 98125, USA
location/Qualifiers
1. 395
/organism="Macaque gamma virus"
/mol_type="genomic DNA"
/strain="Macaque mulatta gamma virus"
/db_xref="taxon:111468"
/gene="gB"
/gene="gB"
/gene="gB"
/codon_start=3
/product="glycoprotein B"
/protein_id="AAE23091.1"
/db_xref="GI:6671091"
/translation="GTEDKTHQESILVFKKNIVPIHFKRRIRKVAITSVYRGWTE
TAVTGKQEVIRPVQYIEINMDTTYOCFSSMRVNVNIVTYTDRDPTNOTVFLQPE
GLINDIORYESQVLYTTPGMFPGIYIVR"

BASE COUNT 106 a 113 c 108 g 68 t
ORIGIN

Query Match 0.8%; Score 331; DB 1; Length 395;
Best Local Similarity 99.7%; Pred. No. 3.3e-183;
Matches 381; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11759 CGGGCAGCGAGACAAAGCAGCAAGAGCATCGATGCTTTAAAAAATATPTG 11818
Db 1 CGGGCAGCGAGACAAAGCAGCAAGAGCATCTGATGCTTTAAAAAATATTTG 60

QY 11819 TCCCGACATCTTTAAGGTACAGAGGTAACCGCAAGGTGGCCACCTGGTGGACCGTCTATC 11878
|||||
Db 61 TCCCGACATCTTTAAGGTACAGAGGTAACCGCAAGGTGGCCACCTGGTGGACCGTCTATC 120
QY 11879 GAGGCTGACCGAGAGACCCCGCTGACCGGCAAGCAGAGAGTATCCGACCGGTGGCCAGT 11938
|||||
Db 121 GAGGCTGACCGAGAGACCCCGCTGACCGGCAAGCAGAGAGTATCCGACCGGTGGCCAGT 180
QY 11939 ACGAGATCAACCAACATGACACAGACCTTACCAAGTGTTCAGTCTCACGCGCGTAAACGTCA 11998
|||||
Db 181 ACGAGATCAACCAACATGACACAGACCTTACCAAGTGTTCAGTCTCACGCGCGTAAACGTCA 240
QY 11999 ACGGATGTAAACACCTACACAGGAGGAGTCTTACCTACCAAGACCGGTGTTCGCAAC 12058
|||||
Db 241 ACGGATGTAAACACCTACACAGGAGGAGTCTTACCTACCAAGACCGGTGTTCGCAAC 300
QY 12059 CGGTGAGAGGCTCAGCATTAACATCCAGCATCTTACAGTACAGCGGTGTTCGATACAGA 12118
|||||
Db 301 CGGTGAGAGGCTCAGCATTAACATCCAGCATCTTACAGTACAGCGGTGTTCGATACAGA 360
QY 12119 CACCGGATGTTTCCGGGAAT 12140
|||||
Db 361 CACCGGATGTTTCCGGGAAT 382
RESULT 7
AF159040 320 bp DNA linear VRL 28-APR-2000
LOCUS Macaque gamma virus strain Macaca fascicularis gamma virus
ACCESSION AF159040
KEYWORDS glycoprotein B (gB) gene, partial cds.
SOURCE AF159040.1 GI:6671088
ORGANISM Macaque gamma virus
Virus: dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Rhadinovirus.
REFERENCE 1 (bases 1 to 320)
AUTHORS Strand,K., Harper,E., Thormahlen,S., Thoulless,M.E., Tsai,C.,
Rose,T., and Bosch,M.L.
TITLE Two distinct lineages of macaque gamma herpesviruses related to the
Kaposi's sarcoma associated herpesvirus
JOURNAL J. Clin. Virol. 16 (3), 253-269 (2000)
MEDLINE 20204465
PUBMED 10738144
REFERENCE 2 (bases 1 to 320)
AUTHORS Strand,K.B. and Bosch,M.L.
TITLE Direct Submission
JOURNAL Submitted (14-JUN-1999) Pathobiology, University of Washington, Box
357238, Seattle, WA 98125, USA
FEATURES
source
1. 320
/organism="Macaque gamma virus"
/mol_type="genomic DNA"
/strain="Macaque fascicularis gamma virus"
/db_xref="taxon:111468"
<1..>320
/gene="gB"
<1..>320
/gene="gB"
/codon_start=3
/product="glycoprotein B"
/protein_id="AAF23090.1"
/db_xref="GI:6671088"
/translation="VRRYRKVATSVTVYRGWTEFVAVGKQEVNRPVQYEINHDITY
QCFSSMRVNVGVINTYTDREFTNQVFEVLQVPEGLTDNIQRYFSPQVLYTTPGWFPGI
YRVR"
BASE COUNT 78 a 96 c 92 g 54 t
ORIGIN
Query Match 0.3%; Score 106; DB 1; Length 320;
Best Local Similarity 99.4%; Pred. No. 1.2e-50;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11834 AGGTAGACGGTACCGCAAGGTGGCCACCTGGTGGACCGTCTATCAGAGGTGGACCGAGA 11893
|||||
Db 1 AGGTAGACGGTACCGCAAGGTGGCCACCTGGTGGACCGTCTATCAGAGGTGGACCGAGA 60
QY 11894 CCGCGGTGACCGGCAAGAGAGTATCCGACCGGTGGCCAGTATCCGACCGGTGGACCGAGA 11953
|||||
Db 61 CCGCGGTGACCGGCAAGAGAGTATCCGACCGGTGGCCAGTATCCGACCGGTGGACCGAGA 120
QY 11954 TGGACACGACCTACAGGTGTTCACGCTCCATGCGCGT 11990
|||||
Db 121 TGGACACGACCTACAGGTGTTCACGCTCCATGCGCGT 157
RESULT 8
AF204167 2708 bp DNA linear VRL 04-JUL-2000
LOCUS Macaca nemestrina rhadinovirus 2 DNA polymerase and ORF 10-like
DEFINITION protein genes, partial cds.
ACCESSION AF204167
VERSION AF204167.1 GI:8925895
KEYWORDS
SOURCE Macaca nemestrina rhadinovirus 2
ORGANISM Macaca nemestrina rhadinovirus 2
Virus: dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Rhadinovirus.
REFERENCE 1 (bases 1 to 2708)
AUTHORS Schultz,E.R., Rankin,G.W. Jr., Blanc,M.P., Raden,B.W., Tsai,C.C.,
and Rose,T.M.
TITLE Characterization of two divergent lineages of macaque
rhadinoviruses related to Kaposi's sarcoma-associated herpesvirus
JOURNAL J. Virol. 74 (10), 4919-4928 (2000)
MEDLINE 20240083
PUBMED 10775636
REFERENCE 2 (bases 1 to 2708)
AUTHORS Rose,T.M.
TITLE Direct Submission
JOURNAL Submitted (12-NOV-1999) Pathobiology, School of Public Health and
Community Medicine, University of Washington, Seattle, WA 98195, USA
FEATURES
source
1. 2708
/organism="Macaca nemestrina rhadinovirus 2"
/mol_type="genomic DNA"
/isolate="Wne442N"
/db_xref="taxon:123630"
/note="Wnevr-2"
<1..2589
/note="similar to rhesus rhadinovirus ORF 9"
/codon_start=1
/product="DNA polymerase"
/protein_id="AAF81664.1"
/db_xref="GI:8925896"
/translation="ROOYEFYAKVPSSGVNTHVLOALKNTRAGRAAGFSRRTYKRI
LKYDVAHEPVTETITSSGPMLSLTSRIVACGGEVSNDAVRRVLDHGFTEPKR
YSCSRATPRLAARARTRALERDCSMEDLSVQADNDMPRIATPAFDECGEETPRPA
TRDCDAVLIQISCVFTTRDGAFTPPNVLVSFGTCDLRDVLVLPSEYDMLVSFFAM
LRDEVDVLTGYNISNFDPLYLARASQVNVQJNETYTKITGSIIEVHEBAGGGE
MRSVSKIKIGIYVIMDYQVCRKLSLTLTKRYIGVLDNKMVMKGVSKDIPPLFS
GSAGRAKVGSCVMSVLMDLKPMIHEVISEIAKLAKIQAARFVSLDGOQLRPFSC
LLEAARENFTLPVPRPGGSGYGATVNIPEFDEPVPVYVDFASLYSIIQAHNL
CYSTMINGRDLHAPRTLPDYEFTFVLSGGGVNHRVKKHKSRLGRLLTYWLEKRAI
RRTLAACDDPSLKTILDKOQALVTCNAVYGFVAGSGLPCINIAETVYLRGTMIL
EMSKSYEALTVSDLRLRLEVTAGPAARFVYGDTSLELACDGPADAASAFCF
DLARITADLEVPPIKLEAEETKCLLTLTKRYIGVLDNKMVMKGVSKDIPPLFS
VOEGRALIDLVLHDPEVKAARLCKKPPRAYVEGLPRFKIIVLVNLSYDIND
DAVPIEILFTSTELSRVCDYKTKTNPLHLYVOKLASRCELTPOVHRIRIPVFDVAG
TKSDLAEPHDYVAGHRIPAVLDLPFKLVKGAANIQLCEFGNDADTVAALNNFLNV
PYKLS"
2683..>2708
/note="similar to rhesus rhadinovirus ORF 10"
/codon_start=1
/product="ORF 10-like protein"

```

/protein_id="AA081665.1"
/db_xref="GI:8925897"
/translation="MLVDKLSV"
BASE COUNT      559 a      852 c      811 g      486 t
ORIGIN
Query Match      0.2%; Score 80; DB 1; Length 2708;
Best Local Similarity 100.0%; Pred. No. 3.2e-35;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      15703 CAGCCAGGCGCGCTGACGAGCGCCACAGCTCCGCGTGTCTCCTGCTGAG 15762
          |||||||
Db      1126 CAGCCAGGCGCGCTGACGAGCGCCACAGCTCCGCGTGTCTCCTGCTGAG 1185
          |||||||

Oy      15763 GCCGCGCGCAGGAGACTT 15782
          |||||||
Db      1186 GCCGCGCGCAGGAGACTT 1205
          |||||||

RESULT 9
AF159031      475 bp      DNA      linear      VRL 28-APR-2000
LOCUS      Macaque gamma virus strain Macaca nemestrina gamma virus DNA
DEFINITION      polymerase (pol) gene, partial cds.
ACCESSION      AF159031
VERSION      AF159031.1 GI:6671070
KEYWORDS
SOURCE      Macaque gamma virus
ORGANISM      Macaque gamma virus
VIRUSES; dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Rhadinovirus.
REFERENCE      1 (bases 1 to 475)
AUTHORS      Strand,K., Harper,E., Thormahlen,S., Thoulless,M.E., Tsai,C.,
              Rose,T. and Bosch,M.L.
              Two distinct lineages of macaque gamma herpesviruses related to the
              Kaposi's sarcoma associated herpesvirus
              J. Clin. Virol. 16 (3), 253-269 (2000)
JOURNAL      20204465
MEDLINE      10738144
PUBMED
REFERENCE      2 (bases 1 to 475)
AUTHORS      Strand,K.B. and Bosch,M.L.
              Direct Submission
              Submitted (14-JUN-1999) Pathobiology, University of Washington, Box
              357238, Seattle, WA 98125, USA
JOURNAL
FEATURES
source
1. 475
/organism="Macaque gamma virus"
/mol_type="genomic DNA"
/strain="Macaca nemestrina gamma virus"
/db_xref="taxon:111468"
<1..>475
/gene="pol"
<1..>475
/gene="pol"
/codon_start=2
/product="DNA polymerase"
/protein_id="AA081665.1"
/db_xref="GI:6671070"
/translation="STIOAHNLCTSTMHGDLHLPPTPDYETVYLSGPPVHEVK
KKHRESLGLRLTWLEKRAIRRTLAACDPSLTKIDKQDLAIKVTCNAVGETGV
ASGLPCTININIEVTLRGTMLKMSKSVLEALIVSDLERLGRVTAQPAKFRV"
BASE COUNT      100 a      147 c      152 g      76 t
ORIGIN
Query Match      0.2%; Score 71; DB 1; Length 475;
Best Local Similarity 100.0%; Pred. No. 5.2e-30;
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      15903 GAGCATCATCAGGCGCAGACCTGTCTACTCCACCATGATACAGGAGAGACTGCA 15962
          |||||||
Db      1 GAGCATCATCAGGCGCAGACCTGTCTACTCCACCATGATACAGGAGAGACTGCA 60
          |||||||

Oy      15963 CCTGCACCCCA 15973

```

```

DB      61 CCTGCACCCCA 71
          |||||||

RESULT 10
AF159034      336 bp      DNA      linear      VRL 28-APR-2000
LOCUS      Macaque gamma virus strain Macaca nemestrina 116 gamma virus DNA
DEFINITION      polymerase (pol) gene, partial cds.
ACCESSION      AF159034
VERSION      AF159034.1 GI:6671076
KEYWORDS
SOURCE      Macaque gamma virus
ORGANISM      Macaque gamma virus
VIRUSES; dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Rhadinovirus.
REFERENCE      1 (bases 1 to 336)
AUTHORS      Strand,K., Harper,E., Thormahlen,S., Thoulless,M.E., Tsai,C.,
              Rose,T. and Bosch,M.L.
              Two distinct lineages of macaque gamma herpesviruses related to the
              Kaposi's sarcoma associated herpesvirus
              J. Clin. Virol. 16 (3), 253-269 (2000)
JOURNAL      20204465
MEDLINE      10738144
PUBMED
REFERENCE      2 (bases 1 to 336)
AUTHORS      Strand,K.B. and Bosch,M.L.
              Direct Submission
              Submitted (14-JUN-1999) Pathobiology, University of Washington, Box
              357238, Seattle, WA 98125, USA
JOURNAL
FEATURES
source
1. 336
/organism="Macaque gamma virus"
/mol_type="genomic DNA"
/strain="Macaca nemestrina 116 gamma virus"
/db_xref="taxon:111468"
<1..>336
/gene="pol"
<1..>336
/gene="pol"
/codon_start=2
/product="DNA polymerase"
/protein_id="AA081665.1"
/db_xref="GI:6671070"
/translation="TMHGRDLHLPPTPDYETVYLSGPPVHKHRESLGLRL
LTVMLEKRAIRRTLAACDPSLTKIDKQDLAIKVTCNAVGETGVASGLPCTINIA
ETVTLRGRT"
BASE COUNT      75 a      103 c      105 g      53 t
ORIGIN
Query Match      0.1%; Score 56; DB 1; Length 336;
Best Local Similarity 100.0%; Pred. No. 3.4e-21;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      15976 CTGACGCGGAGCAGTACGAGAGCTGTCTGACGCGGAGCGGAGTATTGT 16031
          |||||||
Db      41 CTGACGCGGAGCAGTACGAGAGCTGTCTGACGCGGAGCGGAGTATTGT 96
          |||||||

RESULT 11
AF159032      475 bp      DNA      linear      VRL 28-APR-2000
LOCUS      Macaque gamma virus strain Macaca fascicularis gamma virus DNA
DEFINITION      polymerase (pol) gene, partial cds.
ACCESSION      AF159032
VERSION      AF159032.1 GI:6671072
KEYWORDS
SOURCE      Macaque gamma virus
ORGANISM      Macaque gamma virus
VIRUSES; dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Rhadinovirus.
REFERENCE      1 (bases 1 to 475)
AUTHORS      Strand,K., Harper,E., Thormahlen,S., Thoulless,M.E., Tsai,C.,
              Rose,T. and Bosch,M.L.

```

TITLE Two distinct lineages of macaque gamma herpesviruses related to the
JOURNAL Kaposi's sarcoma associated herpesvirus
MEDLINE J. Clin. Virol. 16 (3), 253-269 (2000)
PUBMED 20204465
10738144
REFERENCE 2 (bases 1 to 475)
AUTHORS Strand,K.B. and Bosch,M.L.
TITLE Direct Submission
JOURNAL Submitted (14-JUN-1999) Pathobiology, University of Washington, Box
357238, Seattle, WA 98125, USA
FEATURES
source 1..475
/organism="Macaque gamma virus"
/mol_type="genomic DNA"
/strain="Macaque fascicularis gamma virus"
/db_xref="taxon:111468"
<1..>475
/gene="pol"
<1..>475
/gene="pol"
/codon_start=2
/product="DNA polymerase"
/protein_id="AA23082.1"
/db_xref="GI:6671073"
/translation="STIQAHNCYSTMINGODLHHPITLPDDYEFVLSGCPVHFVK
KHRESLGRLLTWLEKRRIRRTLAACDDPSLKTILDKQDLAIKVTNNAVYGFVGV
ASGLPCINIAETVTLRGRTLMESKSYEALTTDLRTRLGRTVAGHGRFRV"
CDS
gene
CDS
BASE COUNT 99 a 144 c 152 g 80 t
ORIGIN
Query Match 0.1%; Score 50; DB 1; Length 475;
Best Local Similarity 100.0%; Pred. No. 1.2e-17;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 15903 GAGCATCATCCAGCGACACCTGTCCTACTCCACCATGATACGAC 15952
Db 1 GAGCATCATCCAGCGACACCTGTCCTACTCCACCATGATACGAC 50
RESULT 12
AF159036 336 bp DNA linear VRL 28-APR-2000
LOCUS Macaque gamma virus strain Macaca fascicularis 037 gamma virus DNA
DEFINITION Polymerase (pol) gene, partial cds.
ACCESSION AF159036
VERSION AF159036.1 GI:6671080
KEYWORDS
SOURCE Macaque gamma virus
ORGANISM Macaque gamma virus
VIRUSES; dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Rhadinovirus.
REFERENCE 1 (bases 1 to 336)
AUTHORS Strand,K., Harper,E., Thormahlen,S., Thoulless,M.E., Tsai,C.,
Rose,T. and Bosch,M.L.
TITLE Two distinct lineages of macaque gamma herpesviruses related to the
JOURNAL Kaposi's sarcoma associated herpesvirus
MEDLINE J. Clin. Virol. 16 (3), 253-269 (2000)
PUBMED 20204465
10738144
REFERENCE 2 (bases 1 to 336)
AUTHORS Strand,K.B. and Bosch,M.L.
TITLE Direct Submission
JOURNAL Submitted (14-JUN-1999) Pathobiology, University of Washington, Box
357238, Seattle, WA 98125, USA
FEATURES
source 1..336
/organism="Macaque gamma virus"
/mol_type="genomic DNA"
/strain="Macaque fascicularis 037 gamma virus"
/db_xref="taxon:111468"
<1..>336
/gene="pol"
<1..>336
/gene="pol"

/gene="pol"
/codon_start=2
/product="DNA polymerase"
/protein_id="AA23086.1"
/db_xref="GI:6671081"
/translation="TWIHRDLHHPITLPDDYEFVLSGCPVHFVKKHRESLGRRL
LTWLEKRRIRRTLAACDDPSLKTILDKQDLAIKVTNNAVYGFVGVASGLPCINIA
ETVTLRGRT"
CDS
gene
CDS
BASE COUNT 75 a 101 c 107 g 53 t
ORIGIN
Query Match 0.1%; Score 48; DB 1; Length 336;
Best Local Similarity 100.0%; Pred. No. 1.8e-16;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 15975 CCTGACCGCGGAGCAGACTACGAGCGTTCGCTGAGCGGAGCGGT 16022
Db 40 CCTGACCGCGGAGCAGACTACGAGCGTTCGCTGAGCGGAGCGGT 87

RESULT 13
AF159037 336 bp DNA linear VRL 28-APR-2000
LOCUS Macaque gamma virus strain Macaca fascicularis 040 gamma virus DNA
DEFINITION Polymerase (pol) gene, partial cds.
ACCESSION AF159037
VERSION AF159037.1 GI:6671082
KEYWORDS
SOURCE Macaque gamma virus
ORGANISM Macaque gamma virus
VIRUSES; dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Rhadinovirus.
REFERENCE 1 (bases 1 to 336)
AUTHORS Strand,K., Harper,E., Thormahlen,S., Thoulless,M.E., Tsai,C.,
Rose,T. and Bosch,M.L.
TITLE Two distinct lineages of macaque gamma herpesviruses related to the
JOURNAL Kaposi's sarcoma associated herpesvirus
MEDLINE J. Clin. Virol. 16 (3), 253-269 (2000)
PUBMED 20204465
10738144
REFERENCE 2 (bases 1 to 336)
AUTHORS Strand,K.B. and Bosch,M.L.
TITLE Direct Submission
JOURNAL Submitted (14-JUN-1999) Pathobiology, University of Washington, Box
357238, Seattle, WA 98125, USA
FEATURES
source 1..336
/organism="Macaque gamma virus"
/mol_type="genomic DNA"
/strain="Macaque fascicularis 040 gamma virus"
/db_xref="taxon:111468"
<1..>336
/gene="pol"
<1..>336
/gene="pol"
/codon_start=2
/product="DNA polymerase"
/protein_id="AA23087.1"
/db_xref="GI:6671083"
/translation="TWIHRDLHHPITLPDDYEFVLSGCPVHFVKKHRESLGRRL
LTWLEKRRIRRTLAACDDPSLKTILDKQDLAIKVTNNAVYGFVGVASGLPCINIA
ETVTLRGRT"
CDS
gene
CDS
BASE COUNT 75 a 101 c 107 g 53 t
ORIGIN
Query Match 0.1%; Score 48; DB 1; Length 336;
Best Local Similarity 100.0%; Pred. No. 1.8e-16;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 15975 CCTGACCGCGGAGCAGACTACGAGCGTTCGCTGAGCGGAGCGGT 16022
Db 40 CCTGACCGCGGAGCAGACTACGAGCGTTCGCTGAGCGGAGCGGT 87

RESULT 14	AF159035	336 bp	DNA	linear	VRL 28-APR-2000
LOCUS	AF159035				
DEFINITION	Macaque gamma virus strain Macaca nemestrina 139 gamma virus DNA polymerase (pol) gene, partial cds.				
ACCESSION	AF159035				
VERSION	AF159035.1	GI:6671078			
KEYWORDS					
SOURCE	Macaque gamma virus				
ORGANISM	Macaque gamma virus				
REFERENCE	Viruses; dsDNA viruses, no RNA stage; Herpesviridae; Gammaherpesvirinae; Rhadinovirus.				
AUTHORS	1 (bases 1 to 336)				
TITLE	Strand, K., Harper, E., Thormahlen, S., Thoulless, M.E., Tsai, C., Rose, T., and Bosch, M.L.				
JOURNAL	Two distinct lineages of macaque gamma herpesviruses related to the Kaposi's sarcoma associated herpesvirus				
MEDLINE	J. Clin. Virol. 16 (3), 253-269 (2000)				
PUBMED	20204465				
REFERENCE	10738144				
AUTHORS	2 (bases 1 to 336)				
TITLE	Strand, K.B. and Bosch, M.L.				
JOURNAL	Direct Submission				
FEATURES	Submitted (14-JUN-1999) Pathobiology, University of Washington, Box 357238, Seattle, WA 98125, USA				
source	Location/Qualifiers				
gene	1..336				
CDS	/organism="Macaque gamma virus"				
	/mol_type="genomic DNA"				
	/strain="Macaque nemestrina 139 gamma virus"				
	/db_xref="taxon:111468"				
	<1..>336				
	/gene="pol"				
	<1..>336				
	/gene="pol"				
	/codon_start=2				
	/product="DNA polymerase"				
	/protein_id="AAF23085.1"				
	/db_xref="GI:6671079"				
	/translation="MTIHRGLHPILTPDYTEFVLSGSGPIFVKHKHRESLLGRILTVLEKRRRIARTLACDDPSLTLTDKQDLAIKVCNAYVGTGVAASGLPCINIIAAETVLRGT"				
BASE COUNT	74 a	103 c	106 g	53 t	
ORIGIN					
Query Match	0.1%; Score 47; DB 1; Length 336;				
Best Local Similarity	100.0%; Prid. No. 6.9e-16;				
Matches	47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
QY	15976 CTGACGCCGCGAGCTACGACGCTGCTGCGTACGCGCGGACCGCGT 16022.				
DB	41 CTGACGCCGCGAGCTACGACGCTGCTGCGTACGCGCGGACCGCGT 87				
RESULT 15	SH1DNA POLA	3144 bp	DNA	linear	VRL 14-AUG-1995
LOCUS	SH1DNA POLA				
DEFINITION	Pseudorabies virus DNA polymerase gene, partial cds.				
ACCESSION	L24487				
VERSION	L24487.1	GI:438894			
KEYWORDS	DNA polymerase.				
SOURCE	Pseudorabies virus				
ORGANISM	Pseudorabies virus				
REFERENCE	Viruses; dsDNA viruses, no RNA stage; Herpesviridae; Alphaherpesvirinae; Varicellovirus.				
AUTHORS	1 (bases 1 to 3144)				
TITLE	Berthomme, H., Monahan, S.J., Parris, D.S., Jacquemont, B. and Epstein, A.L.				
JOURNAL	Cloning, sequencing, and functional characterization of the two subunits of the pseudorabies virus DNA polymerase holoenzyme: evidence for specificity of interaction				
FEATURES	J. Virol. 69 (5), 2811-2818 (1995)				

FEATURES	source	location/Qualifiers
COMMENT	Original source text: Pseudorabies virus (individual_isolate Kaplan) DNA.	
FEATURES		1..3144
source		/organism="Pseudorabies virus"
		/mol_type="genomic DNA"
		/isolate="Kaplan"
		/db_xref="taxon:10345"
		1..>3144
		/codon_start=1
		/product="DNA polymerase"
		/protein_id="AA74383.1"
		/db_xref="GI:438895"
		/translation="MAARQGSVYTRLESEFKFIARCDLADPQRGVHVTGLAREPTVYC GGARPLIRGEPEPRRYAAWEGAPERPVSRFRPHYYDDIVESTEYASADPRPNGT VVTLLGSACGRVAHVHYGVRRHFFLGKADADALGASAEOLARLAAAGAPRI GPADVARVNDAAVYVYDAPRRPFVSSNSGRGLALRFTVCAGLVTIHEAGVADATT RLLDHDLPTSGRTYRLRGPAGEVYVLRHQRLTSDVEVNTPLANLADGEGPPTVTK LLCDIECKAGDDAFAPAENPEDLVIOISLTVSLATQLEHTLFLSGSDSDDP VTLEPSEFELLAFTVFLKQVAPRATGNIINPMAFVHTLTVYVGLADGYS FNRGQFRVYDAGONSFOKRSKVKINCLVSDMAYADAKLFLSKVAAEALGEE RKLDLQKDPRIYVYAAAGRERGVGRQVOSALVGLKFLFHLLELSAVARLANITTE LARVYDGOOTRVFTCLIKLAGSRGFLPKRRRIADPDGQYOGAKVLEPDSGFHY DPVULDFRSLTSPSTIOAHNLCTPTLLALARPAGLREDFSAFVNGERLYVHAGVRE SLSILRLDWLAMRRKAIARAPITSPAPEVAVLLDQQAIAKYCNSVYGFVANGLLLE CLPAPATVTTIGRDLVATRDYVOTRMAITRLEDRDLPARPAGEVAVRVYGDTS FIRPAGIATDVCELDLGEIMAIRITRDLRPIKLECEKTFRRLLITRKKIYINGC KMKACQGLVKNKCAFINAYARLVLDLFEDEAVVAAASAAATIRAPAPARLERLP FAACGRVLAENHARVAGAGGADVADFYMTALSSPPAASVTRPLHLYTKIKLMRRHG EVPSKERVSTVITAPTPAEARDGAVAPGLAPQKLLVSDLAEDPATVAVHGVPLNTE YVPSHLLSTLSTVEFKALGEGNDTKITERLKRIFETAPGAPFHEAFALITGEGSES LQTLRTTCCTPTAAPRRS"
BASE COUNT	463 a 1172 c 1050 g 459 t	
ORIGIN		
Query Match	0.1%; Score 46; DB 1; Length 3144;	
Best Local Similarity	100.0%; Pred. No. 3.5e-15;	
Matches	46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	15886 TTTCGCAGCCCTGATCCGAGCATCATCCAGCGCACACACGTCGCT 15931	
Db	1720 TTTCGCAGCCCTGATCCGAGCATCATCCAGCGCACACACGTCGCT 1765	
LOCUS	AF159038	336 bp DNA linear VRL 28-APR-2000
DEFINITION	Macaque gamma virus strain Macaca fascicularis 050 gamma virus DNA	
ACCESSION	AF159038	
VERSION	AF159038.1	GI:6671084
KEYWORDS		
SOURCE		
ORGANISM		Macaque gamma virus
		Macaque gamma virus
		Viruses: dsDNA viruses, no RNA stage: Herpesviridae;
		Gammaherpesvirinae: Rhadinovirus.
REFERENCE		1 (bases 1 to 336)
AUTHORS		Strand,K., Harper,E., Thormahlen,S., Thoulless,M.E., Tsai,C.,
TITLE		Rose,T., and Bosch,M.L.
JOURNAL		Two distinct lineages of macaque gamma herpesviruses related to the
PUBMED		Kaposi's sarcoma associated herpesvirus
MEETING		J. Clin. Virol. 16 (3), 253-269 (2000)
REFERENCE		2 (bases 1 to 336)
AUTHORS		Strand,K.B. and Bosch,M.L.
TITLE		Direct Submission
JOURNAL		Submitted (14-JUN-1999) Pathobiology, University of Washington, Box
		357238, Seattle, WA 98125, USA
FEATURES		Location/Qualifiers
source		1..336

/organism="Macaque gamma virus"
/mol_type="genomic DNA"
/strain="Macaque fascicularis 050 gamma virus"
/db_xref="taxon:111468"
<1..>336
/gene="pol"
<1..>336
/gene="pol"
/codon_start=2
/product="DNA polymerase"
/protein_id="AAF23088.1"
/db_xref="GI:6671085"
/translation="MTMGSDLHLHPTLPDDYETFFVSGEPVHFKKRESLIGRL
LTVLDEKRRARLRLAACDDPSLKITLEDKQDLAKVTCNAVYGFVAGSLDPCINIA
ETVTLRGRT"
BASE COUNT 76 a 101 c 106 g 53 t
ORIGIN

Query Match 0.1%; Score 41; DB 1; Length 336;
Best Local Similarity 100.0%; Pred. No. 2.4e-12;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 15975 CCTGACGCCGACGACTACGAGACGTTGCTGCGCGCG 16015
|||||
40 CCTGACGCCGACGACTACGAGACGTTGCTGCGCGCG 80

RESULT 17
AF282937
LOCUS AF282937 475 bp DNA linear VRL 13-DEC-2000
DEFINITION Mandrillus herpesvirus 2 isolate animal Mnd15 DNA polymerase (pol)
gene, partial cds.
ACCESSION AF282937
VERSION AF282937.1 GI:11611783
KEYWORDS
SOURCE
ORGANISM
Mandrillus herpesvirus 2
Mandrillus herpesvirus 2
Viruses; dsDNA viruses, no RNA stage: Herpesviridae;
Gammaherpesvirinae; Rhadinovirus.
REFERENCE
AUTHORS 1 (bases 1 to 475)
Lacoste,V., Maucletre,P., Dubreuil,G., Lewis,J.,
Georges-Courbot,M.C., Rigoulet,J., Petit,T. and Gessain,A.
Simian homologues of human gamma-2 and betaherpesviruses in
mandrill and drill monkeys
J. Virol. 74 (24), 11993-11999 (2000)

TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCES
AUTHORS
TITLES
JOURNALS
SUBMITTED (28-JUN-2000) Departement du SIDA et des Retrovirus,
Institut Pasteur, 28, rue du Dr. Roux, Paris cedex 15 75724, France
location/Qualifiers
1..475
/organism="Mandrillus herpesvirus 2"
/mol_type="genomic DNA"
/isolate="animal Mnd15"
/specific_host="Mandrillus sphinx"
/db_xref="taxon:144208"
/country="Gabon"
/note="MndRHV2"
<1..>475
/gene="pol"
<1..>475
/codon_start=2
/product="DNA polymerase"
/protein_id="AAG39060.1"
/db_xref="GI:11611784"
/translation="SITQAHNLGVSTWIGHGDLHLHPTLPDDYETFLSGGPVHFVK
KHRESLIGRLTVLWDRKREIRRLAKACDDPSLKITLEDKQDLAKVTCNAVYGFVAG
ASGLPCLISIAETVTLRGRTMLEMSKSTVEALTPDELQTRLRRAVHGPSARFRV"

FEATURES
source

BASE COUNT 105 a 151 c 139 g 80 t
ORIGIN

Query Match 0.1%; Score 38; DB 1; Length 475;
Best Local Similarity 100.0%; Pred. No. 1.4e-10;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 16270 ATGCTGAGAGTCAAGCTTTAGCTGAGGCGCTGAC 16307
|||||
368 ATGCTGAGAGTCAAGCTTTAGCTGAGGCGCTGAC 405

RESULT 18
AF282938
LOCUS AF282938 475 bp DNA linear VRL 13-DEC-2000
DEFINITION Mandrillus herpesvirus 2 isolate animal Mnd204 DNA polymerase (pol)
gene, partial cds.
ACCESSION AF282938
VERSION AF282938.1 GI:11611785
KEYWORDS
SOURCE
ORGANISM
Mandrillus herpesvirus 2
Mandrillus herpesvirus 2
Viruses; dsDNA viruses, no RNA stage: Herpesviridae;
Gammaherpesvirinae; Rhadinovirus.
REFERENCE
AUTHORS 1 (bases 1 to 475)
Lacoste,V., Maucletre,P., Dubreuil,G., Lewis,J.,
Georges-Courbot,M.C., Rigoulet,J., Petit,T. and Gessain,A.
Simian homologues of human gamma-2 and betaherpesviruses in
mandrill and drill monkeys
J. Virol. 74 (24), 11993-11999 (2000)

TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCES
AUTHORS
TITLES
JOURNALS
SUBMITTED (28-JUN-2000) Departement du SIDA et des Retrovirus,
Institut Pasteur, 28, rue du Dr. Roux, Paris cedex 15 75724, France
location/Qualifiers
1..475
/organism="Mandrillus herpesvirus 2"
/mol_type="genomic DNA"
/isolate="animal Mnd204"
/specific_host="Mandrillus leucophaeus"
/db_xref="taxon:144208"
/country="Cameroon"
/note="MndRHV2"
<1..>475
/gene="pol"
<1..>475
/codon_start=2
/product="DNA polymerase"
/protein_id="AAG39061.1"
/db_xref="GI:11611786"
/translation="SITQAHNLGVSTWIGHGDLHLHPTLPDDYETFLSGGPVHFVK
KHRESLIGRLTVLWDRKREIRRLAKACDDPSLKITLEDKQDLAKVTCNAVYGFVAG
ASGLPCLISIAETVTLRGRTMLEMSKSTVEALTPDELQTRLRRAVHGPSARFRV"

FEATURES
source

BASE COUNT 109 a 149 c 137 g 80 t
ORIGIN

Query Match 0.1%; Score 38; DB 1; Length 475;
Best Local Similarity 100.0%; Pred. No. 1.4e-10;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 16270 ATGCTGAGAGTCAAGCTTTAGCTGAGGCGCTGAC 16307
|||||
368 ATGCTGAGAGTCAAGCTTTAGCTGAGGCGCTGAC 405

RESULT 19
AF282939
LOCUS AF282939 475 bp DNA linear VRL 13-DEC-2000

FEATURES	source
<p>MDLINE 20542003</p> <p>PUBMED 11090203</p> <p>REFERENCE 2 (bases 1 to 475)</p> <p>AUTHORS Lacoste,Y., Mauciere,P., Dubreuil,G., Lewis,J., Georges-Courbot,M.C., Rigoulet,J., Petit,T. and Gessain,A.</p> <p>TITLE Direct Submission</p> <p>JOURNAL Submitted (28-JUN-2000) Departement du SIDA et des Retrovirus, Institut Pasteur, 28, rue du Dr. Roux, Paris cedex 15 75724, France</p>	<p>organism="Mandrilus herpesvirus 2"</p> <p>/mol_type="genomic DNA"</p> <p>/isolate="animal Mnd402"</p> <p>/specific_host="Mandrilus leucophaeus/sphinx"</p> <p>/db_xref="taxon:144208"</p> <p>/country="Cameroon"</p> <p>/note="MndRHV2"</p> <p><1..>475</p> <p>/gene="Pol"</p> <p><1..>475</p> <p>/gene="Pol"</p> <p>/codon_start=2</p> <p>/product="DNA polymerase"</p> <p>/protein_id="AAC39063.1"</p> <p>/db_xref="GI:11611790"</p> <p>/translation="SIQAHNLVCSYIMHGRDLHPTLVQDDYETELLSCGPVHPFWKHKRESLIGRLTWLDKRRIRKALACDPSKTLIDKQALIKVTCNAVYGTGASGILPSTIAETVTLGRFTLEKSKSVETALPDEQTRLRRAVHGPSARFRV"</p>
<p>BASE COUNT 109 a 149 c 137 g 80 t</p> <p>ORIGIN</p>	
<p>Query Match 0.1%; Score 38; DB 1; Length 475;</p> <p>Best Local Similarity 100.0%; Pred. No. 1.4e-10;</p> <p>Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</p>	
<p>Oy 16270 ATGCTGGAGATGTCAAAGTCTTACGTGAGGCCCTGC 16307</p> <p>Db 368 ATGCTGGAGATGTCAAAGTCTTACGTGAGGCCCTGC 405</p>	
<p>RESULT 21</p> <p>AF210726/c</p> <p>LOCUS AF210726 130733 bp DNA linear VRL 27-MAR-2000</p> <p>DEFINITION Macaca mulatta rhadinovirus 26-95 long unique region L-DNA, complete sequence.</p> <p>ACCESSION AF210726</p> <p>VERSION AF210726.1 GI:7329990</p> <p>KEYWORDS Macaca mulatta rhadinovirus 26-95</p> <p>SOURCE Macaca mulatta rhadinovirus 26-95</p> <p>ORGANISM Vitruses; dsDNA viruses, no RNA stage; Herpesviridae; Gammaherpesvirinae; Rhadinovirus.</p> <p>REFERENCE 1 (bases 1 to 130733)</p> <p>AUTHORS Alexander,L., Denekamp,L., Knapp,A., Auerbach,M.R., Damania,B. and Desrosiers,R.C.</p> <p>TITLE The primary sequence of rhesus monkey rhadinovirus isolate 26-95: sequence similarities to Kaposi's sarcoma-associated herpesvirus and rhesus monkey rhadinovirus isolate 17577</p> <p>JOURNAL J. Virol. 74 (7), 3388-3398 (2000)</p> <p>MEDLINE 20173730</p> <p>PUBMED 10708456</p> <p>REFERENCE 2 (bases 1 to 130733)</p> <p>AUTHORS Alexander,L., Denekamp,L.M., Knapp,A., Auerbach,M., Czajak,S., Damania,B. and Desrosiers,R.C.</p> <p>TITLE Direct Submission</p> <p>JOURNAL Submitted (02-DEC-1999) Microbiology, New England Regional Primate Research Center, One Pinehill Dr, Southborough, MA 01772, USA</p> <p>FEATURES location/Qualifiers</p> <p>source 1..130733</p> <p>/organism="Macaca mulatta rhadinovirus 26-95"</p> <p>/mol_type="genomic DNA"</p> <p>/isolate="Macaca mulatta rhadinovirus isolate 26-95"</p> <p>/db_xref="taxon:119193"</p>	

gene
513. .1784
/gene="R1"
CDS
513. .1784
/gene="R1"
/codon_start=1
/product="ORF1"
/protein_id="AAFS9980.1"
/db_xref="GI:732991"
/translation="MFVLVLEMLQPVSVELLPAKLTSVPTWCPHPHGDTYLLTGRGT
STARQSTOMFRNNITLMGRSNGEXGRVSVTPNATISDRYACQKTTTSSNNIDFRS
SRLTLQERCSASYTYANNTRVLRGSGGVTLRANVLRGAVINGRTNRITHTYV
LTKETGGTFCASAFIGNKFTYSOTINVEFTSPFKPPTNIDPNESHFNKGTGLOOTAYV
OHBNRYVESVPVPSISGLVIGTALSTLMCHLPTTRCNSNSSTNSASQSYOTQSH
NORSNTVECSNHTYRNAHQESITELNQHTSETDSCQVLLEVKNAVAIDGPEENT
NEVEQYDDVAVENIEQTSYEDNVEHMDYSOTINPNFYSGLLILEEVEFYNELN
QYHGLILENDHNEYNHLNELMIEQDWLE"
complement(1852. .2418)
/gene="ORF02"
CDS
complement(1852. .2418)
/gene="ORF02"
/codon_start=1
/product="DHF8"
/protein_id="AAF59981.1"
/db_xref="GI:732992"
/translation="MDIAVNCIVAVDEOLGIGKNGTMDPYLRNEMMYFOKMTSPSV
VCEKNVYIMKRTWFSIPEKKRPVYNINITISLELNEPRHGAFILARTIDANFPR
OYLKEDLNTVWYIGKSVYESVLNACPLKLYITRIMESDCDVFPPSIDNTEYTM.
SELPGKDTNEENGIKRYFOYEKFNK"
2595. .3782
/gene="ORF04"
CDS
2595. .3782
/gene="ORF04"
/codon_start=1
/product="complement binding protein"
/protein_id="AAF59982.1"
/db_xref="GI:732993"
/translation="MFWIPITICFICQVILVDSKDGENVTCIKPPDPFMVKTANONE
NYAVGTVELICRPGFICLOANYVECLNSCTWTPRNAECRRKCSBEDLINEVPI
TDSNNAKFGSNITTKCNTGLIGATVTCCLKIDSNLVDMDPAFTCELEKKQV
DIEGRKYVQVEFVNYLETTFCTCNKDFSLIGNTTCTMTGWSVPPKCOQITCSA
PNIDHGLTLVSGSRVYKHQSIVTIGCDGFTLGNHKMCTCEYSLANPPLPCVAINIT
DPTPEVSPSGTQEMPTENPKSHSETTTTETPKTQCHKSETSPSKVFNPTNHP
TTPFAGISKQTTTNRPSKAPSONPPIAPRPSKMKRHYVVLVAFASVSLFLVLAAYCC
FLK"
4213. .7611
/gene="ORF06"
CDS
4213. .7611
/gene="ORF06"
/codon_start=1
/product="ssdbp"
/protein_id="AAF59983.1"
/db_xref="GI:732994"
/translation="MASKGNAGQPLEDNOGRAPIGAGVYAYAKODPPEANSLIG
NRPSSGVSFLPIILYGLTVEHEPLVYKAAKVDITTLAVKTCFHFREYVFNAL
FRPYFGDGTGNEICEEARLEGYTOPIEGPPHSIMNLEPCOLDDEMLGAVVE
GFKERLMRGCLVAVPOTQVOYIAGRAFVPLTDEDLFAPHGRMRPFYKHQVSATL
YDSIFTSIAOLRLKDYTAIHATERKOPMODHYKIATVAKOKOSTTLPTKTTSSSH
IVDSVAEIALSTGCMFLPCPDACCELLNDSWTI FDGCSPEARVNALEKWSQAV
HVAGQLEAANSVYLTVKQAPRGQGDVNVNSPFIQHLGFLNEATIKENSGEAF
KGVPSNALDGSSTPYHILAYAAFSFPLAKLCYMOFIQHHKSTNOANMVAHYGT
AANSEMCTLGHNTPATCLNTLFLRLKDRPEAVTIPORDDYVVTGAGFENDEIIG
NFAFSRREDGNDADBEPRKYTWOLCOQVTEKLSAIGTEDHNNHNLITNDSFLR
VFKGIDSIYDGEYWKFPVNSMIKNNFNREHVKSVHILQFCNVYQAPCAVFLNTLY
KSLWLIQIDICLPYCMYEDQNPAMGILPSEWLMKHFOITLNTNKAACLDGVTJGGE
LKIVHRMPCDFDPTDAGSNGMAPFMQVRIARAMNVFKSIKRNRIIFSNTAGE
AVOSGEAFPTGRTDYVAGPVKFLNSLRHLEPPTKTAALYLHKIISOTNPPVLK
DVDDDELAELYSVKTNSLAPEETNVDVVPDLSMSYARIKNGAILRAGGOIOFYAT
TILCLTPVLOTIDAEYPRHYLGSNAITPAYIYLAETIGRTALTYOTTAROPVATGTL
RPVITVPMVNNKTTGVNGNNVFEHCGMLGTFAGGAGVRLNMPSSPKKTVGSAMLRK
RHVMWMPIDRLIRAGAGTISTFEASVSGVRGVALLEDNDPNMLKSVILELRLHIG
KCGODLSSEVOYIAGDYCMITDVELFTLIDNIAOSGVPTIEDAGALIEDRODADLQ
FVSDDIATASACPPPEQLPTPSAGALLACKRRKRNALLSDLDL"
7636. .9696

gene
CDS
/gene="ORF07"
7636. .9696
/gene="ORF07"
/codon_start=1
/product="transport protein"
/protein_id="AAF59984.1"
/db_xref="GI:732995"
/translation="MARELAALYAQLSALAVDLSLVTFADPRSIDGARILIKYTOIEN
LNRDLLELRQNSVERTSSLSLEVEHLAKNITEKLGLESLRLQRYSSRHEFTLHR
PECHYSTVFEFOYGGGLIDVNMCLINDVELICKRLGSEVYICGANALSGLRVLE
LSTLRGSLSPHPDLVYTVSVCOCLEIDVELVAPOGSSLLAVADRCDHCKKVRAE
PIHGFETSELISGLKATKRSADATOHGVRSSADOLRRSSLAIQDHNIFFRVSAME
LSNLIYNAACQTCGTCQTEBNCSSMALLIHEADMRHRLITPKISATIFQYOCERD
PIESLFCGGLFNSIDDTINALSRDCASTTFFQOANTYMKRONELFRLNSILRQGA
GSOCPAPSEPTRTTVAATASDVIKAOYRKQEQMYVARDEGFKRLCELOQTQAVL
ANALCMRWGGAAGAESAELVNHRLRRRRLVAPWARCRSDQLIFENSRVYIKNSLS
ORLSREHVEITTLQFYGLITPLTRQSDLEFPANVYLAOCFEAAGMLPHHKMLVSM
IMPOIKRDMITDQENFRFOLPEGLDIAVOKSAWCFIRELVLSVALYNRMEKTLRIE
SIAREKLSISNLDVKKGLTSGILYILEDDAPLVLSQNTGMIFNDVLAALVHHQLDSG
HDDN"
9683. .12172
/gene="ORF08"
CDS
9683. .12172
/gene="ORF08"
/codon_start=1
/product="ORF08"
/protein_id="AAF59985.1"
/db_xref="GI:732996"
/translation="IMTITNTRRLRLRAVNYIIAIGTAVGENVTPKGAATTAKPTPSP
STPPNPPRAEAFKFRVCASATGELFEFNELEKTCPGTEKDHOGLIMVEKKNV
PHIFKVRKRVATSVTVYRGMEETATGEOEVIRPVQYEINMDITOCFSSMRVN
VNGIVNTYTRDPTNQTPIQAPVEGLIDQVSGIOTRCSOPVLATTPGMPGITYRVRTVNC
EIVDMIRASAPESYEVYALGDVYEVSPFCHNDSTCSVAEKTEGCLVRALNTTYD
FATRKPTTETRVEFADSEBYVSMKAEOPKCAVCLLMKTFPPRAIQTHESAHFVAN
DVATFTSPLESEVNFETGYSCDDEVLOKTLNDIKLSIHTVHNGSAQYIKGEGFL
LMQPLTPLSLVDNMRGLNTGTPAPPATSTVSRSVRNINTEADNTIAAPLOQFAY
DKIRASINKVLEELSRAMCREQVADTYMWEKLSINPTSWATLYGGRPSKFEGLDI
SYDVCASVADVASVSIHKSLSRSPGCMYSRBPVFRRLNSTTLEKQOLGRNETIIL
NOVEACKEITCEHTFIASNVITYYYKDYFVKKINTSETSLGTFLALNLTENTDFRY
IELVSRAEKKSIVGSVFDTIMFPERVNYTORLAGLRDLMDLITDLNVAIVLVAFLNR
ADLDVSRKTKIVANASVITLFGSLVSGFINIKSPFGMMLIIVAVNVLIVFLNLR
TNIAQAPLIRNIYDIDIKMOPSGGVQEOEIKNLIAQHOLQOERRRRDDEORSAPS
LERRASDGLKRRFGYKPLNEEAQOEYEMSK"
12290. .15334
/gene="ORF09"
CDS
12290. .15334
/gene="ORF09"
/codon_start=1
/product="polymerase"
/protein_id="AAF59986.1"
/db_xref="GI:732997"
/translation="MDFNRYLGRGFRPHSHRGTDAAPAGAGAVOPPPDVCRLITA
CLRTPGAGMIPVATIPPPYFENGAGADVLANERSMWTARORPAAPPODSTIF
HADYVVTYTAADCAVPSRFQDILPSTGVLLKLGRTEDGSSVCVNRQOYYFA
KVPAGIVNTRILQOALKNFAGRAAGSGSTRVNRILKTFDVAHAPTELTLSGSM
STLSDRILVAGCEVESNDVAVRFGVSDHPTFMGPGSCARAPRIAAARATLEED
CSMEDLSVOQADBSMPRYVARDIETCTGAGFPCCARDQVQIQCIVYITTEGAP
NPPIILFVSGCDIPIPTDVAEPSEEDMLVSPFAMLRDEVDVLIQISNDFPL
ITRASQVYNNRLMEYTKIKGSIJEVHEPRGGGGEFMRVSKIKIAGIYIDMVOYR
EKLSISYKIDTVARQCIGKEDEVSXKDIPLFRSPGRARAKGSCVMDSVYQML
LKMEHIVELISEIKLAKIOARVLTGQOOLRVKSCLEAARHNFLLPPTPGQCG
YGCATVNIPEISGLVAVDPASVLTSTIIQAHNCYSIMHGRDHLHPDTPDXY
ETVPLSGCPYHFAKKHRESILGHLTVMLEKRAIRRTIACDDPSLKITLDKQOLA
IKVYCNNAVYFVAGSLDPCINIAEVYTLGRFMEKSSVYEALTTEDRLRLKLEGE
VTARHGFRFVYVGDTSFLIADGVSAEAVSAFCDDLAARITADLPPIIKLEAKT
FKCLLTLTKRYIGVILNDMMKMGVGLIKRTACKFVQERCAILIDLVDPEVKAAL
RICKLRPHVYEEGILPAGFKLIEYVINAASYLDLRNSVVPIDEQTFSTELSRPVCVK
TTNIDPHAYOKLASRCELPOVHNDRIPIYFVYVARGSLKSDLAENHYVYQHOIPAV
DLTFDKLVHGAANLIQCLFGNADTVAILINFLNPLYKLPs"
15429. .16679
/gene="ORF10"
CDS
15429. .16679
/gene="ORF10"

gene

```

Query Match      0.1%; Score 33; DB 1; Length 130733;
Best Local Similarity 100.0%; Pred. No. 2.5e-07;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23879 GTTGGGTTTGTGTTTACAACTCCCTATATATAT 23911
      |||||||
Db 115354 GTTGGGTTTGTGTTTACAACTCCCTATATATAT 115322

RESULT 22
AF083501/c 133719 bp DNA linear VRL 26-JUN-2000
LOCUS Macaca mulatta rhadinovirus 17577, complete genome.
ACCESSION AF083501
VERSION AF083501.3 GI:8714565
KEYWORDS
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
99174001
10074154
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
REMARK
AUTHORS
TITLE
JOURNAL
COMMENT

```

```

FEATURES
source
repeat_region
CDS
CDS
CDS
Location/Qualifiers
1..133719
/organism="Macaca mulatta rhadinovirus 17577"
/mol_type="genomic DNA"
/db_xref="taxon:83534"
1..840
/note="partial terminal repeat"
1353..2624
/codon_start=1
/product="R1"
/protein_id="AAD21330.1"
/db_xref="GI:4494908"
/translation="MEVLVFMILQPSVELLPKLTISVPTWCPPHGGDTYLTCRGT
STARQORSTQFMFRNNTLMRGSNFGVLVSTPNATISDRACQTKTTRSSNIDFVS
SSRLTQERCSYGYVANTVRLKSGVNTLRVAVAGTAVTNGTNTNHFV
LTKTGCTVFCACATIGNEKFSQITINFTSTSTFRPTNDIPSHKNGQIQOQASV
QHPENTVVFSPVSTIGVLGTAISLIMKMLTIRKNESSESTNSYASQSTIQPSH
NQRSTNECSRHTYRNAHQESIIEELPNQHTSETSCQVLVEKNVAVDPOENTTI
NEVMEQYDDVVKNIEQTSYEDNVEHMDYDTINPNFNYSGILIEEDVEVYENLEEN
OYHGLILENDLHNEYNHLNLENIQDWLE"
complement(2692..3258)
/note="ORF 2: similar to Kaposi's sarcoma-associated
herpesvirus ORF 2"
/codon_start=1
/product="dihydrofolate reductase"
/protein_id="AAD21331.1"
/db_xref="GI:4494909"
/translation="MDITVNCIYAVDEQIGIKNGTMRPPLYRNEMVYRQKMTSPSV
VEKNVYIGKRTWFSIPKRRPLVNRNITILSRLEIRPEPHAGHFLARTLDDNFTR
QYRLKQTLNTVAVIGKSVSESVLANKCPLKLYIRIMESFQCDVFFPIINFEYTM
SEIPGKDTNENEGIKYKFOYVEKNFK"
3676..5613
/note="ORF 4: similar to Kaposi's sarcoma-associated
herpesvirus ORF 4"
/codon_start=1
/product="complement binding protein"
/protein_id="AAD21332.1"
/db_xref="GI:4494910"
/translation="MTFKLFLPLFLHAIYVHCDENCKRPHFTERYKSNTEKDLVSV
GETALRGPGVYVNTKITTTECLQNGCMSTPNPCDRRCRCPADLLGAVIHGGD
NALKRGSNISTECNEGYDILGSNVRCIIQDTBNVMDNSREYCELOKIKRPAVBE
DVLPMQDVNTYDATALTEKCSLYTLVGSTYLLCTSKRKNNSFPCTLMKVCSPQDN
GIDIDLSRNVHQSITVKGSDGVNIVGPELTCTNTTMYVPLVCVPTNTPSPM
PTMPPEPTPPDYOKINLSTAKTATPNAFTVTVSPEDQDVPLCPHREYVAKEN
DKKYSVGSASVELICRPFTKQSTYVSCISNGTATPNAKCRKCPQDLGEC
YIVTSGEADKFKYGTNTTCNGEYOLISGMVIMKDKDLCTADDEPKAPIDIECK
PPQITNGKHYHVKDYQYLDVTVBSCHNDSYDDEMTCTISNTNKKFPREQDITC
SAPNIAHGRLTGSSSVYKVGQSVTIGCTGFTLGSEISTCKDSSWDPPLPTCVAV
SMPDTPKPEKTKKPNTPPEAKRPMTNPVNGTHTPFKPPPNPDIAPPMKMKRHVVL
LFAVSASLFLVLAALYCPLK"
6045..9443
/note="ORF 6: similar to Kaposi's sarcoma-associated
herpesvirus ORF 6"
/codon_start=1
/product="ssDNA binding protein"
/protein_id="AAD21333.1"
/db_xref="GI:4494911"
/translation="NASKGNAGQPLEDNOGSRAPIGAGGVYVAVSKODPPPAEASTLG
MRPSGVSPLDVLGLTYHEHPEPLTVKAAKYKVDPTTAAVYTCHEPRVYVHNASTL
FRPVGDTGLNELCEBARALFSTYQVTEGPRSHSTNPLECPRLPKDEMFLCYVTE
GERERLMRCGLVAVFQVOQVQIAGQKAVPLYDDELAPHGHRPFRYHNDVAVL
YDSEFTSIAQALRLKDVAVIHATERQFQDHYKIKIVQAKQFSTTLRKTGSSHM
YDVSVAELATLGYGCMFLCPDQACELVYDMSPIKDGCDSPARVNALEIRMSAEQAV
HVGAGOLFANSVLYLTKVOKOAPRGQGVVNYNSPFLQHGSLLEATIKENGSAF
KQPSNALDGSSFTPHLAAYASFHLLAKCYWQRPQDHHKSSNQOAPNHYVGT
KANSKCTLCGHTPATCLNTLRYRLKDRPVAVTTQKRDPIYVVTGTAFQNDLELIG
NPAEFDRREDENPADEHRYTYWQLCQVTEKSLAIGTEHDNHNVAQCAVFLNLY
VFKGIDSIVDGEVKNPMSKINNFNRHVSVHHIIOFCCNVVQACAVFLNLY
KSLMTIIOIDICLPYCMITYEODNPAMGILISELKMHFQRLMTNFKACIDRGLTGE
KTIYHDMFCDEFDAGSNGMAPKPMOYKARAWVVPKSIKIKNRITFSVTAGE
AVOSGVRKPTGRTDYVAVGPRYMKPLNSLHRALFPDTRKALALYLMHKISQTNKTPYK
DYPDEELAVSVYKTNSTAFERTNLDVAVPSLMSYAKIKLGAALTLRACGOIOPAT
THCLTPVLQTIIDAEYRPHVLGSAALATPVAVLAELRGRTALTVOVTHARQPAVATGR

```

CDS

RPVITPVWVVKYKTVNGNNGNNVFNHGNLGFAGAGGVDPNINPESSEPFKTKVSANLTK
RHVWMTPIIDILIRAKAGCTITFEAEVSKSVQALLKEDKNDPNLKLKVTIELIRHUG
KGCODLSEEDVQYVLYGDCMLTDEVLFDLNDINAGSVPTLEDAGALLERDQADDLQ
FVSDDIATFASCOPEEDLPPTPSAGALLAGKRRKKNALLSDLLT
9468. .11528
/note="orf 7: similar to Kaposi's sarcoma-associated
herpesvirus orf 7"
/codon_start=1
/product="transport protein"
/protein_id="AAD21334.1"
/db_xref="GI:4494912"
/translation="MARLEALYLAQSLAVALDLSLVIFADPRSIDAGRLTKTQIEN
LNRDLPLREONSVESSLSLEVHLAKNIEDLGLCELSRQYSREPEHLIR
PECHHSTVTFQFGGLIDVNMCLINDVELCKRGVPCIGANEDLSLNRYLT
LSTLNGISPIPHPLDYTVSPVOCLEIRELIVPQSSLLAVLADRHDLCKKVRME
PIHGLETELSQLGLTKRSDATQDHRGSSADQLEBSLAIODHNIFKVSIME
LSNLIYMAAGOTGLQGTENESQOMARLTHEADHHEARLITPELSTHVSYDCRPD
PIESFEGGGLNSIDDTINALSRDQSVTFPOANTNMRKONELFPTLNSLRGSA
GSKPAPSEPTTVAATASDVYKKAQYRKBOYMKVARDGFRKLTECQTOSAVL
ANALCMRWGAVAGEASELYNHLRREYALPWEAKRSDQILFENSKITKSLIS
QRLSREHVEITTLQFGLITGLTRQSDLPFANVALAQCFEAGMLPHIKMLVSEM
IMPOLOPKMDIDQTFNREYQLPEGLDANVOKSANCFLIELYSLAVALNRTWEKTLIF
SLAREKLSISMLDKLTSGLYLFEDQAPLVLLISONTGWIIFKDYALLYHHLQSDG
HDDN"

CDS

11515. .14004
/note="orf 8: similar to Kaposi's sarcoma-associated
herpesvirus orf 8"
/codon_start=1
/product="g1ycoprotein B"
/protein_id="AAD21335.1"
/db_xref="GI:4494913"
/translation="MMITNRTRLIRAMVYIIAIGTAVGEVNTTPKATTTAKPPCP
STPEPPNPRAEAFKFRVCSASATGELFENLKTGCTGDEINKHDEILNFKKNIV
PHIKVRRYRKVATSVTVYRGMTETAVYAKQEVIRPQVEYINMDDTYOCFSSMRV
VNGJAVYITDQDFNQVFLQVPEGLDNIQRYFSQPLVYTPGPIYVRYTVNC
EIVDMIASAEPSYEVYALGDVTFEPCNDSCSAEKTENGILGAVLNTYID
FATROPTETRTVPADSGEYVSMKAEDPKSAVCLTLTKTEPRALIOTHESAEHYAN
DVATPTSPISQVNTFCTYPCINDIYOKITANATIKRSDPHAINSGSOYETEGGLE
LLKQPLPLSLADERELNGTTPAPPTTSTANKRVRSGVNEQATIDDLAPQLOFAY
DKLASINKVLEELSRACRQVBDTYMWYLSKINPTSVATAYGRVSAKFEVGDAL
SVTDCVANDQASVSIHKSIRSTPGICSRPVPFRLNSTYTLFGQGLGPPNEILTD
NOVACKETCHEYTIASNVYKYKDYVKRLINSSEITLGTFLANLSEIFENIDERY
IELYSRAEKKLSGSEVDEIETMRRENYTOCLAGRELDNTLNRRLARDSEIV
ADLDGRTYVAVASVYTLGSIYSGLINIKSPFGMLIIVYAVYLVFALNRR
TMAIQAQIRIMTYPIDIKMOPSGKVDQIKNLLAGHQLOQEBRRRLDQONSAPS
LFRASDGLKRRERKPLENEAEQYEMSK"

CDS

14122. .17166
/note="orf 9: similar to Kaposi's sarcoma-associated
herpesvirus orf 9"
/codon_start=1
/product="DNA polymerase"
/protein_id="AAD21336.1"
/db_xref="GI:4494914"
/translation="MDEFNPYLGPRGPRHSHRGNDAPAPAGACAVOPPPVCRILPA
CLRTPGAGGMIPVTIPPEPPYFENGARGDVLANBRSMWTARDKRPVAPDDOSITP
HAYVETTYADACAEVPSREDDIIPSGVYLLKTEDEGTSCVAVFQOQYFVA
KVPAGINVTHTLQALKNTAGRAAGFSTRVNRKILKTYVAEPTVETILSGSML
STSDRLVACGEVEFESNVADRRVRFVLDHGTFTGWYSCARAPRLAARDRTLEED
CSMEDLSVQADSRDMPPIVADIEDCTGEAGFCARDEGDAVIOISCVETTEGEP
NPNNILFSGTCDIPIDTVLEPSEEDMLVSFAMIEDVDFLGTGYNISNFPYL
ITRASOYVNLINETYKIKGSIIEVHEPRGGGGGSAVSKIKIAGIYVPTDMYOVR
EKLSDYKRLDTVARQCLGKKEDEYSTKIDPLRLRSGGGRKAGVSTVMDV
LKMFMHVEISEIAKLAKIQARVLTGQOQRLVSCLEAARENFLIPVTPGQGG
YQAGTINPIPGFDEPVLVDFASLVSIIQAHNLICSTMIGRDLHLNPLPDY
ETFLVSGPVHFKKRESLLGRLLVWLEKRAIRRTLAACDPSLKTLDLKOOLA
IKVCMNVYGTGASGLIPCINAEVYTLGRTMLEKSKSYVALTEIDLEKTLRRE
VTARHGAERVYVGDTSLEIACGYSASENSAFCDLAARITADIPPRPKLEAKET
FKCLLTLTKRTIYGLANDKMWKGVDIRKTACKFVOERCAITLIDLHPDEKAAK
RLNLKRPHPHAYEGSLPAGFKIYEVINASTYLDLRNSVPIEOLTFSTELSRPCDVK
TTLNPLHAYVOKLASCBEELPOVHDRIPIYEVVDASKSLDAEHPYVVRHQIIPVAV
DLYEDKLVAHGANILQCLFNNADTVAIILYNFLNVPKLFSS"

CDS

17261. .18511
/note="orf 10: similar to Kaposi's sarcoma-associated

herpesvirus orf 10"	
/codon_start=1	
/product="unknown"	
/protein_id="AAD21337.1"	
/db_xref="GI:4494915"	
/translation="MLVNELSVIGDMEVTFHRRGFSPVNLRLQTEFKHGCVARVRL PESLDLHOFARFAGIYVRLKELPEPSSCVALLIPLDSGGADARARVAGVLDSSRP LTVWYMASGRITIRCLFLKPIRDLERAVTVYFENGARSSEGTPKPCATIESLPGGP LRVSGEASQVTHSPHSVAFPTANSVACSLIRLOVRRPSDDAHRDARTSKRYVFSN SGWVCASQVHSLSPSRCKTQMEIIVAPGDPNMEIYVGGSPVLPHTGGVGLGVA DAEKTIOGSSAEVRVOLIFQOGAARGLAFILVTGVAPELFFVTPALLISGCTTHL RLPNDNGPTTIKRTDLVAAAPCPVYVLTSSADAPRDLVASPTGALISINAFITPVG FPGVYASCHYVTLSDNGVHERMNH"	
18520. .19749	
/note="orf 11: similar to Kaposi's sarcoma-associated herpesvirus orf 11"	
Query Match	0.1%; Score 33; DB 1; Length 133719;
Best Local Similarity	100.0%; Pred. No. 2.5e-07;
Matches	33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	23879 GTTGGGTTTGTTCACAGTCCCTATATAT 23911
Db	117575 GTTGGGTTTGTTCACAGTCCCTATATAT 117543
RESULT 23	
CRH251574	
LOCUS	CRH251574 454 bp DNA linear VRL 11-JAN-2000
DEFINITION	Chlorocephus rhadinovirus 2 partial pol gene for DNA polymerase.
ACCESSION	AJ251574
VERSION	AJ251574.1 GI:6469147
KEYWORDS	DNA polymerase; pol gene.
SOURCE	Chlorocephus rhadinovirus 2 (CHRV2)
ORGANISM	Chlorocephus rhadinovirus 2
REFERENCE	1 Greensill J., Sheldon J.A., Renwick N.M., Beer B.E., Norley S., Goudsmilt J. and Schulz T.F. Two distinct gamma-2 herpesviruses in African green monkeys: a second gamma-2 herpesvirus lineage among old world primates? J. Virol. 74 (3), 1572-1577 (2000)
TITLE	JOURNAL
AUTHORS	20094948
PUBMED	10627372
REFERENCE	2 (bases 1 to 454)
AUTHORS	Greensill J.
TITLE	Direct Submission
JOURNAL	Submitted (15-NOV-1999) Greensill J., Dept Medical Microbiology and Genito-Urinary Medicine, University of Liverpool, Duncan Building, Daulby Street, Liverpool, L69 3GA, UNITED KINGDOM
FEATURES	Location/Qualifiers
source	1. .454 /organism="Chlorocephus rhadinovirus 2" /viroion /mol_type="genomic DNA" /isolate="animal L1" /specific_host="Chlorocephus aethiops" /db_xref="taxon:109048"
gene	1. .454 /gene="pol" <1. .>454 /gene="pol"
CDS	/codon_start=2 /product="DNA polymerase" /protein_id="CA861754.1" /db_xref="GI:6469148" /translation="LCYSTLPFGDHLHBDPLTPDDYETRLASGPPVHFKKRESL LGRLLTVLSRKRIIRALAACDPSLKTILDKOOLAKVTCNAYGFTGASGLIPC INIAETVTLRRRTMLEMSKAYVALTEDEIOTLRRAVTAADPGARFRV"
BASE COUNT	92 a 153 c 137 g 72 t
ORIGIN	

Query Match 0.1%; Score 32; DB 1; Length 454;
 Best Local Similarity 100.0%; Pred. No. 4.9e-07;
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 16192 TACGGGTTACCGGGGTGGCCACGGCCCTCT 16223
 ||||||||||||||||||||||||||||||||||||
 Db 269 TACGGGTTACCGGGGTGGCCACGGCCCTCT 300

RESULT 24
 AY237372 523 bp DNA linear VRL 14-APR-2003
 LOCUS Caprine herpesvirus 2 glycoprotein B gene, partial cds.
 DEFINITION AY237372
 ACCESSION AY237372
 VERSION AY237372.1 GI:29826255
 KEYWORDS
 SOURCE Caprine herpesvirus 2
 ORGANISM Caprine herpesvirus 2
 Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 Gammaherpesvirinae.
 1 (bases 1 to 523)
 Li, H., Galbreath, K., Flach, E.J., Holmes, E.C., Keller, J. and
 Crawford, T.B. Phylogenetic Relationships of Selected Ruminant Rhadinoviruses
 Unpublished
 2 (bases 1 to 523)
 Li, H., Galbreath, K., Keller, J. and Crawford, T.B.
 Direct Submission
 Submitted (14-FEB-2003) Animal Disease Research Unit, USDA-ARS,
 3003 ADRF, Washington State University, Pullman, WA 99164, USA
 Location/Qualifiers
 1..523
 /organism="Caprine herpesvirus 2"
 /mol_type="genomic DNA"
 /db_xref="taxon:135102"
 <1..>523
 /codon_start=2
 /product="glycoprotein B"
 /protein_id="AA08173.1"
 /db_xref="GI:29826256"
 /translation="NRASIMMNNELSKINTSWSSITGRPVSKRIGDVISHCVV
 DDOVSVLRNNRYPGKDHAECHSRPVFKFTNDHLKLGQGVNNEILTTALEV
 CHEHTEHYFOGDNMYFYKNRYHKVTPVDATLDTFLVNLTVENIDFOVLELYS
 REEKRMSTVFDELT"

BASE COUNT 133 a 151 c 144 g 95 t

ORIGIN

Query Match 0.1%; Score 31; DB 1; Length 523;
 Best Local Similarity 100.0%; Pred. No. 1.9e-06;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12958 CTGAGCAAGATTACCCACGACCGTAATCA 12988
 ||||||||||||||||||||||||||||||||||||
 Db 29 CTGAGCAAGATTACCCACGACCGTAATCA 59

RESULT 25
 AF159039 395 bp DNA linear VRL 28-APR-2000
 LOCUS Macaque gamma virus str. Macaca nemestrina gamma virus
 DEFINITION AF159039
 ACCESSION AF159039
 VERSION AF159039.1 GI:6671086
 KEYWORDS
 SOURCE Macaque gamma virus
 ORGANISM Macaque gamma virus
 Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 Gammaherpesvirinae; Rhadinovirus.
 1 (bases 1 to 395)
 Strand, K., Harper, E., Thormahlen, S., Thoulless, M.E., Tsai, C.,
 Rose, T. and Bosch, M.L.
 Two distinct lineages of macaque gamma herpesviruses related to the
 Kaposi's sarcoma associated herpesvirus

JOURNAL J. Clin. Virol. 16 (3), 253-269 (2000)
 MEDLINE 20204465
 PUBMED 10738144
 REFERENCE 2 (bases 1 to 395)
 AUTHORS Strand, K.B. and Bosch, M.L.
 TITLE Direct Submission
 JOURNAL Submitted (14-JUN-1999) Pathobiology, University of Washington, Box
 357238, Seattle, WA 98125, USA
 Location/Qualifiers
 1..395
 /organism="Macaque gamma virus"
 /mol_type="genomic DNA"
 /strain="Macaque nemestrina gamma virus"
 /db_xref="taxon:111468"
 <1..>395
 /gene="gB"
 <1..>395
 /gene="gB"
 /product="glycoprotein B"
 /protein_id="AA23089.1"
 /db_xref="GI:6671087"
 /translation="GTEDKTHQGIIMVERKNVPIHFYKRRYKRVATSVYRGTE
 TAVTGKQEVPRVPOYEINMDTYQCFSSMRVNVNGIENTYTRDFTNQTFLQPE
 GLTDNIQRFOSQVLYTTPGMPGIVR"

BASE COUNT 98 a 115 c 114 g 68 t

ORIGIN

Query Match 0.1%; Score 29; DB 1; Length 395;
 Best Local Similarity 100.0%; Pred. No. 2.8e-05;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11788 GGCATCTGATGGTGTAAATAAATAT 11816
 ||||||||||||||||||||||||||||||||
 Db 30 GGCATCTGATGGTGTAAATAAATAAT 58

RESULT 26
 AF031811 469 bp DNA linear VRL 27-APR-1998
 LOCUS Bovine Herpesvirus 4 DNA dependent DNA polymerase (pol) gene,
 partial cds.
 DEFINITION AF031811
 ACCESSION AF031811
 VERSION AF031811.1 GI:2832252
 KEYWORDS
 SOURCE Bovine herpesvirus 4
 ORGANISM Bovine herpesvirus 4
 Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 Gammaherpesvirinae.
 1 (bases 1 to 469)
 Rovnak, J., Quackenbush, S.L., Reyes, R.A., Balnes, J.D., Parrish, C.R.
 and Casey, J.W.
 Detection of a novel bovine lymphotropic herpesvirus
 J. Virol. 72 (5), 4237-4242 (1998)
 TITLE
 JOURNAL 98216791
 MEDLINE 9557713
 PUBMED
 REFERENCE 2 (bases 1 to 469)
 AUTHORS Rovnak, J., Quackenbush, S.L. and Casey, J.W.
 TITLE Direct Submission
 JOURNAL Submitted (29-OCT-1997) Microbiology and Immunology, College of
 Veterinary Medicine, Cornell Univ., Ithaca, NY 14853
 REFERENCE 3 (bases 1 to 469)
 AUTHORS Rovnak, J., Quackenbush, S.L. and Casey, J.W.
 TITLE Direct Submission
 JOURNAL Submitted (04-FEB-1998) Microbiology and Immunology, College of
 Veterinary Medicine, Cornell Univ., Ithaca, NY 14853
 REMARK Sequence update by submitter
 On Feb 5, 1998 this sequence version replaced gi:2660736.
 Location/Qualifiers
 1..469
 /organism="Bovine herpesvirus 4"
 /mol_type="genomic DNA"
 /strain="DN 599"

gene
/db_xref="taxon:10385"
<1..>469
/gene="pol"
<1..>469
/gene="pol"
/codon_start=1
/product="DNA dependent DNA polymerase"
/protein_id="AAC59454.1"
/db_xref="GI:2832253"
/translation="SIIQAHNLCTSTMIDONLHLHLHPDDYETFLSTGPIHFVKQ
HKTSLSLTLLTAMLAARKTRKELANDCDGPMKTIIDKQOLAIRKNSVNGFTGVA
SGILCPPIATVTLQGRMTLEKRAFEVMTTPRLSDIYSVPICDDASFRV"

BASE COUNT 150 a 116 c 95 g 108 t

ORIGIN

Query Match 0.1%; Score 29; DB 1; Length 469;
Best Local Similarity 100.0%; Pred. No. 2.9e-05;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 15919 CACACCTGCTGCTACTCCACCATGATACA 15947
|||||
16 CACAACCTGCTGCTACTCCACCATGATACA 44

RESULT 27
AF005477 3638 bp DNA linear VRL 07-JUL-2000
LOCUS
DEFINITION
Kaposi's sarcoma-associated herpesvirus glycoprotein B gene,
partial cds; DNA polymerase (pol) gene, complete cds; and ORF
10-like protein gene, partial cds.
AF005477 AF204169
ACCESSION
AF005477.2 GI:8714518

KEYWORDS
Human herpesvirus 8 (Kaposi's sarcoma-associated herpesvirus -
Human herpesvirus 8)
Human herpesvirus 8
Virus; dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Rhadinovirus.

ORGANISM

REFERENCE
AUTHORS
1 (bases 2226 to 2701)
Rose,T.M., Strand,K.B., Schultz,E.R., Schaefer,G., Rankin,G.W. Jr.,
Thouless,M.E., Tsai,C.C. and Bosch,M.L.
Identification of two homologs of the Kaposi's sarcoma-associated
herpesvirus (human herpesvirus 8) in retroperitoneal fibromatosis
of different macaque species

TITLE

JOURNAL
J. Virol. 71 (5), 4138-4144 (1997)
MEDLINE
97248469
PUBMED
9094697

REFERENCE
AUTHORS
2 (bases 1 to 3638)
Schultz,E.R., Rankin,G.W. Jr., Blanc,M.P., Raden,B.W., Tsai,C.C.
and Rose,T.M.
Characterization of two divergent lineages of macaque
rhadinoviruses related to Kaposi's sarcoma-associated herpesvirus

TITLE

JOURNAL
J. Virol. 74 (10), 4919-4928 (2000)
MEDLINE
20240083
PUBMED
10775636

REFERENCE
AUTHORS
3 (bases 2226 to 2701)
Rose,T.M. and Strand,K.B.
Direct Submission
Submitted (28-MAY-1997) Pathobiology, University of Washington, Box
357238, Seattle, WA 98195, USA

TITLE

JOURNAL
Rose,T.M.
Direct Submission
Submitted (26-JUN-2000) Pathobiology, University of Washington, Box
357238, Seattle, WA 98195, USA

REMARK
COMMENT
Sequence update by submitter
On Jun 26, 2000 this sequence version replaced gi:2245590.
FEATURES
Source
1..3638
/organism="Human herpesvirus 8"
/mol_type="genomic DNA"
/isolate="KS187"
/db_xref="taxon:37296"

gene
/note="isolated from a KS lesion of an HIV-infected
individual"
<1..328
/note="similar to herpesvirus saimiri ORF 8"
/codon_start=2
/product="glycoprotein B"
/protein_id="AAF78828.1"
/db_xref="GI:8714520"
/translation="MIIIVAIILIIIFMLSRNTNTIAQAPVKMIYPDVRRAPSGGA
PTREIKNIIILGMHLOOEEROKADDLKSTPSVFORANGLRQLNGYKPLTQSLDI
SLENGE"
455..3493
/gene="pol"
455..3493
/gene="pol"
/note="similar to herpesvirus saimiri ORF 9"
/codon_start=1
/product="DNA polymerase"
/protein_id="AAC57974.2"
/db_xref="GI:8714519"
/translation="MDEFNPEIDPTRGGRNTVROPTPSQSPVPSSETRCRLIPACF
QTPGRPGVAVDTFPPPTFQGPGRGEVFAETGSIKTRGQARNAHMLIFHYD
IVETTYADRCEDVEPFSFQNDIIPSGVTLKLGRTLDGASVCNVFPRRCYFTLAPQ
GNTLTHVLOALQALGAFGASGSGSTEEVRRKILRAYDQOYAVOKITLSSPMRITLS
DRITTCGCEVPESNVDAIRRPVLDHGSGTEGNCSPARPTQARDSTETLEPSCME
DLKFTPERTMPPTSLISFDECKGEKGFPAATODEMDITIGVLTGVGDKYTRM
LLGFTCDPLPGVVEFEPSEYDMLAFLSMROYNVEFTIGVIANEDLYIIAAT
QVYDFKLODFKIKITGSEVYEHQPRGSDGDNFMRSSKVAISGIVIDMYQCREKL
SLSDYKLDIVAKOCLGRKDDISYKDIPLKSGPDRAGKNGCIVDYSVMDLLR
FOHVEISEIAKLAKIPIRRLVTDGQOIRVPSCLLEAATGYLLPVKGVAVSYOG
ATVTSRSGEPYDPLVVDPAISLPSIIQAHNLCTSTLIPDSGLHLPHLSPDYEF
VLSGCPVHFKKHKKRESILAKLTVWLAKREIKRTIASCIDPDLKTIIDKQQAIRY
TCNAVGPETGASGILPCNLAEVTLQGRMERLSAFAEISPERLAGLPRIDV
SPDARFVYIGDTSLEIFICGMNDSDVSFAEELASITNTLFRSRIKLEAEIFEC
LLLTLLKRYGVLSDDKVLKMGVLDIKRTACRFYQEKSSQVLDLILKPSVKAAKLI
SGQATDMWYREGLEPEGRVKKIIOVNAHSRELCERSVPDKLFTTELSRPLADYKTON
LPRLTVYOKLOAROEELPOLHDIRIPYFVAVAPGSLRSELAHEHPYVQHGLRAVDLY
FDKLVAHANITQCLFQNTSATVYAMLNLTIDIVTPPTP"
3611..>3638
/note="similar to herpesvirus saimiri ORF 10"
/codon_start=1
/product="ORF 10-like protein"
/protein_id="AAF78829.1"
/db_xref="GI:8714521"
/translation="MGTETATFTL"

BASE COUNT 930 a 1037 c 931 g 740 t

ORIGIN

Query Match 0.1%; Score 29; DB 1; Length 3638;
Best Local Similarity 100.0%; Pred. No. 3.7e-05;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 14938 CTGGAGTTTGACTGCAGCTGGAGGACCT 14966
|||||
1259 CTGGAGTTTGACTGCAGCTGGAGGACCT 1287

RESULT 28
AF318573 108873 bp DNA linear VRL 18-MAY-2001
LOCUS
DEFINITION
Bovine herpesvirus 4 long unique region, complete sequence.
AF318573 AF271211
ACCESSION
AF318573.1 GI:12802528
VERSION
AF318573.1 GI:12802528
KEYWORDS
Bovine herpesvirus 4
Bovine herpesvirus 4
Virus; dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae.

ORGANISM

REFERENCE
AUTHORS
1 (bases 1 to 108873)
Zimmermann,W., Broil,H., Ehlers,B., Buhk,H.J., Rosenthal,A. and
Goltz,M.
Genome sequence of bovine herpesvirus 4, a bovine Rhadinovirus, and
identification of an origin of DNA replication

JOURNAL J. Virol. 75 (3), 1186-1194 (2001)
MEDLINE 20583805
REFERENCE 11152491
AUTHORS 2 (bases 1 to 108873)
Zimmermann, W., Broll, H., Ehlers, B., Bukh, H.-J., Rosenthal, A. and
Goltz, M.
TITLE Direct Submission
Submitted (03-NOV-2000) Project P24, Robert Koch-Institut, Nordufer
20, Berlin D-10555, Germany
FEATURES
source
1. 108873
location/Qualifiers
/organism="Bovine herpesvirus 4"
/mol_type="genomic DNA"
/db_xref="taxon:10385"
1. 108873
/note="long unique region; LUR"
complement(445..633)
/note="ORF B01"
/codon_start=1
/evidence="not_experimental"
/product="hypothetical protein pB01"
/protein_id="AAK07921.1"
/db_xref="GI:12802529"
/translation="MGGVSWAVAGRKTRDRLNNSAGNEVCAVLRKNHNSAGC
CAVRNNSFHSLPGMP"
614..4480
/note="segment protein; ORF3 B0FA1"
/codon_start=1
/product="v-FCM-synthase"
/protein_id="AAK07922.1"
/db_xref="GI:12802530"
/translation="MDTSPSIQCFEVSRRAPLSENCVIOQFTSDQLPLTSPLOY
BOVMVLVNGEAOVREPLPDLKFSHGLTFPHESSILKTDSRRSLFTYGSPSA
PEYLSRLVLAIIOSMGLAPMSNLTOILKIVLSITISKNLMPSPKIHSTLRAL
CPSPSLRPYKSGEIVGHAHTHAPGVLSPPKGDILGAVGCFLNAGSGASGEMT
PQHGQITVNOFCFKATIVPDVWIPETISTYSSGHTDGTGLATYGQVQVARNQ
LKLFLYNSPNQWENFVNSQGLASTVITSPSSYELPPRYATIDAMVNNKRC
SLPCTOGYFFPIVESHLPDLSVPEGPIAFGAVCFNRNITDLPETRHKINIVQIGT
FTSSHEDGREVRCILGALKYLMSEGLRPSQKGSAYVCEVMAKLLSCGQYGIK
IYSGALPRLNTGLLPFAVNRQNMIMKOHFNIVAPIVLVAIEATPDNTDVLK
AGCAIHGOYKVLGRROKPHIHYKMGKGNREKISLRKSPSPILSTNNKQKOS
ENMODSSWMDTLPSLTSTLEILKHPVGCKDRTVKHIDRLSSGRAVQOQIGARDI
PISDYSLIVSDLSLAAPDRGSENPWATAESLDLPLVNNPVPFGICSAIGCEPPLS
TYPIKGAHVAIVESLNIIVASPERKIDDVCTENTNTPOTDSHFGLIEARAGER
CSQLGIGVFCTSTSNRQKCLNLSLVRLYATAPCKDVQGLPDLKEDPSI
VWLPSTGEYFEGTVISQLFRSPSGHINIDPLVYKKLITVTKHLINHESISCHDV
GCGGLITACPEMAVAGSIALTVPODEDVPLFSTPGCLMVEYPRKYSTVQKHLE
TSDITIEDVGRTPSVASNTFTVSKETIRRESINLEWENRHPSTKEQRTYPCET
QGTEDEPRKDLQLHLEQPSMCPHGPXYHQVNVYLLPGINTPDLALVLEAGERVN
LVSTFDKTVKIVDTTNVFGICLIGATNIEDATLGDAISMYKHSVLGELKILI
NSPVFSLAIGHTAQILFENKPMGYNPKNTWYCKENSGLMESRMLNFEIPENTH
AVALOSKMSGLPGMIOGTHGFAPHSETVEMELSTHGMVATORYGADISGPAITYP
ONTRAGTISGLCSADGRHLALLHDPGISNNLMQMPHLPKMTPLKSPKRMFLDLH
IWANKVREMDQPPPHDPPLRNKIVM"
4608..4811
/note="ORF B02; B0FA2"
/codon_start=1
/evidence="not_experimental"
/product="hypothetical protein pB02"
/protein_id="AAK07923.1"
/db_xref="GI:12802531"
/translation="MASPTQCHRWVRYHGPRAKSAISYGYKDRDYTHQLTSKNSAYS
GMSPPQSCADLNLKLFVSCDPS"
5286..5513
/note="ORF B03"
/codon_start=1
/evidence="not_experimental"
/product="hypothetical protein pB03"
/protein_id="AAK07924.1"
/db_xref="GI:12802532"
/translation="MGFNPVMLFYHPCNCTPTSLKHGLYIKIYKISYLIRATFLVRNV
HICPPKRDTRPPGCGPPSLIVORLALKR"
5943..9347

/note="ORF 6"
/codon_start=1
/product="single-stranded DNA-binding protein MDPB"
/protein_id="AAK07925.1"
/db_xref="GI:12802533"
/translation="MAKTRAGQOQEDNIGSKAPILGCGYIYYKKKEFPFKESLLG
NGPFGTSMVSPLLGELTVEGFPFINVAVKIKDTTIVSKVSYHHEVIMFENIDC
FTPIFHHGDPOLCGEDRDLGFTHYSPSPSTNTNLSLDLCGDCNDIDEVITLGVIT
EGFKEFVHGHMIPILGHVEEVQISPGAAKPILEDDELSKLAPRMRKFFHSDVS
OYLFNSLYTATAOAIKVYKDVATVIOASGAPRROOHKPKRYVHKHKKDFSSRDGL
SLMIMDSVASELAYSGSLFDAPQDMSALLDYSPMFVCTICEEDLQALHANMK
QSIHVNTOLESTNSMLYLRIOKQNPATKADLVANYSYIQHGLSTSEYTODEYGO
PVFOGVSNNLSGSGTYTIIHLAYASMPNRLARCYLLQCOHQSTQSONSYNSY
VGTAAASDMCMICOGKPAVCINFLFYLRDRFPPIITSHRDPYIITGSGVMDLD
ILGNASFEREKEDGAQVEYOKATYMDLQTLLEKLEGMGIKDTPPEKLVSDIPSF
IKVRKIDAHVDYDTEVLRKINCMVKNNTNIRETKISIHVIOYCCNVAPRCPVLOL
YKKSILITIDVCLPNCMMYEQDNSSMGKGTBYLNKHVOTLMTNFKGCCDRCVLTG
AELVMSHDPDCEFDVDAIINGIFSPKTVORISRAVLVVPKTKLNRIIFSNSSG
SEAIOSGFLKSGSKNDYIVTPYKPLNLIYHKIMFPOTKSSLFMMHTFSTKQIPL
ITGVPKDQVLAVANIIEYNSKLHSEIDVLDIIPNLITYAKIKLNMAILRACQTOFY
STTLHLCLVPTVRVGEEXPHVLENEEFLGTEOYLKVQNRPAQIVQATLKEDYAOAG
KLRLIITVPMVINKYTGINGNNGIFHCGNLGTFMGRGVDRMLIFENAPFRQSTNAVY
RKKHVFMPPIVDNLKRTYTPSSSTFEVENIRRMIMLEEKDNQNIERDVLLEYK
LGQACADLTADLDQFYLGEEYIMSEDEIISLRQSSJSDAGVPCEDSVSFLGEVYSEE
QLEFGLGEQTTSAPTSEDFQASGLSTIAGKRRKRLNCLMDPLD"
9352..11430
/note="ORF 7"
/codon_start=1
/product="transport protein"
/protein_id="AAK07926.1"
/db_xref="GI:12802534"
/translation="MARELAIVYQVDFLSEKTSILTFECPDRHIDLGAFOHNRKRLK
LIDLAYSHLVQONTRECSLELEHLINITYIMOKETOLNENYIKEDFAMHLIS
DLCEHKKVNLCEFGDCVPISTISINDIEFESLNSVFCISNNMLDELEETIN
LGTIRNISPILPDLIYFISICMNCINTSLIPNGENVFTMNSINETHATPAPRE
PVQGFENELHNLINPVDTGNKQVLESDRIQASLEADIDHNEFVQSHILEIS
NLEIYNSHSDMSQPKLSCSQMALTIOETSRIOASVASHLALTPIPIHFPSYRA
YPIESLFCGJFYFSIMONIQALOKOCSSTFLAKSAYKIMRKNELVYRLNNLAPSH
TRKESGIDKPNISIOARHTIGETSEBDFGDAARKVNYKTLGTEDLKITDPLET
QKIMCMTLTLRTGMWVYKRAAILKHFMRKRLRILAPOMHNHTATINELYESKFI
KNSLYOKLSEHDSITLQYSLITGSGVGRPPFSPRLINLANCDAKAVMHNK
MLISVIMPSPKOWIDAEFNAFLNTGKLVNSVQCAWRIRELVASVSLYNWE
KDLNIVSPSTLPSNHLFSPKPLFNSGIVITYEKTAPLIFIDHNGWIFKDLALLYH
LQLSHKNVL"
11420..11404
/gene="gB"
11420..11404
/gene="gB"
/note="ORF 8"
/codon_start=1
/product="glycoprotein B"
/protein_id="AAK07927.1"
/db_xref="GI:12802535"
/translation="WYKYLIFALIKVCSFNQTTSTSTSPSISSTYSSTTSTSK
PSNNTSTNSLAASPONTSTSKPSTDNGSTPIPTVTDYASKNFYKRGCSASS
SGELFREDLDQTCEDTKDKKKEGILLALKNTIYPIFYKRYKRIATSVYRMSQ
AAVNRNDISRAIPNEYISMIDRYTHCSAMATYINGILNTYIDBSENKSVLPDPA
GLTENINRYDSOPLIYARBGWPGIYRRTVYNECVYMARSEVYRHHFTALGDTI
EISPRCHNSOCTGNSSTRATKYMIENNOTYDYERGRHPTDKRFLNDEBTIS
WKAEDREAIQDFYWKTFPRALQTIHESHFVANEYASFLVNOGETSELRGTEI
LKNANSTINTELETVKPFNSKIDEGEVKYYKINGGLFLWQAKKPLNLSLHNVTYI
ERNKTKNRSKRSKSDVTKTFQAGAKGSTAQOYAYADLRTSMNHILLEELRTMCRQ
KQDNLMYELSKINPVSMAIYGPVAVKAMGDAFVSECINVOASVYNIHKSMTRD
DPKYVSRLPTVFPKVNSTATFPGQLGRNELLLNTHVEFCRPTADHYFVKNMHTY
EKDYKVTQMTQNNISTIDFTLNLFTINDIKTYVLESETERKMASALDLEMFR
EYNTYQKLASLREDLWNTIDLNRDLKXDSLSEMAIDGLIGKVVYNTFGSITVYFGS
IVGGEVSEFTNPIGCVTIIILLIVVVFVIVSRRTNMNNAPIKMTYPNIDKASDEQ
NIQPLPEEIKRILILGMHQLQOSEHGKSEBSASHKPGILFOLLGGLDLRLRGYTRLP
TFDPSGNDTSETHQYV"
11484..17201
/gene="Dpol"
14184..17201
/gene="Dpol"
/gene="Dpol"


```

/Note="ORF 9"
/codon_start=1
/product="DNA polymerase"
/protein_id="AAK07928.1"
/db_xref="GI:12802536"
/translation="MEFNPYISKKTDRKISVDDPKNTNRYCLVKKCRTEPT
GVISTITDTPVLFHODKEPIFTSGDHRSWAKPAPLPADKLFYHYDITE
TITPDRCDDIPDIFQETDIIIPNGVYKLLGKTQDQSVNFOQVYVYVDPDVN
LSYVIOQTLNGVKNQCKFSITQERKKILKEKPSLYKRTTAKPTEINQVLN
TSCGCEVEFSNVAASRFRIIDNKSTFFGVSCSNPDRISORSPDLDFEGLDLO
FHEEOOMPPTIMSPDIEICIGEOGPGATCKEDYATIOSCIIMVYCSPPONILS
IGCDPIANDYVEPSEELDMYAFPTLLADRNIDVYVNTNANPEPPTIDRAIVY
NPIRHFRTVISGSTFEVNOQPMATGAGHRSFKITSGVLPIDMQVCKDSIDY
KLNTYAKHCHQKQEDVYKELPSFSGEAGRAIGSCVLDVLYDLKRYFMTH
EISELAKMAKIPARVLTGQOIRVFSCLLEAKKHEFLIPGAKPGGOGATVIN
PIGFEYNTPLVDFASLIYPSIIQAHNLCSYMIODONHLHLKDDYETFLSTGP
IHFKOHTKSLSTLLTAMLAARKTIRKELANCDDGPKMTLLDKOOLIKYMCNSVY
GRTVYASGILPCIPIAETVYLOGRTMLESKAFVETPERISDIYSTVPCDDPASF
RVYIGDPTDLSFTECRQYPMQSVLNFADKLETTTKALEKDPILKEAKTEFQCLMLTK
KRYIGILSSDKLVMGVDLIRKTACSFVQTKSEKILDLVLRDPEVQAQVLCRQAPA
KYVSDGLPGEFKVIVDLNNSYAALATGVSSESLSTELSPFGEYKTTLLPHLT
YRKIMSRELEPOIHDRIPYVFIKGDORCKSDIADMDPYVSQNKIPISVEIYFDKLI
HGVANILOCLFENNSMTVEILYNFVNIYPSFT"
17297..18577
/Note="ORF 10; BORF1; conserved in other
gamma herpesviruses"
/codon_start=1
/product="unknown"
/protein_id="AAK07929.1"
/db_xref="GI:12802537"
/translation="MSTITVESIEGMVONICNGNIITMFIKIDIPVQCGYMLKRY
EIPLSNQLINNYISGLVQSFELBDIAQCTAMLVQCFPGIRPLETTPHVEEN
MPLFEKTONITINSLSLAIIFKPPCPGICSYISTAPEETIPPHSLAHNLP
TQGLFLLTSGAOKCNKHTYTFRPPSPQSGKMHMTVMSGSDLODQCVGMSYD
IKINIMEVYVNPGLKYSVININPKHDHITKLTVMWKPDLVAVLSTSLPS
CKVNNIYDSEKILKPGETLNLKLYTTRNENSKAVMTKGTPTDNLNMTVEIPI
LMTPLQVYIKNPTMILITIKKDLIAACVPPYSTLEDNQPARSPVYINPDLLITW
EDSMVATIGENITISRCHLNKSETPSPMTP"
complement(18848..19345)
/Note="ORF B04; short ORF of immediate early transcript 1
complement(18848..19345)

Query Match      0.1%; Score 29; DB 1; Length 108673;
Best Local Similarity 100.0%; Pred. No. 5.6e-05;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Ox      15919 CACAACTGCTACTCACCACATGATACA 15947
      |||||||
Db      15957 CACAACCTGCTACTCACCACATGATACA 15985

RESULT 29
LOCUS      093872
DEFINITION      133661 bp DNA linear VRL 09-JUL-2001
      Kaposi's sarcoma-associated herpesvirus glycoprotein M, DNA
      replication protein, glycoprotein, DNA replication protein, FLICE
      inhibitory protein and V-cyclin genes, complete cds, and tegument
      protein gene, partial cds.
ACCESSION      093872
VERSION      093872.2 GI:14627174
KEYWORDS
SOURCE      Human herpesvirus 8 (Kaposi's sarcoma-associated herpesvirus -
      Human herpesvirus 8)
ORGANISM      Human herpesvirus 8
      Gammaherpesvirinae: Rhadinovirus.
      Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
      Gammaherpesvirinae: Rhadinovirus.
      1 (bases 29032 to 30108: 117733 to 118431)
      Zhong,W., Wang,H., Herndier,B. and Ganem,D.
      Restricted expression of Kaposi sarcoma-associated herpesvirus
      (human herpesvirus 8) genes in Kaposi sarcoma
      Proc. Natl. Acad. Sci. U.S.A. 93 (13), 6641-6646 (1996)
JOURNAL      96270595
MEDLINE      8692871
PUBMED      2 (bases 17242 to 17856)

AUTHORS      Neipel,F., Albrecht,J.C., Ensser,A., Huang,Y.Q., Li,J.J.,
      Friedman-Kien,A.E. and Fleckenstein,B.
      Human herpesvirus 8 encodes a homolog of interleukin-6
      J. Virol. 71 (1), 839-842 (1997)
JOURNAL      97138401
MEDLINE      8985427
PUBMED      3 (bases 123309 to 124082)
      Li,M., Lee,H., Yoon,D.W., Albrecht,J.C., Fleckenstein,B., Neipel,F.
      and Jung,J.U.
      Kaposi's sarcoma-associated herpesvirus encodes a functional cyclin
      J. Virol. 71 (3), 1984-1991 (1997)
JOURNAL      97184528
MEDLINE      9032330
PUBMED      4 (bases 122660 to 123226)
      Thome,M., Schneider,P., Hofmann,K., Fickenscher,H., Meini,E.,
      Neipel,F., Matmann,C., Burns,K., Bodmer,J.L., Schrotter,M.,
      Scaifdi,C., Kramer,P.H., Peter,M.E. and Tschopp,J.
      Viral FLICE-inhibitory proteins (FLIPs) prevent apoptosis induced
      by death receptors
      Nature 386 (6624), 517-521 (1997)
JOURNAL      97242415
MEDLINE      9087414
PUBMED      5 (bases 1 to 133661)
      Neipel,F., Albrecht,J.C. and Fleckenstein,B.
      Cell-homologous genes in the Kaposi's sarcoma-associated
      rhadinovirus human herpesvirus 8: determinants of its
      pathogenicity?
      J. Virol. 71 (6), 4187-4192 (1997)
JOURNAL      97296220
MEDLINE      9151804
PUBMED      6 (bases 1 to 133661)
      Neipel,F., Albrecht,J.C., Ensser,A., Huang,Y.-Q., Li,J.J.,
      Friedman-Kien,A.E. and Fleckenstein,B.
      The genome of human herpesvirus 8 cloned from Kaposi's sarcoma
      Unpublished
      7 (bases 1 to 133661)
      Neipel,F., Albrecht,J.-C., Ensser,A., Huang,Y.-Q., Li,J.J.,
      Friedman-Kien,A.E. and Fleckenstein,B.
      Direct Submission
      Submitted (17-MAR-1997) Virology, University of Erlangen,
      Schlossgarten 4, Institut für Klinische und Molekulare, Erlangen
      91054, Germany
      8 (bases 1 to 133661)
      Neipel,F., Albrecht,J.-C., Ensser,A., Huang,Y.-Q., Li,J.J.,
      Friedman-Kien,A.E. and Fleckenstein,B.
      Direct Submission
      Submitted (09-JUL-2001) Virology, University of Erlangen,
      Schlossgarten 4, Institut für Klinische und Molekulare, Erlangen
      91054, Germany
      Sequence update by submitter
      On Jul 9, 2001 this sequence version replaced gi:2246466.
      Location/Qualifiers
      1..133661
      /organism="Human herpesvirus 8"
      /mol_type="genomic DNA"
      /db_xref="taxon:37296"
      /Note="sequence derived from overlapping Lambda phage
      clones isolated from two libraries of Saüa partially
      digested DNA from Kaposi's sarcoma biopsies"
      105..959
      /Note="ORF K1"
      /codon_start=1
      /protein_id="AAB62619.1"
      /db_xref="GI:2246494"
      /translation="MPYVYCSLAVCFRGLSLSSQSPNLCPGVISPPYTLCPST
      SIPSYKCDPRLRLRHTQTFYVDPLILCSVSGSGHSHMLTWYPOPVLTCCGQ
      PSNIVYCGQHTVLYCSTSGNNVTVHLPKGRNRYVSQRTVTFILNDEGCTACSG
      LSSRLSNRCLFSARCANLPERHVSVSSTGTFRTFRTTRCTTDLVLYKRAKSTNL
      HVOVHLYEMTVALIGITGWCIGITIIFAHCOKORDSNKTVPOQLQDYVSLHDLCTED
      YTOPVDWY"
      1127..2779
      /Note="ORF 04, complement control protein homolog"
      /codon_start=1

```


/protein_id="AAB62602.1"
/db_xref="GI:2246477"
/translation="MAFLRQLTMTLFTFNVIGODNEKCSOKTLIGVRLKMSRDGIA
VGEVRLRCRSGTYYARNITATCLOGGTMSSEPTAKCNKSCNPGEIONGKVIPIFGG
QDAKRGANISVYCNEGYFLNGREYRYCMIGASGOMANSSPPCEKEKCHPKREN
GDRPKDYEINDAVHECNESITLVGPHSLACAVANNWTSMPTCELAGCFPSVT
HGVPYIGFSLYKHKQSVTACNDGFLKRSPTITCNEMDPLPKVLEDIDDDNN
SNRGLHPNENKPNNGNFORSNYTEPPKPEDTHAATCDNCEQPKLPTSEEGN
ETTSMITIKOLEDEKTSOPNTHLITSLTSMKAKGNFTKNTNSTDLHASTPTSDI
DAPSIISVOTPNVNTNAPRLTSLITSEEGSPNNTSEKATSTLSHSHKNDGDI
YTLNKTTLPTSNKPTNSQAKSTKPRVETHAKTTSNPAISLITSDADVPQREPEPL
PIERPASPKNRLEKOLVIGLTAVALTCGLTTLFHYLEFR"
3194..6592
/note="ORF 06, major ssDNA binding protein homolog"
/codon_start=1
/protein_id="AAB62603.1"
/db_xref="GI:2246478"
/translation="MALKGQTLLENIGSAPTPGCGYLYAVLYTNHPPIGEASLLNG
YPEAKVSLPLHLGLTVESDPLNVAHKKIDATASVKLTYSHREAIYFHTHLEQ
PIEQGKLEKLESRELFGSTFVEQOHGTLMSPEACPOLPCANEIEMAVITVEGF
KERLYGKLVPSVOTTYPVHIGEOAKFIPLDEDELEGPRAOELCFYVDPISLH
DSIFGTIAALARKDYSTVYQASEROFVDQYKIPKLKAKDPOCAACRDTOSTLH
IDSLVAELMSYLSLSTIEGPQDSCEVLTNDTWPIFENCETPPDKALAEVMAEQHL
IGAQLPANSVLTLRVAKLPQKNGRDAMNNSFYLQHGGLYSATVYKNGASAFK
GVPSALDSSSYTLQHLAYASFSFPHLAMCYLQPLPHKNTNSQSVNVYVGT
APSQMCDLQCGCPAVICNTLYFRMKDRFPVLYNKRDPYVITGTAGYNDLEILGN
FATFEREEGNEVEDAPKYTYWOLCONITERKASNGISBGDALRILYIDISFVKY
FKGIDSTVAELIKFINCMKNYNNRENKTSYHILQFACNVYMOACPGVELTLYXK
SLTYIQQDICTLSCMAYEODNPAVGIYPSMELMHQTMNTNFKACDFKAGITGSEL
KLTVHSMFCDELDTDAIGMFAPARMOVARIAMALVPTIKIKRNLIFSNTGASL
IQAGFMKPSARDYSIVGGYKMFALMLHTLTPSTKTSALYLMHKIQQTKNPILPG
VSGEHLTELCNRYKASSQAFEEINVLDPDLTYSKIKLNSILRACQOTPFVAT
LSLSPTQLVPAEEXPHVLYGGLSPDEYRAKVAGRSVYIYSTLTKOAKOYFAT
PITTVLVNKKYTGSGNGNTNVEHCANLGYSGSGVDNRNLPESVPRKKNVSMILKR
HTMTPLVDRLYKRYVINGSGFEFAPAKRSYONVLEDNRNPLPTVILELYKHGGS
SCASLTEDGYITLGPYAVLGDVLSLSTLVGAGAPWTAEGVASYIODITIDCELOF
VGEEPCLLIGOSVVELPEPSPSLTVGKKKRIASLSDLL"
6609..8696
/note="ORF 7, processing and transport protein homolog
(ICP18.5)"
/codon_start=1
/protein_id="AAB62620.1"
/db_xref="GI:2246495"
/translation="MAKELAAYADVADYALAMDLCLSYADPATLDTKSLATLTGKFS
LHGTLPLLRONAHCSGLSELEHLEVAALATYAGTSCRSALBEPHESLHLD
TGNKHSRVENFYGMALKEIKSLINDVEIFPKRLSVYGCSSALBAGEVLEFR
VCKLRGISPYRPGDLYVSNPCLECIQECVLTICNOSTSLDAMPTRACSHITCPAGE
PVAGLENELEKQGLQTPESITPTPCQSRRODETRQSLMAVGHHITGEYTRSLV
EISNLIYWSGSHDQATCGDRDCSHLASLETHADMHKRRVLDLAGCLGERTKHEFD
CFRPSDLERTFCGLGFSVSDTIESLQKDSAFYQOVNTYALOKONERYVRLSKL
AAGQLNLKCSFSCSPSEARROLVGGKPREEYLRDAKHRELLOKVARDFGKSLDC
IRHQHILSOTGLRLMGSVYNEASALONHPLHROFISLPMODILORVADGPFRENSK
XIKNSXCORLGRHVEHILTEFYKILITGKLSKRLHLPSPRPVNTLAQCEAAGMLPH
QKMWSEMIWPSITEPKDWIEPNQFSENDINHLQKAWMYIELVLSVLYLPT
WERELKILTPQSGPGEPRKPAGLTGTGLYLPETSAPIVLVDKKYGMIFKDYALLY
HHILSNHNSQY"
8680..11217
/note="ORF 08, glycoprotein B (gB) homolog"
/codon_start=1
/protein_id="AAB62592.1"
/db_xref="GI:2246467"
/translation="MTPRSRLATLGTVILVCFAGANHSRGDTPTQSSSPRPGSSS
KAPTKEEASGKSVDEQFRCVCSATITGELFRPNCAGIACGPTKAKIOHEGILLVYK
KNIVPHIFKVRARYKATATSVYRGLTESITDKKLEPRVPLVITSHMSTGYCCFS
MKYNNVGEVTFTRDDVNTVYFLQYEGCLTDIKQYFESPVITYAERGPGIYRPRRT
TNVCEIVDMIAKSAEYNTFVSLGDTVEVSPCYNESSCTPSYKNGNSLAVVNLH
TVVYSDRGTSPPQNRITVEGAYTLVMSASEKTAACVLAAMKTFPRSIGQTHDS
FHFVANEITATFTAPLTPVANEFTDYSLTSDINTLNASKAKLSTHYVNGIQYFHS
TGGGLVYOMPSAINLTHAOGDSGNTPSPSPASPMNTSARRRRKRSSTAAGG
GSTNDLSTYQLOPAGDKLRDGINOVLIELSRACRQVROVMTSARRRRKRSSTAAGG
IYGRPYSAKFVGDAISVTEJCINDOSSVNIHKSRLNRNSKDVCAARPLATFKELNSSL
FTGQLDARNETILTNNOVETCKDTCHEYFTTRNETLYVKYALALRINTINTDISTLNT
IALNLSFIONIDEKALELYSABKRILASVDFLETFMREVNYYTHRLAGREDLDNTI

CDS

DNKRFRVRLSEIVADLGIGKTVNVNASSVVLTCGLSTVGFINEIKHPGLGMLMI
IVIAILLIFMLSRRTNTIAQAPKMIYDVPDRAPSPGAPRREIKNILLGMHOLQ
QEEROKRADLKSTPSVFTQRTANGRLQRLRGKVPPLQNSDISPETGE"
11344..14382
/note="ORF 09, DNA polymerase homolog"
/codon_start=1
/protein_id="AAB62593.1"
/db_xref="GI:2246468"
/translation="MDPEFNFDPTRGPGPNVTRQPTPSQSPVYPSFTRVCRLLIPACF
QPRGRGVAVADPTPPRYFOGKRGEVAFGEGTSLIKPRGQARNAKPHLLEHYD
IVETTTADRCEDVPPSFQDITLPSGTVLKLRRTLDGASVCNVRQRYFTTLAPQ
GVNLTAVLQDLQAGFRASCSTFSPVRKRTILRAVDQOYAVQKLTLSPPMKRTLS
DLRTTCGEVEFESNVDAIRRFVLDHGFSTFGECSNPARTQARSMLEDECSME
DKFIEPEREMEPYTLISFDIECMGEGFPNATQDDMIIOICVLTHTVNDKPYRM
LIGLGTCDPLPGVEFEPPEPEYMLAFLMADYVNEFTGYNINAFDLPYTIART
QYDPRLOPFTKIKTGSVEPHQPRGSGDGNMRSQSKYKISGIVYIDMYQYCREKL
SLSDYKLDVYAKOCLRQKDDISYKQIPLFKSGPGRKAVGNCTYIDSLVNDLLR
FQTHVEISETAKLAKIPTRRVLDGQOIRFSCLEAAATEGILVPGKDAVSGYQ
ATVSPSGEYDPPVLVDFASLYPSLIQAHNLCSYTLIPGSLHLPILSPDYETF
VLSGCVHFEVKKRKRRESLAKLTLVLAKEIRKTLASTCDPALKTILDQOLAIV
TCNAVYGFVNASGILPCNLIAFTVTLQGRKMLERSQAFVETASPERLAGLRPIDV
SPDARKVIYGDPSLFCICMGNMDSYSPAEIASITNTLFRSPRIKLEAKIKC
LLTLTKRKYGVLSDBKVLKMGVDLIRKTRCRVQEKSSOVLILLIREPSVKAANLI
SGQATWVYREGLPBEGFVKIIQVNLNSHRELCSRSVPVDKLTFTTSLRDLAYKTON
LPLRLYVQKLOARQEBLPQIHDIRIPYFVDAPGSLSELSAEHEEYVYKOHLRVAVDLY
FRLVHAVANIIQCLFQONNTSATVAMLYNLDIPVETFP"
14500..15756
/note="ORF 10, herpesvirus saimiri ORF 10 homolog,
conserved in other gamma-herpesviruses"
/codon_start=1
/protein_id="AAB62594.1"
/db_xref="GI:2246469"
/translation="MQTEAFILGDMETIVSNCRFCSSLTGCGPLVRSSTDYTRLRIP

CDS

Query Match 0.18: Score 29; DB 1: Length 133601;
Best Local Similarity 100.0%; Pred. No. 5; 7e-05;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CDS

Oy 14938 CTGAGTTTGACGTCGACGCTGGAGGACCT 14966
Db 12148 CTGAGTTTGACTGTCGACCTGGAGGACCT 12176

RESULT 30
LOCUS KS075698
DEFINITION Kaposi's sarcoma-associated herpesvirus long unique region, 80
putative ORF's and kaposin gene, complete cds.
ACCESSION U75698.1
VERSION GI:2065526
KEYWORDS

SOURCE Human herpesvirus 8 (Kaposi's sarcoma-associated herpesvirus -
Human herpesvirus 8)
ORGANISM Human herpesvirus 8

REFERENCE 1 (bases 47193 to 47522: 133099 to 133729)
Chang, Y., Cesarman, E., Pessin, M.S., Lee, F., Culpepper, J.,
Knowles, D.M. and Moore, P.S.
Identification of herpesvirus-like DNA sequences in AIDS-associated
Kaposi's sarcoma
Science 266 (5192), 1865-1869 (1994)

REFERENCE

TITLE JOURNAL
AUTHORS Moore, P.S., Gao, S.-J., Dominguez, G., Cesarman, E., Lungu, O.,
Knowles, D.M., Garber, R., Pellet, P.E., McGeoch, D.J. and Chang, Y.
Primary characterization of a herpesvirus agent associated with
Kaposi's sarcoma
J. Virol. 70 (1), 549-558 (1996)

REFERENCE

JOURNAL MEDLINE
PUBMED 96099469
8523568
3 (bases 28661 to 29741; 117919 to 118101)

REFERENCE

JOURNAL MEDLINE
PUBMED 96099469
8523568
3 (bases 28661 to 29741; 117919 to 118101)

AUTHORS	Zhong, W., Wang, H, Herndler, B. and Ganem, D.
TITLE	Restricted expression of Kaposi sarcoma-associated herpesvirus (human herpesvirus 8) genes in Kaposi sarcoma
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 93 (13), 6641-6646 (1996)
MEDLINE	96270595
PUBMED	8692871
REFERENCE	4 (bases 122794 to 123567; 123809 to 127297; 129372 to 130400; 130551 to 134441)
AUTHORS	Cesstman, E., Nador, R.G., Bal, F., Bohenzky, R.A., Russo, J.J., Moore, P.S., Chang, Y. and Knowles, D.M.
TITLE	Kaposi's sarcoma-associated herpesvirus contains G protein-coupled receptor and cyclin D homologs which are expressed in Kaposi's sarcoma and malignant lymphoma
JOURNAL	J Virol. 70 (11), 8218-8223 (1996)
MEDLINE	97048116
PUBMED	8892957
REFERENCE	5 (bases 1 to 137508)
AUTHORS	Moore, P.S., Boshoff, C., Weiss, R.A. and Chang, Y.
TITLE	Molecular mimicry of human cytokine and cytokine response pathway genes by KSHV
JOURNAL	Science 274 (5293), 1739-1744 (1996)
MEDLINE	97094384
PUBMED	8939871
REFERENCE	6 (bases 1 to 137508)
AUTHORS	Russo, J.J., Bohenzky, R.A., Chien, M.-C., Chen, J., Yan, M., Maddalena, D., Parry, J.P., Peruzzi, D., Edelman, I.S., Chang, Y. and Moore, P.S.
TITLE	Nucleotide sequence of the Kaposi sarcoma-associated herpesvirus (HHV8)
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 93 (25), 14862-14867 (1996)
MEDLINE	97121480
PUBMED	8962146
REFERENCE	7 (bases 1 to 137508)
AUTHORS	Russo, J.J., Bohenzky, R.A., Chien, M.-C., Chen, J., Yan, M., Maddalena, D., Parry, J.P., Peruzzi, D., Edelman, I.S., Chang, Y. and Moore, P.S.
TITLE	Direct Submission
JOURNAL	Submitted (17-OCT-1996) Dept of Pathology/Genome Center/Division of Epidemiology, Columbia University, 650 West 168th Street, New York, NY 10032, USA
REFERENCE	8 (bases 1 to 137508)
AUTHORS	Russo, J.J., Bohenzky, R.A., Chien, M.-C., Chen, J., Yan, M., Maddalena, D., Parry, J.P., Peruzzi, D., Edelman, I.S., Chang, Y. and Moore, P.S.
TITLE	Direct Submission
JOURNAL	Submitted (02-MAY-1997) Dept of Pathology/Genome Center/Division of Epidemiology, Columbia University, 650 West 168th Street, New York, NY 10032, USA
REMARK	Sequence update by submitter
COMMENT	On May 3, 1997 this sequence version replaced gi:1718251.
FEATURES	location/Qualifiers
source	1. .137508
	/organism="Human herpesvirus 8"
	/mol_type="genomic DNA"
	/db_xref="taxon:37296"
	/cell_line="BC-1; virally infected primary efusion lymphoma derived cell line"
	/note="sequence derived from overlapping lambda phage and cosmid clones isolated from libraries; A prototype sequence for the terminal repeat (TR) unit is deposited under GenBank Accession Number U75699. The left junction variant TR sequence unit immediately preceding base pair 1 of the LTR is deposited under GenBank Accession Number U75700. The remaining LTR sequence extending from this sequence to the right TR unit is not available due to difficulties in cloning and sequencing of this region"
	1. .137508
	/note="Long unique region LUR"
	105. .974
CDS	/note="ORF K1"
	/codon_start=1
	/protein_id="AAC57081.1"
	/db_xref="GI:1718252"
	/translation="MFLVNCVSLACFEGSLISLSSPNLCPCVITSPYTLICLNASLPISWICNNITLRLKERRVLDITACNLTFCVCSGSHKOSTITATTAAGVYLTCLCAQPSMTYVCGQHVLTLCYSTGNNVTWHLNPGNENRVSQRTKINFTLMSQTEGCTCSNGLSRLSNRICEFARCANITPEETHTVSGVSTGEPFRLTSLNSLVKLIHATTDVAVVAKAKSTHFIEVHFPLVEFMTVALVIGTMCGILGTIIIFAHCGKQRDSNKTVPQQLDYYSLHDLCDEYTDVDMY"
	1142. 2794
	/note="ORF 4; The HVS ORF 4 homolog has alternatively spliced messages encoding membrane bound and secreted proteins; complement binding protein VCBP homolog"
	/codon_start=1
	/protein_id="AAC57082.1"
	/db_xref="GI:1718253"
	/translation="MAFLQTLWLTMTTYVIGQDNKSCSKTLCGRILKMSRGDIAVEVEYELRCRSGVTTTARNTATLCLGGTWSSEPATCNKSKCPNPGIQLNGKVIPIHGGQALXKANIISVYCNMEGFVLGREVYRCMIGAGOMASSPPCEKCHREKIKNGPEKPDQYEVYNDVAFHECNEGTYTLVGPHSIACAVNMTSNMPTCEKCEKPSVTHCYPIQGFSLTYKHKOSVFPACNDEGFVRSPTLTCTVEMDPLLPKCYLEDIDPNKNSMGRHLHPNPKNGVNFQNSNTPEPTPEPTHTACOTDPTNCEOPKLTISLSEGNERTTSYITIKOLEDKTISQPTHTITSLTSMKAKGNFTKNTKNSDILHASTPTSDQDAPPSIPSVQTPNVTNMAPRTLTSLHIEEPPSNSTSEATSSSHNSHKNDGTGIYTLTKNTQLPSTNKPITNSOAKSSKTPVEHTNNTSIPALSTLSDASVQBPQREPTLPPIFRPASKNRYLEKQVIGLTFAVALTCGLITLFIHYEER"
	3210. 6611
	/note="ORF 6; ss DNA binding protein ssBP homolog; EBV BALF4 homolog"
	/codon_start=1
	/protein_id="AAC57083.1"
	/db_xref="GI:1718254"
	/translation="MAIKGPTLTENIGSAPTPGCGIYAYLTNHPFGEASILNGNGYBEAVYSFPLRHGTVESDPLNKAHKKIDMTASTYKLTSTHRAIYFHTNHLPOPIFGKGLERKLCRESRELFGSTFVEQDHKTLSPEACPOLPACNITMAVLTBESKRLYGGKLVLPVPSQTPTHVHGEHOAFETPLVDHLCSPQAQELCFNPDIDSRVLIHDSIFLTIQALVKNVSVTVIAEGHQAEPFHDDYKIPKLVQAEPQCSKRTDGSITVLIISVALFELGMSYGLSFIENGPODCEVLVDWYMFENCPEDARLAEVHWAQALHICAOLEFANSVLYLTVKAKLPQKNORGNAMNYSFYLQHGIGYSEATVGENASARKGYPSVALDSSSTTIOHLAYASFSFPHILARCYTLOTLPHKNTNSQSYVNDYVCGTAAPSQMDLCQGGCPAVCTINTLETRKDNFPEVLSNVKRDPIVTGTAGTINDLEILGNFATPFRREBEGNPVDARKYTWOLCONITKELASMGISEGDALRLIYDISEFYKVFQIDISTVEAELEIKINCMIRKNYFNFRNINSHVHILIOFACNYWQAPCFILTYLKSLVEYIDICELSCMYEODNDPANGIVSEWLNKHPMTNPNFGCAFQDAGTGLKIVHOSMPCDLEDDNALIGMPAPAROMVRIARAMLVAPRTIKKNTIFSNISGAEISIOAGTRKPRASQDSITVIGPTRYKPLNALHKLTPSTYSALILNKHIGQTTKNPILPGVSGEHLTELCTNIVKASQAFEBINVLDPVLTISYAKIKUNSLILACQGTQPIATYLSGLSPVQOLVPAEYPRVLGVPVLSDEYRAAVARSVITVQSTLKQAVSTNGRLRPITTYPLVNNKTYTGNGNTNVFHCANLIGFSGRVDNRLREESYFEPKNNVSSMLKRRHYIMPIVLDVRLKTVIYVINGSEFEAKVYVQWLEDRDNLNPKVYLEIVKPPWSSCASITSEEDVYVYIGPVAIVGADDEVLTSLTSTVGQAGVPMTAEGVASTYIQDIIDDCELQEVGPEEPCILCQGSVEELFSPSGVPSLTVYKRRKIASLSDDL"
	6628. 8715
	/note="ORF 7; transport protein homolog; EBV BALF3 homolog"
	/codon_start=1
	/protein_id="AAC57084.1"
	/db_xref="GI:1718255"
	/translation="MAKELAAVYADVSLAMDLCCLSYADPATLDTKLSLTLTGKQOSLHGTLPLPLRQNAHECSGLSLELHEHFKMTLMPMEWALENCLOKISIPSCITWQATNSRVSRYFNGMALLEKLILINDVLEFFRSLFVYGLSGSSGAGLIFSCVTVKLGKISIPPEPLDYVNLPCLECDLQCLTPNQGSLQAMIDPTKISCTIPACGEVPGGLFENETKIQGLQTPRESIPTPGCSRVNODETROSSIMVGDHITGEYTRVLEISNLIYVSSGHSDDTCGGDCHSLASLFTHEADHKRRYDLAAGCIGEGTQKHFEDCRRPSLLELFCGGGLFSSSEVQNTISLQDCSAVYQVNTTALQOKNEFYVLSKLLAAGQNLNKCSTFSCQSEARQOLGGKPEEVLADAHRELYLOKVARQGFKLISQCIKHQHILISQRTGLQELMSQVLYFVNASALONIFILRAQFISLPMDDLVDCDPTFEENSKYIKNSLYCQIRGREHVELITLVEFKLTQNGTSKRHTLPSPPNVTLAOCGEAAGMLPHQKAMYSSEMIWPSIEPKMDIETFNQFVSFENQDINHLQKRAHEVIRELVSVSLYKNTWHERELKILLTPDQSGPGEFEKPRAGLTTLGTLTFTTSAPLVAVDKKGTGWIKRDLYALDYHHLQLSNNDSQV"
	8699. 11236
	/note="ORF 8; glycoprotein B gb homolog; EBV BALF4 homolog"
	/codon_start=1
	/protein_id="AAC57085.1"

```

/translation="MFLVYVSLAVCFRRLSLSLSSPLKCGSVTPVTLTCLNSA
SLPSWICYNNLRLIKERVVLIDTITPCRYCSGHROSITWTRADVLOTCLGQ
PSNTVYQOHVLYLCYSTSNNVTVMHLPNGRETVSYQTYNFTLMSQEGCTCSNG
LSSTRSLNCEFWARNLIPETHTVYSSTITGRLTOSTSLVNLIHATRDVYVVEA
KSTHRIEHLVAFMFLVLTITMCGISLTITIFAGHOKORDSKRTVPOOLQDYSYLD
LCTEYDPOVDVWY"
1142..2794
/note="ORF 4: The HVS ORF 4 homolog has alternatively
spliced messages encoding membrane bound and secreted
proteins; complement binding protein vCBP homolog"
/codon_start=1
/db_xref="GI:1718253"
/translation="MAFLQITWILMTFTWVIGODNEKSOQLTIGRLMSRDGGA
VGEVTELCRSQSYTTPVNRNTVATCLOGTWSSEPTAVCNKSCSNPEELONGKVIPIHGG
ODALYKGNITSYVNEGVEGFLVAREYRYCISAGQMASSSPPECEKCHRPKIKN
GDFKQKRYEYENDVAHFGNCGNLTLYGSHISAGANMNTSMPTCELAGCFPSVT
HGYPIQGSLSITLKHKHSYFAKNDGVLVLEGSPTITCNEMDPEKCPVEDIDDPNN
SNRGLAPLNPKNRKPNQSRNNTPEPTPKPDTTHAICDNPCEKCPKLTPESEPN
ETTSNTITKOLEDETISOPTNITSLTSMKAGNFTNKTNSDHLIASTPTSD
DAPSIPTSQVQPNVMTAPRTLTSLHIEGKSNSTSKASTSLSSHNSKMDGTGI
YTTLLKTKTLOPSTNPKPTNSQAASRTKPRVETPTKLTISNAISLTDSADVPQREPLE
PIFPRPASKNRYLEKQVILGTLTALVCLGTLTFHYFFR"
3210..6611
/note="ORF 6: ss DNA binding protein ssDBP homolog; EBV
BALF2 homolog"
/codon_start=1
/protein_id="AAC57083.1"
/db_xref="GI:1718254"
/translation="MAKRODPLEENIGSAPPCGCVLYATVIRPIGEASLILGQ
VPEAKVSLPIHLGLVEDBPFLNKANHKIKDATATSVKITSYHEALFVHTMTLFO
PIFQKRGELKRESRELGEFTVEQOKGTLMSPEACQDLCEANETMAVIVTBEF
KERLQGLKVPVSSQTPTHVIEHQAFLPYDEDLFGSRABOELCFNPNDISRYLH
DISFGLIKQALVKNQVSTVIGASERQFHYDQKIPFLYAKQEPQCARFYNPDISTVYH
IDSLIAEANSVLSGSLSEIPEOSQCEVLANTDMPFENCSTPDMLRLAEWMAEOALH
IGAOFLVANSVLYLRAVKLPOKNOGDAMNTNPFLOGLGLTSLATYANESAAFK
GVYSALDGSSTTIDHLAASSFPHLLARMCYILOFLPHKKTNSQSYVNDYVGTGA
APSSQDLOQGGQCAVCTVITLYLRMKNDRPVALSNVKNRQPVITGTAGTYNDLELGN
FATPEREENEGNVDAPKVTWYLOLQNTREKLASNGISEGDAITLIVDIPSELYKX
FKGDISYVEALELTKINCIMKNNYNERENIKSVNHLQFCAVYMOAPCFVETLYGK
SLVAYDIOELTSCMAYBEDNPVAGVPESELMKHMPOTWNTNKGCAFDGALITGGL
KIVGSMCDLDDTDPAIGMPARMAVORIARAMIMVKTIKIRILFNSNTEGAS
IOAGMKRASPQSDITVGGPYKFLNALAKLTLPSTRTSALYIMNHIGOTQPTPILG
VSGHEMLTELCTNVKASSQAFBEINVLVDLPULTSTAKITLNSILRACQOTPIVAT
LPIYPLVQLVPAEYEPHYLGVGLSSPDEYRAKAVAGSVTVYQSLTKQAVSNGRLR
PLITPLVPLQVLTGSGNGNTNHCANLGFESRGVDNRNLPESEVPKKNVSSMLRR
HYIMPLVDLRAKTVIYGLISGEEAAVYRSVONTVLEEDNDNPLPKTVYLEIKPPM
SSCALITEDVEDYVITGVAVAGDEVLTSLISTYSGQGVPMTPBEVAVIQIDIDCELO
FVGPERPOLIGQSYVEELFSPGYSLTVGKKRKIASLSLDL"
6628..8715
/note="ORF 7: transport protein homolog; EBV BALF3
homolog"
/codon_start=1
/protein_id="AAC57084.1"
/db_xref="GI:1718255"
/translation="MAKELAAVYADVSAALAMDCLSLVADPATLDTKSLALTGKQOS
LHGTSLPLLRONAHGCSGLSLSEHFWMTLMLPRMCAALAELOLSGSEPCVLT
OHATNSRNVSRVYENMNALELISLINDVEITFFKRLSYVIGSSALAEQISFECWT
VGRKILSIEVPEDLPVLSLPCLEQCEVCLPNQSTLOAMVPDACHISGIPACAGE
PVKGLFEMELKQIGLYTNSLPTTECCOEVCLPNQSTLOAMVPDACHISGIPACAGE
EISNLTIVSSGHSDDTCGDRDCSHLASLFTEDBAMHKRRVLDAGTGLERGTPKHFDD
CFERPDLSLTFEGGLFSEVEDTIESIQKSSAFAQVANYTALQKONEYVYKSLDC
AAGQNLKCTGSCSESESRARLSDVGGKEEVLRAKHQEYLTLQKAVADGFKSLSDC
IRKHSHLISOTGLREGLVLSITVNEASALONHFLHRAOFLSLPMODLTVOPTFEENS
YIYKHOITLQSGREHVELLITFEYKILNSPLSKRHLTPSPNVTALQCFEAGMLPH
OKMAYSEMIWPSIERKDMIEPWFNOFSPENDINHLQKRAEYIRELVLSVLYNPT
WERELSLTIDGSGSESEKPKAGLITGLTYLTFEYSAPLVLDVKTKGWLFKDLYALY
HRLQSLNNDSQV"
8699..11236
/note="ORF 8: glycoprotein B gb homolog; EBV BALF4
homolog"
/codon_start=1
/protein_id="AAC57085.1"

```

```

/db_xref="GI:1718256"
/translation="MTPRSRLATLGVILVCFACAGAAHSGDPTFOTSSSPPTGSSS
KAPTKPEEASGPKSVDFQFVCSATISGELREFNLEQCPDTRKDYOEGLLYK
KNVPHIFVRYRRKATATSVYRGLTESAITKYLPRVPLVETISHMDTQCFS
MKVNVGVENTFTDRDDVNTYVFLQVEGLTDNIQTFSPVYIAERGPFGITRRRT
TVNCELVDMTARSAPRYNFVSLGDTVEVSPCYNESSCTTPSKNGLSVOVLNH
TVVYSDRGTSPQNRIFETGAYTLNMASESKTTAVCPALMKTFFPRIGIOTHDS
FHVANEITATFAPLTPVANFTDYCLSDINTNLNASKAKLASTHYVNGVQYFH
TGGLLVNOMPMAIULTHAQSGDNPTSSPPASBMTSASRRKRSSTAAGG
GSDNLSTYQLOFAVDKLRDGINOVLELSRAMCREOVNDMLMVELSKINPTSWTA
IKGRVSAKRVGAISVTECINDQSSVINHKSRLTRNSKDVCAAPLVTRFKFLNSSNL
FTQGLAREEILITNNVEFCQDCEHFTTRNETLVYKQVALRTINTDITNTE
IALNLSFIONIDKAELEYSSAKELASSVDETFMERENYTHRAGLRDELDNTI
DMKREFVDSIEVADLGIGIKTVNVASSVYLCGLSVTGFINKHGLGMLMI
IYVAILITFMSLRNTTAQAPVKMIYPPVDRAPSGGAPRREIKNTLLGMHQLO
OPEKRAADLKSTPSVFORLANGLRGRGKPLVQSDISPETGE"
11363..14401
/note="orf 9; DNA polymerase homolog; EBV BALF5 homolog"
/codon_start=1
/protein_id="AAC57086.1"
/db_xref="GI:1718257"
/translation="MDFNPTDPTRGPRNTVROPSPQSPVSEPTRYCLIPAC
QTPGRGVAVADTPPTPTQCPKRCSEVFAGETGIMKTRRGARNAHNSHLFHYD
IVETTYADRCEDVPFSQTDIIPSGTVAKLLGRTLDGASVCVNVRRQCYFTLAPQ
GVNLTHVLQALQAGFGRASCFSTEPVRKRLRAYDIOQYAVOKITLLSSPMKRTL
DRLTGCGEVEFSNVDAIRFRVLDHGFSTFGWYECSPAPARTQARDSWTELEFDCSWE

```

Query Match 0.1%; Score 29; DB 1; Length 137508;
 Best Local Similarity 100.0%; Pred. No. 5.7e-05;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14938 CTGAGTTGACTGACGCTGGAGACCT 14966
 Db 12167 CTGAGTTTACGCTGAGGAGACCT 12195

RESULT 31
 AF031808 480 bp DNA linear VRL 27-Apr-1998
 LOCUS Bovine lymphotropic herpesvirus DNA dependent DNA polymerase (Pol)
 DEFINITION gene, partial cds.
 ACCESSION AF031808
 VERSION AF031808.1 GI:2832250
 KEYWORDS .
 SOURCE Bovine lymphotropic herpesvirus
 ORGANISM Bovine lymphotropic herpesvirus
 viruses; dsDNA viruses, no RNA stage; Herpesviridae; unclassified
 Herpesviridae.
 REFERENCE 1 (bases 1 to 480)
 AUTHORS Rovnak,J., Quackenbush,S.L., Reyes,R.A., Baines,J.D., Parrish,C.R.
 and Casey,J.W.
 TITLE Detection of a novel bovine lymphotropic herpesvirus
 JOURNAL J Virol. 72 (5), 4237-4242 (1998)
 MEDLINE 98216791
 PUBMED 9557713
 REFERENCE 2 (bases 1 to 480)
 AUTHORS Rovnak,J., Quackenbush,S.L. and Casey,J.W.
 JOURNAL Unpublished (1998)
 REFERENCE 3 (bases 1 to 480)
 AUTHORS Rovnak,J., Quackenbush,S.L. and Casey,J.W.
 TITLE Direct Submission
 JOURNAL Submitted (29-OCT-1997) Microbiology and Immunology, College of
 Veterinary Medicine, Cornell Univ., Ithaca, NY 14853
 REFERENCE 4 (bases 1 to 480)
 AUTHORS Rovnak,J., Quackenbush,S.L. and Casey,J.W.
 TITLE Direct Submission
 JOURNAL Submitted (04-FEB-1998) Microbiology and Immunology, College of
 Veterinary Medicine, Cornell Univ., Ithaca, NY 14853
 REMARK Sequence update by submitter
 COMMENT On Feb 5, 1998 this sequence version replaced gi:2660730.
 FEATURES
 source
 1..480
 /organism="Bovine lymphotropic herpesvirus"

```

/mol_type="genomic DNA"
/db_xref="taxon:69955"
<1..>480
/gene="Pol"
<1..>480
/gene="Pol"
/codon_start=1
/product="DNA dependent DNA polymerase"
/protein_id="AAC59451.1"
/db_xref="GI:2832251"
/translation="STIQAHNLCYSTMIENDQLSRPELKADYERFVYSSGPVHYK
KHHTESLASLTLAWLAKRAIKRELATCODSKLTLLDQOLAIVTCAVYGFVGV
ASGLPLCKIAETVTLQGRMTLERTHYVESLQPVLEICORPIAVAEGRADPSLRV
"

```

BASE COUNT 134 a 123 c 118 g 105 t
 ORIGIN

Query Match 0.1%; Score 27; DB 1; Length 480;
 Best Local Similarity 100.0%; Pred. No. 0.00044;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15919 CACAACCTGCTACTCCACCATGATA 15945
 Db 16 CACAACCTGCTACTCCACCATGATA 42

RESULT 32
 AF327830 1295 bp DNA linear VRL 03-Apr-2001
 LOCUS Bovine lymphotropic herpesvirus DNA polymerase (Dpol) gene, partial
 DEFINITION cds.
 ACCESSION AF327830
 VERSION AF327830.1 GI:13517547
 KEYWORDS .
 SOURCE Bovine lymphotropic herpesvirus
 ORGANISM Bovine lymphotropic herpesvirus
 viruses; dsDNA viruses, no RNA stage; Herpesviridae; unclassified
 Herpesviridae.
 REFERENCE 1 (bases 1 to 1295)
 AUTHORS Chmielewicz,B., Goltz,M. and Ehlers,B.
 TITLE Detection and multigenic characterization of a novel
 gammaherpesvirus in goats
 JOURNAL Virus Res. 75 (1), 87-94 (2001)
 MEDLINE 21212029
 PUBMED 11311431
 REFERENCE 2 (bases 1 to 1295)
 AUTHORS Chmielewicz,B., Goltz,M. and Ehlers,B.
 TITLE Direct Submission
 JOURNAL Submitted (12-DEC-2000) P24 Xenotransplantation, Robert
 Koch-Institut, Nordufer 20, Berlin, 13353, Germany
 FEATURES
 source
 1..1295
 /organism="Bovine lymphotropic herpesvirus"
 /mol_type="genomic DNA"
 /db_xref="taxon:69955"
 /note="isolated from infected peripheral blood
 lymphocytes"
 <1..>1295
 /gene="Dpol"
 <1..>1295
 /gene="Dpol"
 /codon_start=3
 /product="DNA polymerase"
 /protein_id="AAK28843.1"
 /db_xref="GI:13517548"
 /translation="YVYNIKPSYTRKSTIRAVHKPRDGNFRSHTKKLAGYIV
 DMVLYCKEKLNLNSKNTVAKECTGKRDVYKEIPVLEKGTADRAHGLCYVD
 SVAVIDLKHFMTHVEISEIAKIANIPTFRVYDGOIIVFSCLLAAKRNRYLPLP
 SAGNTDQOGATYINPLSGFYNTPLVDFASLYPSSTIOAHNLCYSTMIENDQLSRP
 EIKKADYERFVYSSGPVHYKHTESLASLTLAWLAKRAIKRELATCODSKIKTI
 LDKOOLAIKTCAVYGFVYASGLPLCKIAETVTLQGRMTLERTHYVESIQPVLE
 ERICORPIAVAEGRADPSLRVYGDQDLSLFINCIGDIEVLAFGDOLAEHTSNLNF
 KPIKLESEKVKCLLLTKRRYLGILSNKIKMKGVLV"

BASE COUNT 371 a 310 c 302 g 312 t
ORIGIN
Query Match 0.1%; Score 27; DB 1; Length 1295;
Best Local Similarity 100.0%; Pred. No. 0.00049;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 15919 CACAACTGTGTACTCCACCATGATA 15945
|||||
DB 603 CACAACCTGTGTACTCCACCATGATA 629
RESULT 33
LOCUS AF005478 475 bp DNA linear VRL 26-JUN-2000
DEFINITION Retroperitoneal fibromatosis-associated herpesvirus DNA polymerase
ACCESSION AF005478
VERSION AF005478.1 GI:2245592
KEYWORDS
SOURCE Retroperitoneal fibromatosis-associated herpesvirus
ORGANISM Retroperitoneal fibromatosis-associated herpesvirus
REFERENCE 1 (bases 1 to 475)
AUTHORS Rose,T.M., Strand,K.B., Schultz,E.R., Schaefer,G., Rankin,G.W. Jr.,
Thouless,M.E., Tsai,C.C., and Bosch,M.L.
TITLE Identification of two homologs of the Kaposi's sarcoma-associated
herpesvirus (human herpesvirus 8) in retroperitoneal fibromatosis
of different macaque species
JOURNAL J. Virol. 71 (5), 4138-4144 (1997)
MEDLINE 97248469
PUBMED 9094697
REFERENCE 2 (bases 1 to 475)
AUTHORS Rose,T.M. and Strand,K.B.
TITLE Direct Submission
JOURNAL Submitted (28-MAY-1997) Pathobiology, University of Washington, Box
357238, Seattle, WA 98195, USA
FEATURES
source
1. 475
/organism="Retroperitoneal fibromatosis-associated
herpesvirus"
/mol_type="genomic DNA"
/isolate="Mme78114"
/specific_host="Macaca nemestrina"
/db_xref="taxon:111469"
/note="Isolated from a retroperitoneal fibromatosis lesion
of a Macaca nemestrina"
<1..>475
/gene="pol"
<1..>475
/gene="pol"
/codon_start=2
/product="DNA polymerase"
/protein_id="AAC57975.1"
/db_xref="GI:2245593"
/translation="SIMOAHNLCSYLTITGSLHGHPELPDDYETPHLSGCTVAFVK
KHVESLTKLLTWLAKEIKRLNLSCTDPTMTITDKQALIKVCNMYGFTG
ASGILPCINIEYETVLOGRKMLTFOAFVEGISTPALDLORPIEASPEARFYI"
BASE COUNT 129 a 145 c 120 g 81 t
ORIGIN
Query Match 0.1%; Score 26; DB 1; Length 475;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 16150 GATAAACACAGCTGGCATCAAGT 16175
|||||
DB 248 GATAAACACAGCTGGCATCAAGT 273
RESULT 34
AF204166

LOCUS AF204166 3554 bp DNA linear VRL 04-JUL-2000
DEFINITION Retroperitoneal fibromatosis-associated herpesvirus glycoprotein B
gene, partial cds; DNA polymerase gene, complete cds; and ORF
10-like protein gene, partial cds.
ACCESSION AF204166
VERSION AF204166.1 GI:8925891
KEYWORDS
SOURCE Retroperitoneal fibromatosis-associated herpesvirus
ORGANISM Retroperitoneal fibromatosis-associated herpesvirus
REFERENCE 1 (bases 1 to 3554)
AUTHORS Schultz,E.R., Rankin,G.W. Jr., Blanc,M.P., Raden,B.W., Tsai,C.C.
and Rose,T.M.
TITLE Characterization of two divergent lineages of macaque
herpesviruses related to Kaposi's sarcoma-associated herpesvirus
J. Virol. 74 (10), 4919-4928 (2000)
MEDLINE 20240083
PUBMED 10775636
REFERENCE 2 (bases 1 to 3554)
AUTHORS Rose,T.M.
TITLE Direct Submission
JOURNAL Submitted (12-NOV-1999) Pathobiology, School of Public Health and
Community Medicine, University of Washington, Seattle, WA 98195,
USA
FEATURES
source
1. 3554
/organism="Retroperitoneal fibromatosis-associated
herpesvirus"
/mol_type="genomic DNA"
/isolate="Mme442N"
/specific_host="Macaca nemestrina"
/db_xref="taxon:111469"
<1..334
/codon_start=2
/product="glycoprotein B"
/protein_id="AAF81661.1"
/db_xref="GI:8925892"
/translation="MIVIVGIVILIEMLNRTNMAQAPYKMIYPEIDRHGGGTT
VDKDEIKRILGLMHQHOEROKERKRETPSMFORANEIRORIRKQYKPLROOETE
LEAEASV"
373..3414
/note="Similar to Kaposi's sarcoma-associated herpesvirus
ORF 9"
/codon_start=1
/product="DNA polymerase"
/protein_id="AAF81662.1"
/db_xref="GI:8925893"
/translation="MDPFPFLDRTHRNPRANARAPSPNPANPALQICRLIPAC
REGLPGVVPDTPPPYRPGPRGDIYKBRASMTTRASGVPTGEPAPVPHY
YDIVETTYAERGSDVPRFOTDIIIPSGVILKLGRTVDGTSVCVNFROKCYTTRA
PPGVNLHVLQOOSLQSTVGRAPCAFTTELVKKILRYVDIEEYEVRYVILSSPMMA
LSDRLTACGCEVESNDALRRFVLDROGTFYFGWACARARQADAMWLEFDCS
WEDLELRDLHTMPRYRLISFDICMGEEGPRATRGDVLITQSCFHGDEAPYT
RMELSLGTGDPLEMTIEFPEPEXDMGLAFTMTLDVDVIDTYNLANPDLPIITR
ATQYNDPLKNTYKIKGSMFEVNEPAGSGGFRSSQKVISSIVPIDMYQVRDL
SLSDYKLDITVAKHCLSKQKDDISTRDIPPRPSAGAGAKIGRCVDSVLMDLKRA
FQTHVEIAEIKRILRIPARVLTGGOQIRVPSCLAEASRGVILPVPNGTGGYGG
ATVISPJEGFYDDVLVWFASLPSIMQANILSYLTITGSLHGHPELPDDYETP
HLSCGVHVKKHYRESLSKLLFTTWLAKEIKRLNLSCTDPTMTITDKQALIKVCN
TCNAVGTGVAAGSILPCINIAETVTLQGRKMLTFOAFVEGISTPALDLORPIE
SPERFVITGDDTSLFVCCVGSNESYSPADDLAITTYTLKPAIKIAEAFIQC
LLLTAKRYGVGLTDEVLNMGVDLIRKTAQCFVQETSRLELLLRDPVAKAAKLI
SHQPADWYREGIPGGLVKIITLHNSRRLEHGDVVEKLTFTTELGPRACEYKTN
LPHLSVYRKQLROEELPOLHDIRIPYFIRAPGMLKSDLAHEPPEYVARHGLQVAVDLY
FKAVHGANTLQCLFHNDAATVAAALYNFLDPPRMPFSR"
3528..>3554
/note="Similar to Kaposi's sarcoma-associated herpesvirus
ORF 10"
/codon_start=1
/product="ORF 10-like protein"
/protein_id="AAF81663.1"
/db_xref="GI:8925894"

BASE COUNT 865 a 1078 c 935 g 676 t
ORIGIN

Query Match 0.1%; Score 26; DB 1; Length 3554;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 16150 GATTAACACAGCGGCGCATCAGCT 16175
Db 2392 GATTAACACAGCGTGGCATCAGCT 2417

RESULT 35
AF250880 475 bp DNA linear VRL 12-OCT-2000
LOCUS Pan troglodytes rhadinovirus 1a isolate Pancandja DNA polymerase
DEFINITION (pol) gene, partial cds.
ACCESSION AF250880
VERSION AF250880.1 GI:10798913
KEYWORDS
SOURCE Pan troglodytes rhadinovirus 1a
ORGANISM Pan troglodytes rhadinovirus 1a
Virus; dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Rhadinovirus.
REFERENCE 1 (bases 1 to 475)
AUTHORS Lacoste, Y., Maucelere, P., Dubreuil, G., Lewis, J.,
Georges-Courbot, M.C. and Gessain, A.
TITLE KSHV-like herpesviruses in chimps and gorillas
JOURNAL Nature 407 (6801), 151-152 (2000)
MEDLINE 20454683
PUBMED 11001045
REFERENCE 2 (bases 1 to 475)
AUTHORS Lacoste, Y., Dubreuil, G., Maucelere, P., Lewis, J.,
Georges-Courbot, M.C. and Gessain, A.
TITLE Direct Submission
JOURNAL Submitted (30-MAR-2000) Unité d'Oncologie Virale-Département du
SIDA et des Retrovirus, Institut Pasteur, 28, rue du Dr. Roux,
Paris cedex 15 75724, France
FEATURES
source location/Qualifiers
1..475
/organism="Pan troglodytes rhadinovirus 1a"
/mol_type="genomic DNA"
/isolate="Pancandja"
/specific_host="Pan troglodytes troglodytes"
/db_xref="taxon:138896"
/country="Cameroon"
/note="PanrhV1a"
gene
/gene="pol"
/gene="pol"
/codon_start=2
/product="DNA polymerase"
/protein_id="AAG3140.1"
/db_xref="GI:10798914"
translation="SITQAHNLICSTLIPGDSLHLPHLSPPDYETFLISGPVHFVK
KHKRESLRLTLTWLAKREIKRTLASCDPTKTLDQQLAIKYTCNAVYGFYV
ASGLPLNLAEYTLQGRKMLRSQAFVEAISPRLVGLRKFINVSTDRFVY"
BASE COUNT 130 a 143 c 107 g 95 t
ORIGIN

Query Match 0.1%; Score 23; DB 1; Length 475;
Best Local Similarity 100.0%; Pred. No. 0.099;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 15904 AGCATCATCCAGCGCACACACT 15926
Db 2 AGCATCATCCAGCGCACACACT 24

RESULT 36
AF327831

LOCUS AF327831 1297 bp DNA linear VRL 03-APR-2001
DEFINITION Ovine herpesvirus 2 DNA polymerase (DPOU) gene, partial cds.
ACCESSION AF327831
VERSION AF327831.1 GI:13517549
KEYWORDS
SOURCE Ovine herpesvirus 2
ORGANISM Ovine herpesvirus 2
Virus; dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae.
REFERENCE 1 (bases 1 to 1297)
AUTHORS Chmielewicz, B., Goltz, M. and Ehlers, B.
TITLE Detection and multigenic characterization of a novel
JOURNAL gammaherpesvirus in goats
MEDLINE 21212029
PUBMED 11311431
REFERENCE 2 (bases 1 to 1297)
AUTHORS Chmielewicz, B., Goltz, M. and Ehlers, B.
TITLE Direct Submission
JOURNAL Submitted (12-DEC-2000) P24 Xenotransplantation, Robert
Koch-Institut, Nordufer 20, Berlin, 13353, Germany
FEATURES
source location/Qualifiers
1..1297
/organism="Ovine herpesvirus 2"
/mol_type="genomic DNA"
/db_xref="taxon:10398"
/note="isolated from infected organ material"
gene
/gene="DPOU"
/gene="DPOU"
/gene="DPOU"
/codon_start=2
/product="DNA polymerase"
/protein_id="AAK28844.1"
/db_xref="GI:13517550"
translation="SRVQLKPEEYSKRTNSLFYVYKPGEGNFRAHSHKYLSCVVI
DWHICREKLSISNYKNTVAKECMGAKNDVYKDPILFRGSSHRKAGLYCVD
AVLVNLQHMTHIEITELAKINIPPRVITDGOQIRVACLLAAOEGYLLPMP
TAGATSGYOGATVINPISGFYNPVLVDFASLIPSIIOAHNLICSTLIPENSNP
DTPNDDETFEPISSGPVHFVKHKSLSLAKTWAKRAIKRECCODELTAI
LDKQDLAIKTCNSVYGFYVYASMLCMLIAETVTLQGRMLEKTKQFVENDVQSL
QOICPTQTLKIHACHPPTFVYVGDPSLFINCEGDMQVLEFSORLASHSTSLF
SAPRIKSEYFQCLLLTKRVYGLISNNKILMKGVLY"
BASE COUNT 337 a 372 c 314 g 274 t
ORIGIN

Query Match 0.1%; Score 23; DB 1; Length 1297;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 15919 CACAACCTGCTACTCCACCAT 15941
Db 602 CACAACCTGCTACTCCACCAT 624

RESULT 37
AF275657 1339 bp DNA linear VRL 01-JAN-2002
LOCUS Badger herpesvirus DNA polymerase gene, partial cds.
DEFINITION Badger herpesvirus DNA polymerase gene, partial cds.
ACCESSION AF275657
VERSION AF275657.1 GI:18027277
KEYWORDS
SOURCE Badger herpesvirus
ORGANISM Badger herpesvirus
Virus; dsDNA viruses, no RNA stage; Herpesviridae; unclassified
Herpesviridae.
REFERENCE 1 (bases 1 to 1339)
AUTHORS King, D.P. and Banks, M.
TITLE Characterization of a herpesvirus isolated from the Eurasian badger
JOURNAL (Meles meles)
REFERENCE Unpublished
2 (bases 1 to 1339)
AUTHORS King, D.P. and Banks, M.

TITLE Direct Submission
JOURNAL Submitted (05-JUN-2000) Virology, Veterinary Laboratories Agency,
Woodham Lane, Addlestone, Surrey KT15 3NB, UK
FEATURES
source
/organism="Badger herpesvirus"
/vion
/mol_type="genomic DNA"
/specific_host="Eurasian badger (Meles meles)"
/db_xref="taxon:132610"
/note="Isolated from badger lung"
<1..>1339
CDS
/codon_start=2
/product="DNA polymerase"
/protein_id="AAL55728.1"
/db_xref="GI:18027278"
/translation="LGENGFNATRDDEMILOISVLMKGTGENTPRKLLFNIGTCDP
IPDTEVECEPSEIDMLYLFTMLRDNIETIGYNIANDPFIITIDRAOVNPNFKD
FTRINSSMEFVHTPONSAGFMAVSKIKISGFCIDMYNCKEKLISNKNLMTVA
KOCISGOKEDVSKDIPHLFRGPRGAKLGYCYKDSIYVLOLRFETHTIESEA
KIAKIPTRRVLTGQOIRVSCLLVADQNYILPQKDGSDGYOGAVIDIPGFY
NPIIVVFPASLYPTIQAANNLCYSMTAPHEKLIHYNISPHDYQTFNLSGPFHVKK
HKVOSLALTLDAWLSKRAIKTKTQSVDPMLRILDKQOLAIVTCNAVYGFVGS
SGILPCKIAETITTEGRMRLEKSNFENITPVELERLIHKPINCAVDANRV"

BASE COUNT 441 a 242 c 259 g 397 t

ORIGIN

Query Match 0.1%; Score 23; DB 1; Length 1339;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16162 CTGGCCATCAGTCGACATGTAA 16184
AAAAAAAAAAAAAAAAAAAAAAAAA
Db 1127 CTGGCCATCAGTCGACATGTAA 1149

RESULT 38
AF376034 6165 bp DNA linear VRL 25-JUN-2002
DEFINITION Badger herpesvirus envelope glycoprotein B (gB) and DNA polymerase
(pol) genes, complete cds.
ACCESSION AF376034
VERSION AF376034.1 GI:21552713
KEYWORDS
SOURCE
ORGANISM
Badger herpesvirus
Badger herpesvirus
Viruses; dsDNA viruses, no RNA stage; Herpesviridae; unclassified
Herpesviridae.
1 (bases 1 to 6165)
Banks, M., King, D. P., Danielis, C., Stagg, D. A. and Gavriel-Widen, D.
Partial characterization of a novel gammaherpesvirus isolated from
a European badger (Meles meles)
J. Gen. Virol. 83 (Pt 6), 1325-1330 (2002)
22024835
12029147
2 (bases 1 to 6165)
King, D. P. and Banks, M.
Direct Submission
Submitted (03-MAY-2001) Virology, Veterinary Laboratories Agency,
Woodham Lane, Addlestone, Surrey KT15 3NB, UK
FEATURES
source
1..6165
/organism="Badger herpesvirus"
/mol_type="genomic DNA"
/specific_host="Meles meles"
/db_xref="taxon:132610"
69..2623
/gene="gB"
69..2516
/gene="gB"
/codon_start=1
/product="envelope glycoprotein B"
/protein_id="AAM62281.1"

/db_xref="GI:21552714"
/translation="WMNKVLPNYITVVCFFHHINNTPVKSGSTPPSDGKYNLTNLSLN
ISTIVMPFVRCASATGVEIFRRPVHDHCPDVEDHEHNEGIAIVIKNLIPMFIRK
YKRLVSTVYVGLDYALITNQFNSTSPQYELVLDIROFCFNAIVOTENGELFNAY
TDRDYNKTKVMLOPYDGLTGNIMRYASOKLYVDGMAVGFRTRTTYNVECTMMAK
SVHPREYFTASGDFVEMSPFLDNNMTRKSPFRESLIVNLTITNTFTISYDRAFSM
KHAFVNTGDHYISMARESENSTCKFCGKMFPTALIQTKOTNSHFLIANEYTAFT
PLEPDSFNSTHSCIMEETINNOIQSLASINTFKTNGSVQFTKTTGNTLTAMQFLIP
IELLSALNALNDSSQAQTNNSSVRRKRRLSPSSNSIATAQLOAYONLRASIKVL
HELISKAWCEQHOARAQMFEISKINPTSVMSAIYGRPVASRLAGIVSTEVCYVDOA
KYDLHSGMHPGPDVNCYSRPVTEFKSGTDVFGOLGPRNEILLSTNVECTCKDSA
VHYFOSGHOMHKFENVYHHNSTIDINHFSTLNFALNLTFTENIDFEVELEYSKREK
LANVLDIESMFEYNYTQRLSGISKELHNTYENNRDAIIRQFNIDIDIGISGVV
NVAAGVTLFGSITVGLINFTHPTGMLTITLIGAAVYVLMRRTRMAREATIK
LYPHIDQSAQDEPVQPIDQOQKSTILAMHNPQDBHAKLLEKESNKKSGSLIANI
ATKFLRNRRGYALKTS"
2618..2623
/gene="gB"
/note="putative"
2875..6050
/gene="pol"
2875..5865
/gene="pol"
/codon_start=1
/product="DNA polymerase"
/protein_id="AAM62282.1"
/db_xref="GI:21552715"
/translation="MAGNFYNYLNPKKFKIKTQSCVENLEEYTRLIPLEKTPHQP
GVPTTHRVPTPEFFNGKEELVFPQGRKSIWKHNSNPVDKTRRELTFFHVDIETTY
HSOQFPNVPEDIHPSGTVALKILGRTEDNYSVNVVQOYVYVDTGAMHIDQTL
RQHTGYSIVIMKKKILREYQGCNRYKVSITSKNDITITIDKORAGCELFENNQ
AVKRFVINDGSTEGYHCKLAHPRLNRRDSTDPDEPSCMKQTLFLDERIDMPPNOY
LSEFIECUGENGFNATRDDEMILOISVLMKGTGENTPRKILFNIGTCDPDTVEF
ECPESEIDMLYLFTMLRDNIETIGYNIANDPFIITIDRAOVNPNLKDPTRLKNS
SMFEVHTPONSAGFMAVSKIKISGFCIDMYNCKEKLISNKNLMTVAKOCIGGO
KEDVSKDIPHLFRGPRGAKLGYCYKDSIYVLOLRFETHTIESEIAKIAKIP
RRVLTGQOIRVSCLLVADQNYILPQKDGSDGYOGAVIDIPGFNPTPLVY
DPAISYPTITQAANNLCYSMTAPHEKLIHYNISPHDYQTFNLSGPFHVKKHKOYSL
ATLDAWLSKRAIKTKTQSVDPMLRILDKQOLAIVTCNAVYGFVGSGLPCL
KIAETITTEGRMRLEKSNFENITPVELERLIHKPINCAVDANRVLYGDSLEIE
COGYSISEVSGFDOLAKITTEALFEPEIKLEAEKIFQCLILSKRYIGILSKGL
MKGVDLIRKTSCKFIQNTSKYEVNLILLDHTVEKALNLSKQINSVSEGLPLPK
VIDILNDSYKTKKENTVPIDETLFTTESKAPSEKVSITPLPIVYHKIISNEEPPQ
IHDRIPVYFVASPNATKSDMAEDPAFOQNIPLAVLDYFDKVKRGAANILQCFGN
SDKRAVSVLNPLDPTVNAVHR"
6045..6050
/gene="pol"
/note="putative"

BASE COUNT 2045 a 1164 c 1150 g 1806 t

ORIGIN

Query Match 0.1%; Score 23; DB 1; Length 6165;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16162 CTGGCCATCAGTCGACATGTAA 16184
AAAAAAAAAAAAAAAAAAAAAAAAA
Db 4849 CTGGCCATCAGTCGACATGTAA 4871

RESULT 39
EHVU20824
LOCUS EHVU20824 184427 bp DNA linear VRL 02-FEB-1996
DEFINITION Equine herpesvirus 2, complete genome.
ACCESSION U20824
VERSION U20824.1 GI:695172
KEYWORDS
SOURCE
ORGANISM
Equine herpesvirus 2
Equine herpesvirus 2
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae.
1 (bases 1 to 184427)
Telford, E. A., Watson, M. S., Aird, H. C., Perry, J. and Davison, A. J.

TITLE The DNA sequence of equine herpesvirus 2
JOURNAL J. Mol. Biol. 249 (3), 520-528 (1995)
MEDLINE 95302501
PubMed 7783207
REFERENCE 2 (bases 1 to 184427)
AUTHORS Telford, E.A.R.
TITLE Direct Submission
Submitted (09-FEB-1995) Elizabeth A.R. Telford, Institute of
Virology, MRC Virology Unit, University of Glasgow, Church Street,
Glasgow G11 5JR, United Kingdom
FEATURES
source Location/Qualifiers
1..184427
/organism="Equine herpesvirus 2"
/mol_type="genomic DNA"
/strain="86/67"
/db_xref="taxon:133899"
1..17553
/ftc_type=direct
9248..10399
/note="ORF E1"
/codon_start=1
/product="G. protein-coupled receptor"
/protein_id="AAC13788.1"
/db_xref="GI:695173"
/translation="MATTSATSTVNTSLATMTNTNFTSLTSVTTIASLVPSTNNS
EDYDDLDDVDEESAPCYSDTTLAAOVPAIYLVLFGILGNILVILVIRMK
IKNTNMLNLNLAISDLFLTLTFPMHIGWYHDMTFGISCLKLRGCMSTISOV
RCIILLTDRYLAIVYAVPALBPRTVTCIYVCVCPWLAGLSLPEFFRHODNG
RVQCDPYRPMSTNWRRAHAKVIMLSLIDPLINAVCTIYIRLRLRPSKKTKA
IKLIFVIMAVFVFWTPYNNIIVLSTFHTLTLNLCALSSNLDMALLITKTYATYHCC
INPVYAFVGEKFRHLHFHTYVAIYLCKYIFLPSGDEGEGPTRI"
10494..10499
/note="ORF E1"
10660..10665
/note="ORF E1"
12533..13114
14197..14541
18810..19733
/note="ORF E2: product has hydrophobic N-terminus"
/codon_start=1
/protein_id="AAC13789.1"
/db_xref="GI:695174"
/translation="MILGLVLSLASTASATIQAMMPQVITGHEGRPLVRCRVAK
NPSKPTMLMLKTIEGSAEGTIVPRFKPVYTKSSCGSTGVFTSDLSHMDAGRYA
CAVSEDDKDEKSCSDYHTATNIVLETRRRSLGPGLPPTAGPSTGOTGP
LSSQSEESVAVRKGVKYVGSLSLHVECOFGATAGLISAVLFFKVEGAYOAST
ISTSSLTITDLSPIVIEGTQAKWCMGNATKEDSGEYMCMTIGMDFPGEDESGDEDESG
VDFKITVTEGEGEDDDLYLTSSSEKK"
19761..19766
/note="ORF E2"
19784..19789
/note="ORF E2"
20320..20844
/note="ORF E3: product has N- and C- hydrophobic domains
and 6 N-linked glycosylation sites"
/codon_start=1
/protein_id="AAC13790.1"
/db_xref="GI:695175"
/translation="MATEYQFACALVYLGCYAGTPTPSKSTLIYNSQNTTYSIE
NQSSLYYNGSWFIRIEFNCSSGYLEQMPYTCJLFWPKNGTIWNPPSCVKLNTT
TLMTSTSTPTPTGTGTFPDPONTHTHTPTRRPINLRFGYTPMAITLVIL
LVWVINCMMPMF"
21360..25319
/note="ORF 03"
/codon_start=1
/product="tegument protein"
/protein_id="AAC13791.1"
/db_xref="GI:695176"
/translation="MDSTSKRSSFRKARAGRATVYFVPTWQHGPGCGPVSSAFSL
VNEVGVFLVGGACGTGATGARAADPCVASFAPMEILRTVILPGRNVAISLP
AGISGTYTSGDGAAGPCTLSRDVAPMOMALBHLTRGOOUARPLVGAGAGACGP
GGEATPTPKILAAVFEHTLWSLHSHKOHAVMCLNQLSSPASFCRTGYLGFTPLG
DGERPDLKFARVPVPALAHPRADALAKLPEMREHDSOVLGTGTRGAIKIRPFENGL

LGVLORLYAPTSRVEIDRDVFSSNGKPDYFGVYOVGGISTGASELDLTSBAGTFGW
GNVLHLGVVSGDEDFALQELSHIMLAQCSGAPTLGFRVWDGSAAPGMPA
SRPSHETGATRASITSPKACLSPVKGGASVAMLGFEFORPQAGAVASHGRLA
STIAVOPFINAVGGRVILSTCOSPLEGTMHAKIAACGMKLTITSLPREAVSEL
SHFSPGMASMRNSILSKLNLVNAQVILVTYNTTRNRIITLEGVKTREGCRSLGLH
ARAKTIVLYDDSRSPDYCCGPRYLCKFKMKPRYALPIDRWCSTASIRPAPSRVPS
SDAGPPSDAREVLGILRHPTVGCNKYIKYHADRCSAGVAAQCCGPIDLVADYSK
VYVEPSAGPPSSMEPWMTETPOVDDCFILHEDGVGVCASALGEKNSPFPYBGAOK
MAIASSVLSIALAPIARIEDVYVNLISLAMPKAGQGEVFTTLTRCKRCEGAGVSCN
VTSACSSRRAGGDDPEGADIKSFYASFAYPGAFMKLTPDILKARVITLPLASP
GKHARASYQOVRGQKRTYGSVINSGATLGLARVILHLRAKLAVSHDYGDDGLM
AALAEAMAGMRSLOVEVPRLDGPMDGLTSETGEALVEPLSSAAVEALRSYTI
LCRYGVGHKTCERMFITRRDOVYLCEQEOVEAMSHSVRMERGPCNRRHAG
EGPYREREAFLAYTPFRLNRPNNKRRVAVLLGCGPYPLAALDRLRSGRDALYS
HDLAVHLDEVGAYTFLVAGVNTSPDRTSDATLSLVHNRNGVIRDFLSDQTSIG
VGSMACRILIFDGDMAVSPALOSDRICVAPVCFKESRDLNFINOSPVAPVRLTLP
SILPCMAOHTHIGFGAPSPEDCLDRVLSQAASMTGSDVYASGAPMAVPAVNTETLPV
AGICSRDGHVLVLDHDTASVYLMQPHVPKSNIPYASPMKQVFLDLHAWTAHSH"
25639..26190
/note="ORF E4"
/codon_start=1
/protein_id="AAC13792.1"
/db_xref="GI:695177"
/translation="WVPSRFEFEEMDRVLENDAOKLSLTNLKNVFAOTLDMKPEGV
LITTEALMLVDECKEYIHLIELVMQVPVSVAPPTSAIINNSLIGITROTGOGED
NFGRLCSLSPASCFLELVLOSDECLVSFASELAKFYVESQNLMLAYSGLSGLIRE
RPPSWMLYFALKOKMRLFYFPFK"
26436..29873
/note="ORF 06"
/codon_start=1
/product="single-stranded DNA binding protein"
/protein_id="AAC13793.1"
/db_xref="GI:695178"
/translation="MNSNRAAGPVENYGTQASVPCGPFVLYLPEDTTPVEASILG
NLHAGEVSLPLSGITVEADPHVNAKAVHKLDPATYSAKASATHRVTFPANAC
FKPIFAGPLEGICAAARQLFGYAEFEBAEGAAARFELIADGLHLLGMESHIAGVY
TESFKERLRCOLVAVESQIQSVRVEGCAPFVPLDGLFAKSPCLREMLRYFYHAGV
SYLFEAHTSLAQLRLRVDRVGLIGLALRGOSFHDPYKLPKYECEEPFATGIRGAD
CSLTIVDSATVELAVSYGLSFLVEPDEGALLSHDYKPIFECEPEEOPAEVALTOGNA
KQAVHYHSQLPFGSGSVLYLAROKASQSGGGENYVNFPMHGLACLAEPKQNG
LSPFPVPASALSGSNYSLHLIAYASESPOMLRHCYTLQROHOKSSNNSGYNPT
VYGTANTPWCLEICRSGCPASCNTLTFYLRLRFPVAVSVRDPVTVGVAGVANDL
DLAGNFANRDKDDESNQSEBEKFTYQVOTVTLERLEAGICEGEDEVGAIAHNG
SFLKVEKEIDGIVDEGARFINSQVNNVANSIESIKSHIHYQVYVWOPCPYFL
NLXYRCVLWODICLPTCMYEOENRPAVSGEMLKMHYOTLMFNKNSIDKGLV
TGEYKVVYAKDQCPDPODSARAGFVCSQKQVRSRLMMAPRMKIKNRTIENS
PGTESIQANFVAGTRKDCSCVYSGPMRLSTYHSOLFPGAKISPLFLMHTSKKRLQ
PVPNVPRESVTELAVYVQNSRLHGETSIDVPEPNFYAKVRLNMLFRACQTO
FYATITHCLTPKIQTVPABEYFHALCARVAVGEYLGARLCTVPTVQCTSDNICE
VGKCRPIVTLPLVANKYTGVTGNSQIFOCANLGFYGVDDKNLIPDAGSFKQGVST
SMKRRIWETPLSDHLRLRSVQGAVAFLIEGVRRVVOOILSDGONPHYIRDVLOLV
KSLGECRSVSEYDLEYWGOYYIRAGVSEBRLQSLSDIGOMSEMAISVIGEEDP
LGGELEFEKVEDECLGHPQODEFALAPAAPVQYSGSSSVAKKRAVILIGDLQ"
29997..32183
/function="role in capsid maturation/DNA packaging"
/note="ORF 07"
/codon_start=1
/protein_id="AAC13794.1"
/db_xref="GI:695179"
/translation="MAKRELAAYVAYOYFDLAEVSLLGYCDPSSIDKRCYMANSKYFK
LCEISLPLRLQNTDECSPLSELQHLQNTDEBALVLDLSDGSRSEYEAALPS
RPLEGCRKHARVRVPEYGAERTVSLDELQVLEFFKRLNSYFVLLPAGELALAGE
TVAFILGRKRGVSPIPADAVYSSVPCASFARVAMPNGEGSVLSMLAVNCHVRCO
VPSDPYIGVFENELRHLDGADARAAGAGGREGSERGRADADEDEDEPEPDGCGDA
GGGAALRVLTSSLSVLAGHTIIEBEDGLAIESLVLSNLYVSSAADRGCVGCTARATSS
HNAKLAHARHMRSRAMWLGKAPSHFPFAHPSPLTSCGCVFNSIDDTIAALQKD
CSATFLKKSNTOTLLQOONELVYRLNLEYLNGRDEGCGAKGALADAPKLPDGGAS
CPDRVILSDARVRLDYLTKLRLDGLRLTDCIETNGRYVLSPTLSLADVGSALYSAA
RLVNHRLFRORVYIGWADLTAGGEAEPFNSYIKKALHQLNREHDLISYVHVFH
TNGPLSLQNSHRFPVDPVNALVACIAAGAMPKOKIYLTMPKIPGSKKIMQICNPSF
YSTETGDLNLTOKTLNTYIRVAVLSISLNRWBSLSLSTELRGSLASASGSEL
GGGVYLTTEGTAPVLAIVPDSKGVKFDVLTLLTYTLQLTQSGRQASV"
30114..30119

polyA_signal

CDS	/note="ORF E3, 03, E4 and 06" 32195..34619 /note="ORF 08" /codon_start=1 /product="glycoprotein B" /protein_id="AAC13795.1" /db_xref="GI:595180"	
	/translation="MGVGGPRVYLCLMCVALLCCGVAQAEVAETTPPYTHREPV AEENPAPFLEPRVCGASPTGGEIIFREPLESSCPTEKDKIDEGITALYKNIYEPV NRRKRIIMTSTTIYKGSSEDAITNOMHRAVYALQMDHYOCFSAOVNEG VNTYRDDGNETAFILKPADGITSITRYOQPPVAPYAPRLIMSTYRTVNEEVE MSARSMKPEEFVSVGDTIEMSPLEKNGEIKLRKPSLITLKNYATKAGVGL GQADNATPEFAIEDGYLSMKATENSICYLLIMKGSNAIQOHNSLFIANDIT ASESTPLEEANEETKCLNNNTQEEIOKLAKVEYKTHRNQAKYKTKGNYLYV QPLIQIDLTLHAKLYNLNTNATASPTSTPTSPRRRRDTSVSGGNGNGNKS VAAQVOFADNLRKISINRYGELSRAMCRQYALSMWELSKINPTSVMSAYGR VSAKIDGVSVSDCIYVDKSVFVHKMKKYGKEDLCYTPVGVKFEINSELPAG LGPNEIYLTISOVEVCOHSCHEHYFOAGNOMYKKKDYVYSTLNLTDIPIHTMTN LSIENIDFKYIELKSTKERTLSNVEDIETMFRYNYTQNLNLRDLDSIDHGR SFIOITLDMODLTIGKVVYVNAVSFSLDSVGSVTSFKKPGMLDVLILIG VVVYLFMTSRSTYSAPITRMLYPGVEAAQEPGAPVSEQIINILMGHFOQOR AEEARREEEYKGRITLFYVIRDSATSVLRRRGGGYORLDRGSDDEGYEPLRQ DGYDDVDVEAGTADTV"	
polyA-signal	34855..34860 /note="ORF 07 and 08" 35089..38115 /note="ORF 09" /codon_start=1 /product="DNA polymerase replicative subunit" /protein_id="AAC13796.1" /db_xref="GI:595181"	
CDS	/translation="MSFVNPYLKRTFLKRAAPSPRIKERTRIIPKCEKTPGAGVVP HTSLDPVCYFGDEKTEPILIGDGRSLMSAGRGPGAGQGHTPALFFHVDTIE TVYQDNCDFVQFQTDIIPSGIVLILGRTSDRSVCVAVFQELIYFVRYVDTIE LDPLIQOCSRENENFSQGRYREKTSKGLREYCEVAREYRVASSQGFVDLGLG TAAACEVFETVDAARFIIIDNGESTFGWYCAAVPROGAAVSTWTELEDDAAG LEFAGRADNGVNLSEDIICGENCEPNAISREDMILIOISYINMGASGARVYL LNGTCEIEGVEYVCCPSLEDILYLFTMRDVEDVEYGVNINSDRPVIDRATD VYNLNKFTFRVRSSTSFVHKPKNSASGRARVSKVAVGVITDITQVCRDLSTS NYKLIVAGCEVCAKKEVDVSKETIPHLFRQDGGARAGLYCVASDALVLDLLEFMT HVEISEIAKIAKIPTRVLDGQIRVSCLDVAGREGVILPVDRIADAGYCGAAY IDPSGFYNTPLVDFASLPTIIOAHNLCYSTMIHPCGRDLCLPHLGGPEYFEEL SGPVHFKHKAVALSLATLLVWLAKRAIRRELATVSDAEVRIITLKKQALAVTGN	
Query Match	0.14; Score 23; DB 1; Length 18442;	
Best Local Similarity	100.0%; Pred. No. 0.2;	
Matches	23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
OY	15445 CCATAGACATGTACGAGGTG 15467 	
Db	36394 CCATAGACATGTACGAGGTG 36416	
RESULT 40	AY037858 171096 bp DNA circular VRL_19-NOV-2002	
LOCUS	AY037858 herpesvirus 15 strain LC18664, complete genome.	
DEFINITION	AY037858 AF148640 AF159308 AF227125 AF159309 AF159310	
ACCESSION	AF227123 AF227124 045963 093160 093909	
VERSION	AY037858.1 GI:18025465	
KEYWORDS	Cercopithecine herpesvirus 15	
SOURCE	Cercopithecine herpesvirus 15	
ORGANISM	Viruses; dsDNA viruses, no RNA stage; Herpesviridae; Gammaherpesvirinae; Lymphocryptovirus.	
REFERENCE	1 (bases 1 to 171096)	
AUTHORS	Franken,M., Devergne,O., Rosenzweig,M., Annis,B., Kieff,E. and Wang,F.	
TITLE	Comparative analysis identifies conserved tumor necrosis factor receptor-associated factor 3 binding sites in the human and simian Epstein-Barr virus oncogene LMP1	
JOURNAL	J. Virol. 70 (11), 7819-7826 (1996)	
MEDLINE	97048062	
PUBMED	8892903	
REFERENCE	2 (bases 1 to 171096)	
AUTHORS	Rivallier,P., Quink,C. and Wang,F.	
TITLE	Strong selective pressure for evolution of an Epstein-Barr virus LMP2B homologue in the rhesus lymphocryptovirus	
JOURNAL	J. Virol. 73 (10), 8867-8872 (1999)	
MEDLINE	99412410	
PUBMED	10482645	
REFERENCE	3 (bases 1 to 171096)	
AUTHORS	Jiang,H., Cho,Y.G. and Wang,F.	
TITLE	Structural, functional, and genetic comparisons of Epstein-Barr virus nuclear antigen 3a, 3b, and 3c homologues encoded by the rhesus lymphocryptovirus	
JOURNAL	J. Virol. 74 (13), 5921-5932 (2000)	
MEDLINE	20304984	
PUBMED	10846073	
REFERENCE	4 (bases 1 to 171096)	
AUTHORS	Rao,P., Jiang,H. and Wang,F.	
TITLE	Cloning of the rhesus lymphocryptovirus viral capsid antigen and Epstein-Barr virus-encoded small RNA homologues and use in diagnosis of acute and persistent infections	
JOURNAL	J. Clin. Microbiol. 38 (9), 3219-3225 (2000)	
MEDLINE	20440633	
PUBMED	10970361	
REFERENCE	5 (bases 1 to 171096)	
AUTHORS	Rivallier,P., Jiang,H., Cho,Y.G., Quink,C. and Wang,F.	
TITLE	Complete nucleotide sequence of the rhesus lymphocryptovirus: genetic validation for an Epstein-Barr virus animal model	
JOURNAL	J. Virol. 76 (1), 421-426 (2002)	
MEDLINE	21602573	
PUBMED	11739708	
REFERENCE	6 (bases 1 to 171096)	
AUTHORS	Wang,F., Franken,M. and Annis,B.	
TITLE	Direct Submission	
JOURNAL	Submitted (11-JAN-1996) Medicine, Brigham and Women's Hospital, 181 Longwood Avenue, Boston, MA 02115, USA	
REFERENCE	7 (bases 1 to 171096)	
AUTHORS	Moghaddam,A., Koch,J., Annis,B. and Wang,F.	
TITLE	Direct Submission	
JOURNAL	Submitted (12-MAR-1997) Medicine, Brigham and Women's Hospital, 181 Longwood Avenue, Boston, MA 02115, USA	
REFERENCE	8 (bases 1 to 171096)	
AUTHORS	Moghaddam,A., Annis,B. and Wang,F.	
TITLE	Direct Submission	
JOURNAL	Submitted (17-MAR-1997) Medicine, Brigham and Women's Hospital, 181 Longwood Avenue, Boston, MA 02115, USA	
REFERENCE	9 (bases 1 to 171096)	
AUTHORS	Rivallier,P., Quink,C. and Wang,F.	
TITLE	Direct Submission	
JOURNAL	Submitted (04-MAY-1999) Medicine, Brigham and Women's Hospital, 181 Longwood Avenue, Boston, MA 02115, USA	
REFERENCE	10 (bases 1 to 171096)	
AUTHORS	Jiang,H. and Wang,F.	
TITLE	Direct Submission	
JOURNAL	Submitted (16-JUN-1999) Medicine, Brigham and Women's Hospital, 181 Longwood Avenue, Boston, MA 02115, USA	
REFERENCE	11 (bases 1 to 171096)	
AUTHORS	Rao,P.V., Jiang,H. and Wang,F.	
TITLE	Direct Submission	
JOURNAL	Submitted (21-JAN-2000) Medicine, Brigham and Women's Hospital, 181 Longwood Avenue, Boston, MA 02115, USA	
REFERENCE	12 (bases 1 to 171096)	
AUTHORS	Rivallier,P., Jiang,H., Cho,Y.-G., Quink,C. and Wang,F.	
TITLE	Submitted (01-JUN-2001) Medicine, Brigham and Women's Hospital, 181 Longwood Avenue, Boston, MA 02115, USA	
REMARK	Sequence updated by submitter	
COMMENT	On or before Dec 31, 2001 this sequence version replaced	
FEATURES	g1:9651728, g1:9651730, g1:9651731, g1:5929880, g1:5929882, g1:8745308, g1:8745310, g1:8745312, g1:3342233, g1:3342231, g1:1477526	
SOURCE	Location/Qualifiers 1..171096	


```

/organism="Cercopithecine herpesvirus 15"
/mol_type="genomic DNA"
/strain="IC18664"
/db_xref="taxon:104228"
join(<162521..162879,137..354,437..535,644..892,974..1054,
1134..1289,1377..1592,1673..>1779)
/product="LMP2a"
join(162521..162879,137..354,437..535,644..892,974..1054,
1134..1289,1377..1592,1673..1779)
/note="similar to Epstein-Barr virus LMP2a"
/codon_start=1
/product="LMP2a"
/protein_id="A056624.2"
/db_xref="GI:18025544"
/translation="MSALEMEPLGAPAPGPGVGDGEGSGRESYPSSPPSPCP
QGDYEDPPDDNPPPYDAEDGDGDPYQPLRGDPNOLYARLGGGGNGTLPPEPY
SPQRETSLSLIEIHPQRTAPGMLPVNSAPYLEFWLAGIASCSASVALVTTGTA
LSLLAALVNSVAQQRKAVTKLTIVGIVTFEAILTWIQKPRDAIVFALLTGA
AVLOATYIVMLFLPTPYRRRMKIVCVLLFCAVLVDAIMQISFLGSMTV
VALTLLLAFTIILSSPMSGALGALLTAAALALGSLVGLGNLATWFLMWT
LVITLCSTPOTMYLMSRWLYALSLLLASALLAGSITLQTMGNDNTEFPSTLGM
LLIVAGLFIILALITENKSGSKTYGPVYCSGLTMAAGLVVYLMIKVLSANIT
TAGCTFFELGELFGLKFCRLCCFCLRLSDSDPOVATYQNNV"
join(166602..166718,137..354,437..535,644..892,974..1054,
1134..1289,1377..1592,1673..1781,5496..5930)
/product="LMP2b"
/note="similar to Epstein-Barr virus LMP2b"
join(<141..354,437..535,644..892,974..1054,1134..1289,
1377..1592,1673..>1779)
/product="LMP2b"
join(141..354,437..535,644..892,974..1054,1134..1289,
1377..1592,1673..1779)
/note="similar to Epstein-Barr virus LMP2b"
/codon_start=1
/product="LMP2b"
/protein_id="A095410.1"
/db_xref="GI:18025466"
/translation="MAPGMLPVNSAPYLEFWLAGIASCSASVALVTTGALSLL
LALVNSVAQQRKAVTKLTIVGIVTFEAILTWIQKPRDAIVFALLTGAVAL
IYLVMLFLPTPYRRRMKIVCVLLFCAVLVDAIMQISFLGSMTVALLT
LLAFITMSSPMGICAGALLTAAALALGSLVGLGNLATWFLMWTLLVITL
LCSTPOTMYLMSRWLYALSLLLASALLAGSITLQTMGNDNTEFPSTLGM
AGLFIILALITENKSGSKTYGPVYCSGLTMAAGLVVYLMIKVLSANITTAGC
IFELGELFGLKFCRLCCFCLRLSDSDPOVATYQNNV"
<1836..>5780
/product="BNRF1"
1836..5780
/note="similar to Epstein-Barr virus BNRF1"
/codon_start=1
/product="BNRF1"
/protein_id="A095411.1"
/db_xref="GI:18025467"
/translation="MAGHSRVPOAHGSQPLMITLCTDGGANVOERLYLISNPSE
LGSTGLVSENLITVALRGNDPRRQERARELALVGLGNSBQGRILGTESAL
NALRNKYVYVAGDDMMARPTWSAEIQOFLRLGTGYVLELROFGVGTARSEF
ROFOALINHYLFNDNLRYKPEYGOASAGFALLPGPPTVDVPRDTLVEVMEFGGA
GGGROLADELMTYSLPLADYNSGHLIOPFALVYALNAGSNRERATSLSEGFVHTGT
IOPCNPQLPMRHPGLPFRVSAIASSLCGYPALGPRSDVEDARQOAFPTKVA
ECHANSGVYVAGFRTVDTTLTGEGELVTMTGELGVIRHOLDIARPEIQYLVN
LGFHPWSNLTPAPCPYASBALAQAIVOTALFESGLYPRPCVSSHARPGPALLIEH
LRSLVQGGILFLSHLPEDVKGIGIDLGAQTSRGIKQYVETVLELNPSCSVFLIE
ROGERKINGVGLQALRKACEVAGCOYVYVSGVPLGGLFVNDLASPVSTAMTDF
APPEVSEPPSIPIGEMKSPVSHTEEMDVPASHESNLSTSLTSVLSHPVSGKE
HLVHNDRVASGGVALQCGVPLDPLADYARAHQOYVYRPGAPPLPRYTRDRNME
KLIVSARPTDEAKVSGTYITTEGQCYKTYLDIEGKLLMVALMAMAFAPLVNED
VLLTLNADPGKVDSTAVMDLMTAASDARDLGVLKLTGASCPGEGSAPFPMYV
VWSARGESAPLTPLYLQSGSLISVRGDKIQGSLFEDLFSVNAAPAPQAD
AMKIIERTVQGLVKSGLVLSGHDVSGGLVTCVEMALAOQRYTTSVPAAYLPLD
FTEHPGLVEVEEGNEMVQOTLRAONIVAVAGVGENAGAGVAGVLSHPSVSGKE
LSLLSTMSFTEATEQYELRPGRLNSMHNYSVDGENALASPLTGKNLGLRTVTER
DPICRYAVLIDPGTRGHESLLAFITNAGCICQYVTRDVENETTFDITACLAGVSHA
ARDAPLAGRATVALIDRSPLALDLKFLARPEFTSLGELGVOYVLAGVAGSGSDP
TPBPGEINQORSPLILITTNASGLFESRWLNFVSFPHDTKSVMLRGIRGCVLPCWIGDS

```

```

misc_feature
653..6824
/note="similar to Epstein-Barr virus EBR-1"
6967..7136
/note="similar to Epstein-Barr virus EBR-2"
<9920..>10453
/product="BNRF1"
9920..10453
/note="similar to Epstein-Barr virus BNRF1"
/codon_start=1
/product="BNRF1"
/protein_id="A095412.1"
/db_xref="GI:18025468"
/translation="MGLRSGITLQCVIIQCLVIMYIAPKCGVNSGNNPMLRLDR
DAFSRKTFQMDOLDNLILKSLSEDFRGYCGALSIMQIFLEEVNPOANDP
HAREHNSGLENLTKLRLRRCHRELPCENKSAEQVNAASKLOEKGVYAMSEF
DIRINYEAVYMKIR"
join(11765..11771,11930..11959,15018..15078,15160..15294,
18100..18159,18241..18375,21181..21240,21322..21456,
24262..24321,24403..24537,27343..27402,27484..27618,
29839..29871,29956..30060)
/product="EBNA-LP"
/note="similar to Epstein-Barr virus EBNA-LP"
join(<11958..11959,15018..15078,15160..15294,18100..18159,
18241..18375,21181..21240,21322..21456,24262..24321,
24403..24537,27343..27402,27484..27618,29839..29871,
29956..30060)
/product="EBNA-LP"
join(11958..11959,15018..15078,15160..15294,18100..18159,
18241..18375,21181..21240,21322..21456,24262..24321,
24403..24537,27343..27402,27484..27618,29839..29871,
29956..30060)
/note="similar to Epstein-Barr virus EBNA-LP"
/codon_start=1
/product="EBNA-LP"

Query Match 0.1% Score 22: DB 1: Length 171096;
Best Local Similarity 100.0% Pred. No. 0.78;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14555 CCAGCGTGTCGTGACGTGT 14576
Db 151918 CCAGCGTGTCGTGACGTGT 151897

RESULT 41
AF292063 949 bp DNA linear VRL 15-MAR-2001
LOCUS
DEFINITION
Unidentified herpesvirus natural-host Pan troglodytes DNA
ACCESSION
AF292063
VERSION
AF292063.1 GI:13345036
KEYWORDS
SOURCE
ORGANISM
unidentified herpesvirus
viruses: dsDNA viruses, no RNA stage; Herpesviridae; unclassified
Herpesviridae.
1 (bases 1 to 949)
AUTHORS
Worley,M.B.
TITLE
A herpesvirus of the slow loris related to the HHV6/HHV7 group of
betaherpesviruses
JOURNAL
REFERENCE
2 (bases 1 to 949)
Worley,M.B.
Direct Submission
Submitted (02-AUG-2000) Research, San Diego Zoo, P.O. Box 120551,
San Diego, CA 92112, USA
FEATURES
location/Qualifiers
1..949
/organism="unidentified herpesvirus"
/virion
/mol_type="genomic DNA"

```

CDS

/specific_host="Pan troglodytes"
/db_xref="taxon:39059"
/note="Betaherpesvirus"
<1..>949
/codon_start=2
/product="DNA polymerase"
/protein_id="AAK19167.1"
/db_xref="GI:13345037"
/translation="SIMAHNICYSTLLVPGGEYVPDADYVSTLLENGITTHREYRAS
VRVSVLELLKRWKSORKARECEKEDPAPRMILLDEOMALKVTCNAFYGFVNV
GAMPCLPIAASITRIGRDMLEPRTAFIEDNFSGPCFLNPNQEDYAAVSEDEARE
EEEGDVGHLGLEMVEEKGGGGNGGRTSHVLTAAAGATPRTRRIRHHTIP
KRRPRGEARRRGGGSGGNTVERVYTCGTDVSFYHRTIGTADALVSRPALADY
TACLPNEVKLEFKEVFLSMICKRRTIGAVEGAAGLSM"

BASE COUNT 172 a 281 c 331 g 165 t

ORIGIN

Query Match 0.1%; Score 21; DB 1; Length 949;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 15919 CACAACCTGTGCTACTCCACC 15939
|||||
17 CACAACCTGTGCTACTCCACC 37

Db

RESULT 42
AF283477 3623 bp DNA linear VRL 26-MAR-2001
LOCUS Caprine herpesvirus 2 glycoprotein B (gB) and DNA polymerase (DPOL)
DEFINITION genes, partial cds.
ACCESSION AF283477 AF327829
VERSION AF283477.2 GI:13447464
KEYWORDS
SOURCE
ORGANISM
Caprine herpesvirus 2
Caprine herpesvirus 2
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae.
REFERENCE
AUTHORS 1 (bases 1 to 3623)
TITLE Chmielewicz, B., Goltz, M. and Ehlers, B.
DETECTION and multigenic characterization of a novel
gammaherpesvirus in goats
JOURNAL Virus Res. 75 (1), 87-94 (2001)
MEDLINE 21212029
JOURNAL 11311431
PUBMED 2 (bases 1 to 3623)
REFERENCE Chmielewicz, B., Goltz, M. and Ehlers, B.
AUTHORS Direct Submission
TITLE Submitted (29-JUN-2000) P24, Robert Koch-Institut, Nordufer 20,
JOURNAL Berlin 13353, Germany
3 (bases 1 to 3623)
REFERENCE Chmielewicz, B., Goltz, M. and Ehlers, B.
AUTHORS Direct Submission
TITLE Submitted (11-DEC-2000) P24, Robert Koch-Institut, Nordufer 20,
JOURNAL Berlin 13353, Germany
REMARK Sequence update by submitter
COMMENT On Mar 26, 2001 this sequence version replaced gi:10121846.
FEATURES
location/Qualifiers
source 1..3623
/organism="Caprine herpesvirus 2"
/mol_type="genomic DNA"
/db_xref="taxon:135102"
/note="Isolated from infected peripheral blood leucocytes"
<1..1050
/gene="gB"
<1..1050
/gene="gB"
/codon_start=1
/product="glycoprotein B"
/protein_id="AAK26669.1"
/db_xref="GI:13447466"
/translation="STSYGRVSAKRIGDVTSVSHGVVVOOVSLSHNMVPPCKDHA
HECYSRPVTYTKFINDSHLYKGGLGVNNEILLTTTALFVCHENIEHYFGGDNMTFYK

gene
1222..>3623
/gene="DPOL"
1222..>3623
/gene="DPOL"
/codon_start=1
/product="DNA polymerase"
/protein_id="AAK13396.2"
/db_xref="GI:13447465"
/translation="WLSFWNPYLKGFCKPPSTPLTPLPSTHRLIPKCFKSDPEPKHG
VESIKTSIPPTAFHOGRELPAVLEGRPSLMDAASSPPSNGKLFTHYDIVEALXYA
ERCDIIPHLQADIVPSGIVLKEFGTEGGOSACVNVGCGYFVNDVYVNLQDYL
OHVLESGRSAGVMTPTRRKFLSGYSTSEIYQITLMSSSARSLANGSGWYQ
VPEANVDAPTREITIDNKFSTFGWYCHHMSARPSRSHOLEDCAVSPVPSER
VDMRYNLSLSDIECLGREGPPSARDSDITIIQISCTTMAVGSBDPRRIILCVCTD
PLEGIDVFEPSSELDMLAFTFLIRDIYEMITGINICNFDPPVLDRAHYNFKPE
EYKTKSNSLEFYVKKPHEGNFMRAHSKVLGGVADIMYHICRDKLSLDKLNLTAK
ECLGEKTDVTKDIPILFGRSSRDRAKGLYCDAVLVNLQHEWTHIEIETIAK
IAHPPRRAVISDGOQIRVFACILAAQREGVILPPTGATAGYOGATVNPISGFVN
TPVLVVDRAVSLYPSIIQAHNLCYSLVPEHMSLDPDLDPDYEFESTISSGPVHVKR
HKTESLASLITAMLAARKARIRRELAKQDDKRLITLQKQALIKVPCNSYGFQVA
SGMLPCLTIAETVTLQGRVLEKTRFVEYVDIQRLQDPSITGLPQNPSPRLTV
VYGDPSLFLINCEGFHIDTVLQPSRLAHTSSLPDPILKSEKVFQCLLLTKRR
YVG"

BASE COUNT 827 a 1085 c 997 g 714 t

ORIGIN

Query Match 0.1%; Score 21; DB 1; Length 3623;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 15919 CACAACCTGTGCTACTCCACC 15939
|||||
Db 2974 CACAACCTGTGCTACTCCACC 2994

RESULT 43
AF033822 12708 bp RNA linear VRL 03-DEC-1998
LOCUS Walleye dermal sarcoma virus complete genome.
DEFINITION AF033822
ACCESSION AF033822
VERSION AF033822.1 GI:2801519
KEYWORDS
SOURCE
ORGANISM
Walleye dermal sarcoma virus
Viruses; Retroid viruses; Retroviridae; Epsilonretrovirus.
REFERENCE
AUTHORS 1 (bases 1 to 12708)
TITLE Petropoulos, C.J.
APPENDIX 2: Retroviral taxonomy, protein structure, sequences, and
genetic maps
JOURNAL (in) Coffin, J. M. (Ed.):
RETROVIRUSES: 757;
NY, USA (1997)
Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York,
2 (bases 1 to 12708)
REFERENCE Chappay, C.
AUTHORS Direct Submission
TITLE Submitted (12-NOV-1997) NIH, NLM, Rockville Pike, Bethesda, MD
JOURNAL 20894, USA
FEATURES
location/Qualifiers
source 1..12708
/organism="Walleye dermal sarcoma virus"
/mol_type="genomic RNA"
/db_xref="taxon:35720"
1..12708
/gene="gag-pro-pol"
join(1..246,5856..12708)
/gene="env"
78..153

Casey, J.W.
Nucleotide sequence and protein analysis of a complex piscine
retrovirus, walleye dermal sarcoma virus
JOURNAL
J. Virol. 69 (9), 5320-5331 (1995)
95363939
MEDLINE
PUBMED
7636975

FEATURES
Source
1..12708
/organism="Walleye dermal sarcoma virus"
/mol_type="genomic RNA"
/db_xref="taxon:39720"
1..590
/evidence=experimental
870..1232
/note="ORF-C"
/codon_start=1
/protein_id="AA09528.1"
/db_xref="GI:786143"
/translation="MANYHQRHMLDYSIPRONQAPLTTITTFIDPOFKIOENGLTBS
EYKQIVKQIIPOLCRIPNONSPPPIWVGPRIGKDPWIKINKFTTELLPKQKGRK
NISTKYLSTRLEFVIMLON"
1240..2988
/gene="GAG"
1240..2988
/gene="GAG"
/gene="GAG"
/codon_start=1
/evidence=experimental
/product="gag polyprotein"
/protein_id="AA09528.1"
/db_xref="GI:786144"
/translation="MGNSSTPPPSALKNSDLFTKMLRTQYSSGVKTRRINODIKKQY
PLMDGTCATKHEQAVLIPDSVSEETAVLNLVFNKIQARGETAROMTAHTIK
LIVGTIDKRNQOETLLOKIDESDEMDTNTMLPIANKRERIRAOOQADIAOQOVL
LLOREQOREOREDIKKRDEKKKILPDTQKQOTDIEGESSDASAOKPISYDNP
DKYDGVLTROHTTVPSSNITIKKGGTSVOQPHIRNYPGEGLNTAORNPFRPEL
OOLKDDPALPEGIPOLAEMLTOMALYNODEAEVDEALARYPTPTVQIAGVINGHA
AANTRAKIQNTVTRCROHYPAYCDWGTIOAFTTTPPOAHYKHAETIRKNSGLE
OHATVPFINNVQGLPRTKVTSLMSGNPDWSTKITPQIIPLMQHYLNQSDOKIKQ
TPVLQDAMPQNTNGNGYGSYPTENEPYSFOQOORPARAPGVNPSVTCFCCKO
PGHWKADCPNKTRNLRMNGMNGRGMGPYRSPYPAFIQPPQNHQNGYHMDRS
OLOQAQEWLPGCTYPA"
6414..10091
/gene="ENV"
6414..10091
/gene="ENV"
/codon_start=1
/evidence=experimental
/product="envelope polyprotein"
/protein_id="AA09527.1"
/db_xref="GI:786145"
/translation="MDTPGSLQVIAIISLLVGSQAPAFLEKALPTDGSLETIEH
KTEWNTTRESSESPVRSKTRQOLIDETPEICANAWIRLITEPELGMSSOKQT
IAIQVNTTMEETVSLVSHVKNKNEIHNVSIGTKQLVGNFTCSRKISOT
KERKISTVQKTEYVLPFAMSOKEPGGKYPPOIYGTGRLNOMNMDEPVIQ
CKRRKROITVPSLPTGTDPTKTPPISPNSTALNETEOKTPTCTDEPFNN
EKONLIFGINVTMPCQEAELFOQNISDKIVQAEKVTSLGQNTISCAITNTH
GINTENKNCVISILKENRKAIAHYITRTGSYEYAAQVNSKGIQGVNRNLVITVEE
CPYKPLPOGIIPLTMPRVLTNPSPILHSAKFDLSKFGSPCSFSPSEWQYIT
KPLKRAMHGEVHQRKRDGLIGLSTLMMWNNANSLGLVESADOKDOKLKLAL
ONLAVOORTVKNQOCTGKALEPITYITITLQALANSLAAILKHEQOONVGTCDIAI
LYVQIAFYLRDIOHEHLPMVFETIQNTQILLPVGQYIMEITAPILNPLIGNQSV
LVIGLTHQLITTTVOQPLKANKNGFQDMTPPEPFLANKTHGFSIDCPLMKRSFLC
HTLPTPKLSBERKSTIYQTSQVWITPEGKACLNHRNITVQDRTCLNPKSPCLP
KHPWSAGKQITVPTQOONFVPDPTIDEDNOTVLOKEMIEAISAKRQYGVYKQCO
IALIRHHEAITTIGQEAATYIKETQALISSIEQEAANYNMLFESWYDGSVSOLOLIV
VITCTIPLWLWNLCTCFEKLRAIRREDDNNIYVEQAOARTGRRTHEPTTKORAK
LIRAKTRRLPRSLRATPRVSAFAEWTTPDQETVEYINRIRDSHENNDGCPNNAP
IISADSTALPTPTITLMDRELNOGRKAVITLLNDPAREVFNKAINLVTTNHTLAY
GCDSAGVNOHAETMGKPVITVLGAVITPVGLAWIPDQOEPLKLFVNPSPMAY
TVAMADYHETREKEMKIVKIDINNELLVKPOLFKMDRVRFCSLPCYKRSCHWQFAA
YRMPCYGSGTGRDLOSASTLCITSLFLEKVLILFQMLIPMIVQHLLLLLVLYEFV
LSLYEIFYFLIFLTYTYNV"
10114..11007

BASE COUNT
4196 a 2806 c 2456 g 3250 t
ORIGIN

Query Match
Best Local Similarity 100.0%; Score 21; DB 1; Length 12708;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OR 33762 TATTAGTTTATATTTT 33782
Db 10000 TATTAGTTTATATTTT 10020
|||||
|||||

RESULT 45
AF005370
LOCUS AF005370 130608 bp DNA linear VRL 19-OCT-2001
DEFINITION Alcelaphine herpesvirus 1 L-DNA, complete sequence.
ACCESSION AF005370
VERSION AF005370.1 GI:2337967
KEYWORDS
SOURCE Alcelaphine herpesvirus 1 (wildbeest herpesvirus)
ORGANISM Alcelaphine herpesvirus 1
VIRUSES; dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Rhadinovirus.
REFERENCE
1 (bases 1 to 130608)
Essner, A., Pflanz, R., and Fleckenstein, B.
Primary structure of the alcelaphine herpesvirus 1 genome
J. Virol. 71 (9), 6517-6525 (1997)
JOURNAL
MEDLINE
PUBMED
9261371
REFERENCE
2 (bases 1 to 130608)
Essner, A., Pflanz, R., and Fleckenstein, B.
Direct Submission
Submitted (27-MAY-1997) Institut fuer Klinische und Molekulare
Virologie, Friedrich-Alexander-Universitaet Erlangen-Nuernberg,
Schlossgarten 4, Erlangen 91054, Germany
TITLE
JOURNAL
FEATURES
Source
1..130608
/organism="Alcelaphine herpesvirus 1"
/mol_type="genomic DNA"
/strain="C500"
/specific_host="Canis lupus familiaris taurinus"
/db_xref="taxon:35252"
/lab_host="MDBK bovine epithelial kidney cells; ATCC
CCR-22"
918..1211
/note="putative ORF"
/codon_start=1
/evidence=not_experimental
/product="A1"
/protein_id="AAC58052.1"

polYA_signal
/db_xref="GI:2337968"
/translation="MRLHFLYRSIEFMWYKKSRLKIFCITLSLYFLTAHKRPSANP
ITDFSRINGPCFYKMSRHQLLVNLQMLSPCRNKSCLTSADOCITANEDTTR"
1248..1254
/evidence=not_experimental
complement(1300..1305)
/note="spliced cDNA detected by 5'RACE-PCR"
/codon_start=1
/evidence=experimental
/product="A2"
/protein_id="AAC58053.1"
/db_xref="GI:2337969"
/translation="MSQNSNSNPSPRRKRYVMCDLTREOKERRSRINRASKNFKL
RRRIFEEOQEGKLINLKYSNRLRCOVERKREIRILEMLYHKCTTLONTYGPPE
PRKYVNSLEMCATFALNDOYTTNNINIPETVSGNNTNGFAATATLHNCYER
TLANNNTNBEAKNCEVLPSTALDDLISIDNNINYL"
3492..3493
/note="A3: AHV-sema, similar to Vacinia A39"
/codon_start=1
/evidence=not_experimental
/product="semaphorin homolog"
/protein_id="AAC58054.1"
/db_xref="GI:2337970"
/translation="MAYLNATVSKPVISLSKVKLKEKCGEGCGLITFEVYIH
PAMGTLGVSRILMILSAITAAKSRFDKPLILVLDGFGQHRFEGPEPTVLEH
LSSSDVYVGANNITLIFDPFASSNASSTALINTSTHNTRLSTCENFETLLHNTD
GLIACCTNSOKSCPKLNNLTQFLGPKIGLAPSPSGNLVLPDONDRYSTNLKKS
LSGSKFRRIAGOVELYTSDTAMHRPQVQATVHKNESIDKITYFFEDNSIDTKO
PPIYVPRVQVCSDDGEGSSLSVYKWTFLKARLACVDYDGRITVNELODIEIWAP
ENSMETLILYGLFSPWNFSAVCFVAKDIDHYKTSKLNHHKLPTPFGCKMNH
OHVETPEQVADRYPEVADPVYQKNNAKPEIIOISKYITKILVRYEYGVEMATIEY
LMTIKGTHIYVREDSNSTALNILEINPEFOKPAIIONTILDNMTLKLIVNSEWVS
EYPLDLSYVGNDCFSCMSRDLCTWYNNTGSEKORVSEGGCPANRLTSEMGCHY
APVYVHQVSIPLSNSYISCPAVSHADYFTKDKGTEKRCVKYTKHKNDCTILLIANS
TTATNGTHVCNMKEDSVYKLVLEVNVTLM"
5590..5597
/note="ORF containing putative signal peptide: detected by
5'RACE-PCR"
/codon_start=1
/evidence=experimental
/product="A4"
/protein_id="AAC58055.1"
/db_xref="GI:2337971"
/translation="MYAOLYHNLITLISYITFEFNAAPLYEDDEEDNSREYVF
LBSDSQFPRRRNSCNCITREARITLLEALKRALQITAGINETDIBELTYPTMTT
PLETPTLDTSPVLPISAIP"
6123..6128
/evidence=not_experimental
6333..10442
/note="ORF03: similar to H. salmieri and EHV2 ORF3, similar
to ORF75"
/codon_start=1
/evidence=not_experimental
/product="tegument protein"
/protein_id="AAC58056.1"
/db_xref="GI:2337972"
/translation="MTRRELQALATTAESALETAAIALRSTPGLONYIOTQAYL
VTFSTPRPLREHQLKILETLFKALRTFDEQVYLPILSALSSSFTEYVGGDILRL
PQSQNELTAILOTRDAREKVFVNERIHOGRLLFFSGPGEQLONHAYLARILICGD
LTLQPFRENEFSSLDIFYATYPPRFLDKVRHYVAGDINLITGAASVYNNASPT
AVYDSEIFRIPTYHVVFIDRMEIRVVRPDVPGSGRVRROHGAAYVCSILNST
GATGCLQKGMTSFTISOPTLGOGLITPEPCCGGOELSATATOMLTKYANTVEATK
TUNYAGVPLVCGSVTISPTLRKRAMATGSSLSITSPYILKPTPRTETIDAMERRR
QULLEVGTPDTEGKLVHNPVNIIMNSESQHNAHILHQAALQMLTITPFGVYHICDM
QVNEKVTMKRIAAACGDLGISMARSILPAHTLRLKWNFRNLNYYNRILIKNSMLVD
SAALVYIADNEOVDSKMDIALSGMCEPHILGNLTSPNSNTIVISDKNOGEIYDI
QYKMHKQPSGEETEDTPIADMSNIQLEKNDLVETDILLQVLRHPTVSGKAHIVH
DRGNGHIAQPGVPEDTPIADGFSYVHNLVDGDI REGMESVPRVMAADWARYARLI
EROYSTPGDITDATALANNKGLTYHITPSEHQVYVESKKYGCIGIKETITFYORDPL
GITLAI VESCTNCLGPEVNYEFLIGLSISVEGTHYHREVSIMAMADFCSSMNF
GFQVNSAENGNCILRSVVAITANPCVVPGLSKPYFKKPGSAILRVNLHTHPLSGGI

polYA_signal
/evidence=not_experimental
11260..14643
/note="ORF06"
/codon_start=1
/evidence=not_experimental
/product="major ss DNA binding protein"
/protein_id="AAC58057.1"
/db_xref="GI:2337973"
/translation="MALKHQLNHVNEDNLGSKAPIGPCGFIYIYPETHFNKEISLIG
DKYAEAGAFSLPLHGVTEAEVNPVNAKAYKKIDMTVYEVKLSFTFNRAIIFHNNEK
FESIFSGPGISLCKEACDLFGVVPFPIGEGSDVSDICPVMOEKDALMAVYVTEG
FKRILHLGKIYIYAKSOMSHWIKTEYVRPLVDDELFTKSSLRILYIPAVEYLYX
TLYTSIAQSLRVHNAASLVBAIDQFPHDKYKAKLYSEFEYPLATYAGACDTLLMYID
AVAAELGLSYSLSEFEAPQETKVQDYYSMDIEASCEQSDRLAELASKMAQAIIH
AQLESTNSIYYVRRVARQAPIPNSKVEPNYSYVLOHGLANICEETLEFGSGPAPFG
APASLDSSEFTLOHLYAAAFSPNLAIRMCYVLOFCQHOXSTLNPAYNTIEVGSNA
NSPVGSLGSGCCPCVCIINTFLYFLKBFPPVLOGSRDPPVITGINVNEFLGAF
ASPRDDDEONQREPTRYMOTLNOTITREKILDAAGIYSDPDEACGSGCSNLEK
VRFPSIDSLVDABAAKFIYTMTRKNVNFRESIKGVSHYQVNCNTYQWPCSLMLL
YYSILITLITDIALPISVYESENPAGVKPNWMLKHQVLTQNTNERSFETIDGVTIG
TEMKVYAEQFSDPEVDATNNMYSFVQVVAROYLARVALANIKVKNRILFSGJPC
SEHYOAAFLKTARNDNYILAGYVKEFLVHQLPFLKISCLYLMSNFKKQJLSC
VPGVSAELNKFESYIINNSKOREVNMIDVPLDLYVYVYKORLNYAIIAACGOTOP
AVYHISFEPVQTCALIEYHVTCTGSSVDSVEVYVNNQALATLYNVSISRESANLA
RSRPITLPPVYVAKYTGIAQNAOLFQSANLCYMGKRCVQNLIGDSIFPKQOQNSYR
KKYLEMPLVGNLKLPSYTHQGAFFELVYKRIQSLLEQQAEDVYINRVYCGELVSL
GAGCADDITDDIOFLYSGYGMFSENILEKIDQILRELVPWTHEMAESVLGTCETDE
VQFAVEEEOVKLTSMDSGKVVGGKKRIATMFDDLL"
14725..16767
/note="ORF07"
/codon_start=1
/evidence=not_experimental
/product="transport protein"
/protein_id="AAC58058.1"
/db_xref="GI:2337974"
/translation="MGQYLAALYSQIYIGCLDVSIVGFCPTSLCTIKIADACNVYK
IHREVASLIDQNSLEKALSTELSHLEMLKRLFTYIHALDNPTYERKLSSVGL
CDLHKRLNVQFYNWEGILEVNLTLINDERLSLUNCVFCYSSSALLAKLEALTEFG
QLRGISVPRTDIYITSSSCLCEVLLETSVVPNGEVLNELLHNCHHLLVERVPEPI
KGLFESLONLGLKVHIAITDTIEQSVGKEHVAIOESLAYLAKATIENNPKOVLELSN
LLYWSGQONQSDSGVSKSELKIMSRENNLOKVRPLKNGDEPFGFEDLHSGOETL
LRGGIJSSTHDTITALKODCSNTPMKQRTLVYAKRONLIMRLSNITLYGEEYPRP
KOTESALKTCDQSDASKNOYLQEAELREKAYLNLKLSVSGEGRKIQACLSITHEMBNSOL
SLKTIWGSVYKQSAITLNLHFLFROSQWYQASLPSVSGSEQFENSKFISLSLYKSL
SREYLSLRLHFPALITVGLTTOEGLEFPSPPNVOLAHCLEAARHMPQKMLNEMIRP
TMPEODMCSNFENEFYIHTETDLNGVLEGCMKILRELVLVLAVALYNTIMEKNLIDYRD
HSCPTACSSGIGKGLVYVESHPVLIVYSNKKWIFKDIYVALLIYAHMQLANNGAHR"
15048..15053
/evidence=not_experimental
16751..19315
/note="ORF08: similar to EBV BALF4, CMV UL55, HSV UL27"
/codon_start=1
/evidence=not_experimental
/product="glycoprotein B"
/protein_id="AAC58059.1"
/db_xref="GI:2337975"
/translation="MAHTGSTVCAFLIFAVLKNVFCQPTSSSEVEDVIDEANTVSDN
IIRQQRNNTAKGJHSDSAPFPVCSASNGIDJFRQTSKSCPTKDKKENEGLILTF
KENIVYVFEVYKRIKIVTSTIYNGIYADAVNOHFSKSVIYETRRMDTYOCYN
SLVYTGAVNLVYTDNDGSMYTDIOPVDSLNSVRYHSHQPEITHAEPMGLIGYRBR
TYNCEYETEDAAYVPRFRITINIGDTIEMSPNKSANHETESGCPDPTLYVANDY
RVNDYKFRGQPGGHTRIPEVDEKLYTSMQOQRTNISYCSWAMKSDNATIKTEHGS
LHFVANDITASFTYPTMQRELVGKHVCLNNTIESELKSLRAVNDHSPNGAOYYLL

TNGCLLVWQPLVQOKLLDAKGLDAVKKQONTTITTTTSRRORSVSSGIDVYT
AESTILLTQIOFATDTLRAQIINNVLEELSRACREQHRASLMMNELSKINPTVWSSI
YGRPVSAKRIDVIVSHCVVVDQSVSLHRSRVPGDKTHECVSRPPVTFKFINDS
HLVKGGLGVNNEILLTTTAVEICHENTEHYFOGNNMYFYKNYRHVKTMPIGVATLD
TFVNLNLTLVNIDFOVLEYLSREKREKSTAFDIETMERREYNYTORVYGLRDLTDL
ATNRNPFVDARFSIMDDLGAVGKTYLVNAVSSVATLFFSIVSGIINFTKNPFGMLLFG
LIAAVITVITILLNKAKRFRFQNPVOMIYPDIKITTSORELOVDPISKHELDRIKILAM
HDYHASKOPESKODEQSGSTSGPADMLINKAKNVLRRAKITPLKRTDSFESTGVP"

polya_signal

CDS

/evidence=not_experimental
19314..19319
19428..22508
/note="ORF09; similar to EBV BALF5, CMV UL54, HSV UL30"
/codon_start=1
/evidence=not_experimental
/product="DNA Polymerase"
/protein_id="AAC58060.1"
/db_xref="GI:2337976"
/translation="MCCFFFSIQPCLEKLPPLPLKKNNTAMLSFWNPYLRGFKAPTP"

Query Match

0.1%; Score 21; DB 1; Length 130608;

Best Local Similarity 100.0%; Pred. No. 2.9;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 11042 CCTGATACGGGCCCCCTGAC 11062

Db 16290 CCTGATACGGGCCCCCTGAC 16310

Search completed: September 26, 2003, 12:28:56
Job time : 1258 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 30, 2003, 02:54:04 ; Search time 396 Seconds

(without alignments)
11960.308 Million cell updates/sec

Title: us-09-831-000-1
Perfect score: 14020
Sequence: 1 gcgaccgaagtcactaac.....cggcaccgcgcgacatct 14020

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 189188 seqs, 168911627 residues

Word size : 0

Total number of hits satisfying chosen parameters: 378376

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : gb_v1.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	14020	100.0	133719	1 AF083501	AF083501 Macaca mu
2	7651	54.6	130733	1 AF210726	AF210726 Macaca mu
3	172	1.2	130733	1 AF210726	AF210726 Macaca mu
4	20	0.1	2007	1 CHV1GC	249225 Caprine her
5	20	0.1	5077	1 KSU82242	082242 Kaposi's sa
6	20	0.1	6671	1 AY189899	AY189899 Pseudorab
7	20	0.1	8481	1 KSU40384	U40384 Kaposi's sa
8	20	0.1	28559	1 AF148805	AF148805 Kaposi's
9	20	0.1	133661	1 U93872	U93872 Kaposi's sa
10	20	0.1	137508	1 KSU75698	U75698 Kaposi's sa
11	20	0.1	184427	1 EHVU20824	U20824 Equine herp
12	19	0.1	165	1 AH002374S1	K00659 Middelburg
13	19	0.1	824	1 AF251159	AF251159 Human her
14	19	0.1	947	1 AF251158	AF251158 Human her
15	19	0.1	1213	1 HSL1S81	K01836 HSV-1 (stra
16	19	0.1	1303	1 HEHPSV	V00460 Fragment fr
17	19	0.1	1303	1 HSL1SFA	J02223 HSV-1 (stra
18	19	0.1	1346	1 HSL1CP345B	M33700 Herpes simp
19	19	0.1	1367	1 HSL1CP345C	M33701 Herpes simp
20	19	0.1	1399	1 HSL1CP345A	M33659 Herpes simp
21	19	0.1	1794	1 HSL1CP345A	K01835 HSV-1 (stra
22	19	0.1	1794	1 HSL1CP345A	M12240 Herpes simp
23	19	0.1	2038	1 AF015716	AF015716 Alfalfa m
24	19	0.1	2038	1 AF015717	AF015717 Alfalfa m
25	19	0.1	2121	1 BHV4GH	Z79653 Bovine herp
26	19	0.1	3008	1 AF359760	AF359760 Buffalo h
27	19	0.1	3113	1 AF078726	AF078726 Bovine he
28	19	0.1	5175	1 CP6VTC47	X79773 Cydia pomon
29	19	0.1	7919	1 HPV10	Z74465 Human papil
30	19	0.1	30000	1 BHV130KB	Z48053 Bovine herp
31	19	0.1	35450	1 SV1344259	AJ344259 Sullolodu
32	19	0.1	106873	1 AB096160	AB096160 Cercopit
33	19	0.1	108873	1 AF318573	AF318573 Bovine he

C	34	19	0.1	135301	1 BHV1CGEN	AJ004801 Bovine he
C	35	19	0.1	144575	1 YD1293568	AJ293568 Yaba-like
C	36	19	0.1	152261	1 HE1CG	X14112 Human herpe
C	37	19	0.1	152261	1 HE1CG	X14112 Human herpe
C	38	19	0.1	156789	1 AF533768	AF533768 Cercopit
C	39	19	0.1	232392	1 AF250284	AF250284 Amsacta m
C	40	18	0.1	780	1 HSE1E1	M30497 Equine herp
C	41	18	0.1	824	1 AF251159	AF251159 Human her
C	42	18	0.1	947	1 AF251158	AF251158 Human her
C	43	18	0.1	1047	1 KSU52065	U52065 Kaposi's sa
C	44	18	0.1	1175	1 AF347327	AF347327 HIV-1 iso
C	45	18	0.1	1346	1 HSL1CP345B	M33700 Herpes simp

ALIGNMENTS

RESULT 1	AF083501	133719 bp	DNA	linear	VRL 26-JUN-2000
LOCUS	AF083501				
DEFINITION	Macaca mulatta rhadinovirus 17577, complete genome.				
ACCESSION	AF083501.3	GI:8714565			
VERSION					
KEYWORDS					
SOURCE					
ORGANISM	Macaca mulatta rhadinovirus 17577				
	Viruses; dsDNA viruses, no RNA stage; Herpesviridae; Gammaherpesvirinae; Rhadinovirus.				
REFERENCE	1 (bases 1 to 133719)				
AUTHORS	Searles,R.P., Bergquam,E.P., Axthelm,M.K. and Wong,S.W.				
TITLE	Sequence and genomic analysis of a Rhesus macaque rhadinovirus with similarity to Kaposi's sarcoma-associated herpesvirus/human herpesvirus 8				
JOURNAL	J. Virol. 73 (4), 3040-3053 (1999)				
MEDLINE	99174001				
PUBMED	10074154				
REFERENCE	2 (bases 1 to 133719)				
AUTHORS	Searles,R.P., Bergquam,E.P., Axthelm,M.K. and Wong,S.W.				
TITLE	Direct Submision				
JOURNAL	Submitted (11-AUG-1998) Division of Pathobiology and Immunology, Oregon Health Sciences University/ Oregon Regional Primate Research Center, 505 NW 185th Avenue, Beaverton, OR 97006, USA				
REFERENCE	3 (bases 1 to 133719)				
AUTHORS	Searles,R.P., Bergquam,E.P., Axthelm,M.K. and Wong,S.W.				
TITLE	Direct Submision				
JOURNAL	Submitted (16-JUL-1999) Division of Pathobiology and Immunology, Oregon Health Sciences University/ Oregon Regional Primate Research Center, 505 NW 185th Avenue, Beaverton, OR 97006, USA				
REFERENCE	4 (bases 1 to 133719)				
AUTHORS	Searles,R.P., Bergquam,E.P., Axthelm,M.K. and Wong,S.W.				
TITLE	Direct Submision				
JOURNAL	Submitted (26-JUN-2000) Division of Pathobiology and Immunology, Oregon Health Sciences University/ Oregon Regional Primate Research Center, 505 NW 185th Avenue, Beaverton, OR 97006, USA				
REMARK	Sequence update by submitter				
COMMENT	On Jun 26, 2000 this sequence version replaced gi:5508840.				
FEATURES	location/Qualifiers				
source	1..133719				
	/organism="Macaca mulatta rhadinovirus 17577"				
	/mol_type="genomic DNA"				
	/db_xref="taxon:83534"				
	1..840				
	/note="partial terminal repeat"				
	1353..2624				
CDS	/codon_start=1				
	/product="R1"				
	/protein_id="AAD21330.1"				
	/db_xref="GI:4494908"				
	/translation="MPVIVLFIQGVSELLPAKITSVTPWCPHPCDPIYLLTCGCTSTRDORSTQWFRNNNTLMKGSNFTGLVSTVPARTISDRACOTKTTTSSNIDFRYSSSRLTLQERCSSGYVYANNRYLRVLCVSGGNVTLRVNCHLNGTAIVINCSTNIHFVLTKEITGTYFCFSAFIGNKEKYSQITINVFSTFSEFKPTNDIPNESHKNTGQIDOOTASY				

CDS

OHPENVYVESVPISIGVLTGIAISLMCWLTTRCNENSSSTNSASTSYQPSH
NQRNSTNECSRRRTYRNAQESIEELPQHTSEDSQCLVLEKNVAYGQPEMTI
NEWEQDDVYVKNIEQTSYEDNEHMDYDPTINPNFYSGLLILEEVEVEYNELEN
QYHGLILENDHNEYNHNLNEMTEQDWLE"

complement (2692...3258)

/note="orf 2: similar to kaposi's sarcoma-associated
herpesvirus orf 2"

/codon_start=1

/product="dihydrofolate reductase"

/protein_id="AAD21331.1"

/db_xref="GI:4494909"

/translation="MDITVNCIVAVDEQIGKNGTNPMPILRNEMMYEOKTGNPSV
VGEKNVIMGRMTFSIPEKKRPLVNRNITLSRELREPPGHAFIATLDDAENFR
OYKLKEDLNATWAVIGKSVESVNLNKCPLKLYITRLNESDCDFEPSINFTXTML
SEIQRKDNFEENGIRKRYFOYKFNFK"

3676...5613

CDS

/note="orf 4: similar to kaposi's sarcoma-associated
herpesvirus orf 4"

/codon_start=1

/product="complement binding protein"

/protein_id="AAD21332.1"

/db_xref="GI:4494910"

CDS

/translation="MTKLFPLFLHAIMYHCDECKPHEFTEHYKSNTEKDYV
GETAEILCRBGVYNTKLTITEGCLONGTWSPTNPPCDKRCPTADILNGVHJGSD
NALKRSNITSECBGDLIGSNRRCILODTENVNDSNPVCEIOKICITPRAYERG
DILPNODYNTGDAITFKCSLYTLVGSITLVGTSNKNWSNFPCLMLVCSFOIDN
GYIDIGSRNRYNGHOSITVCKSDGYNITVGPETLICTNKNWNPBPKCLVNSPOTM
PETMPEPTPYDQYKINLSTAKATTPNAFTVAVSPKEDVTCVKPKFEFENKAEN
DKERYSVASVELICRPGFTKQSTVSEVCSNTPWPNAKCHGKCPTEQLLNGE
YIVTSGEDAFYGTNITIKYKNEGQILGSMWIRICMDKLTIDVMEPAPICDIIECK
PPROITNGKYHPKDFYOXLDPTWPFSCNRDSILVDEMTICISNMPKPPRCQITC
SAPNIAHGKLTIGSSVYKIGOSTVIGETGTFILGSEITGCKDSSMDPILTPAV
SMPDTPKPEFKKNTPTPEAPKNTPNVGTHTPEKPPPNPPIAPPMKMKRHVVLV
LEASVASLFLVLAALYCCFLK"

6045...9443

CDS

/note="orf 6: similar to kaposi's sarcoma-associated
herpesvirus orf 6"

/codon_start=1

/product="ssDNA binding protein"

/protein_id="AAD21333.1"

/db_xref="GI:4494911"

CDS

/translation="MASKGNAGOLEDNQSGRAPITGACGYVAVSKODPPPAASITLG
NRPSGSGVFSLPIIXGLTVEHEPPLTYAAKKVDTITLAKQVCFHREYVFNHSL
FRVYDGTGLNEICEBARALFGYTQFIIEBPBHSIWNLECPQLEPKDEMFLGVAYTE
GKEERLMWGCILPAPVFTQVOVIAQROAFKVLVDEDLFAPGHMPEFYKIDVAYLE
YDSLFTSIQALRLKDYAVIHATEKQFMQHYKIAKIVQAKQFSTLPTKTTDSSHM
IVDSVAELIATYSCMFLECPQDACELNYDSMPILFDCDSPEARVNALEMSAEQAV
HVAQGLFAANSVLVLTQVQKQAPRGOKGDVWVNSPFLQHGLFNLNKAITIKENSSEAF
KCVSNALDSSFTPYHLAVASFSPHILALCYMORLOHKSSTNAENMYHYVCT
AANSEKTLCHGNTPATCLNLTLYRLKDRFPAVTPPORRDEYVVTGTAGITNDLEITLG
NEASFRRDEEDGNPADEHPKTYWQLCQTVTEKLSAIGITEDHNDHVALITNIOSELR
VFKGIDSIVDEVCYKFNWSMKNFNEFEHVSYHILIOFCCNYMQAPCFANLYY
KSLMTIODICLPCMIYEODNPMAGLISEMLKMHFOTLMTNFKAAOLDGVLGCE
LKIVHDMFCDFPDNDAGSNGMLAPKMKOVLARAMVVPKSIKNNITISNTAGSE
AVQSGVFKPTGTRDTPYVYAGPYMKFENSLHMLPDDTALYIMHKISQCNKPYLK
DVPEDELAELVSYKNSLAFETNLDVVPDSASTARIKLNGALILACQOTPYAT
RLHCLTVLQITIDAEYEPHYGSAIAIPAYLAIEIRGRIALYQTARQVAAATGRL
PVLTVPMVWYKTYGVNGNNVNFHCGNLGYPAGRGVGNRLNPPESPEFKTSLMLRK
RHVMATPIILIRKRAQOITSTFEAESKRSYQALLKEDKDNPLKSVILELIRLHG
KGCODLSEDOYVILGYCMYLDVLTIDNINIOSGVPTIEDAGALIEDQDADDDQ
PVSDDIATASQCPREQLPPPSAGALLAGKKRIINALSLDLD"

9468...11528

CDS

/note="orf 7: similar to kaposi's sarcoma-associated
herpesvirus orf 7"

/codon_start=1

/product="transport protein"

/protein_id="AAD21334.1"

/db_xref="GI:4494912"

/translation="MARELALVLAQLSALAVDSLVIIFADRSIDGARILTKTQIEN
LNRDLPLAREONSVEVTSLSLEVEHLAKNIEDLIGELERSLRQSSREHFETLHR
PECHSVTVFOFGGLIDVNMCLINDVELLCRLGSLFVCICANENALSINLRF
LSTLRGISPIHPPLVYTVPCVOCLEIETELIYVPOGSSILAVIADRHCDHCKRYRAE
PIHGFETELISQLGLKTKRSDATQHGVRSSADOLRESSLAAIODHNIFKRVASIME

CDS

/note="orf 8: similar to kaposi's sarcoma-associated
herpesvirus orf 8"

/codon_start=1

/product="glycoprotein B"

/protein_id="AAD21335.1"

/db_xref="GI:4494913"

CDS

/translation="MTITNRTRLRLRAVWVILIAIGTAVGENVTTPKGATITAKPTPGP
STPPPEPNPRAEAFKFPVCSASATGELFRNLKCTCGPTGDTHOELIMWFKNIV
PHIKRVRYRKVATSVTRYRGWTEFAVAKQREVRAPQVYINIMDITQOCSFSSRN
VNGIVNTYTTDDPTNQYVFIQDVPBGLDNDIQRYSOPLYTTPTGMPFGIYVPTVNC
EIVMILARSAPYSYFYVALGDIVEVSPFCHNDSTCSVAEKTENGGLARVLTNTIYD
PATROPPTETREVFADSGEYIVSMKAEDEKSAVCALITLKTPEPRAIQTHESYHFVAN
DVATATFSPLSQVNTNFTGYPCILNDVLOKTLNATIKLSDHANGSBOYEETEGLE
LLMOPILFSLADMERLNGTTPAPPTTSTANVRSGVNGEATDIDLAPQOFAY
DKLRASINKVLEELSRAMCREQVADVTWVWLESLNPTSVMTAIGRPVSKAFQGDAL
SVTQCVANDQASVSIHKSIRTPSGICYSRPVTPERPLNSTFLFKGOLGPNELIIND
NOVEACKTCHITFASVNTYITVDYFVKIKINTSEISTGTFALNLSPTENDFRY
IELVSRAEKKISGVFDEIEMFERENYTYQSLAGREDLDTIDLNRDLARLDEIY
ADLDQGVTVNVAVSITLPGSIVGEINIKIPFGGMALILVAVVILVFLNLR
TNALQAQAFIRMIYDIDMKQPSGVQDQIKNIIAGMHQLOQEERRLDEOQRSAPS
LFRASDRLKRRFRGKPLENEAEQVEMSK"

14132...17166

CDS

/note="orf 9: similar to kaposi's sarcoma-associated
herpesvirus orf 9"

/codon_start=1

/product="DNA polymerase"

/protein_id="AAD21336.1"

/db_xref="GI:4494914"

CDS

/translation="MDFFNPYLGRGRGPRPHSRGTDAIPAPGACAVOPPPVCLIPA
CLTRPGAGGMIPVITPEPPTYFENGARQDVILLANRSKWTAIDKRPVAPDQDOSTIF
HAYDVVETTYADARCAEVSRRQDIDIFSGVTLKLGTEGDSVAVNFQOQVFA
KVPAGINVTYTHILOQALKNATAGRAACGSTRVNRRIKITYVABHPVETILSGSML
STLSDRLVACGSESVNDAVRREVLHDHGTGTTGWSACAPATRLAADRTALFED
CSMEDLSVOADRSDMPRYRIARVIECGEGAPGPRGCAVAVIOSVETFTGEGAP
NPPIILSVGTCDDIPIDTVLEPFESEDMALVSFFAMIRDEPVDLTGICNINPDLPL
ITRLASQVNLNLENTYKIKTGSIEVEHPPRGGGGFMKSVKIKIAGIVPIDMVOCR
EKLISLSDKIDTAPROCIGKKEVYSKDIPLRSGGGAKNKSYCVMSVYLMVL
LKMMIHVEISEIARIKIAQARVLTDGOQLRVSCLLEAARENFILPPTPGQGG
YOGATVINPIGTGFDEPVLAVPFLSVPSISOAHNLCSLIMHRDLHNLNPPDY
ETTVLSGPMVHFVKKHRESLIGLLTWTLEKRRARIPTTLAACDDPSIKTILDOOLA
IKVGNNAVYGTGASGILPCINIAEYTLGKRMLEBSKSYVALTIEDRTNLRGREG
VTARHGAERFVYDQDSLFTACQGSYSAVASARCDILAKITADLPPLILKLEKTI
FKCLLLTKRKYIVLNLNDKMMWGMGVDLIRKTACKFVQERARILDLVLPILPEKAA
RLCKLRPHAYEGEILPAGFKIYEIVNLASLIDRNSVPIPEQJLTFSELSRPLCDYK
TTNPLHAYVQKLSRCEELPOVDRIRPYVVDVAGSLKSDLAHPDVVRQHQIPVAV
DIVPDKVLHGALNLOCLCFGNMATTVALILNPLNVPKLES"

17261...18511

CDS

/note="orf 10: similar to kaposi's sarcoma-associated
herpesvirus orf 10"

/codon_start=1

/product="unknown"

/protein_id="unknwn"

/db_xref="GI:4494915"

CDS

/translation="MLVNELSVLGDMEVTFHGRFSEFVNITRLQTEKGGIGYVRVL
PESLDLOHFAFGLVYRLKELPFSPSCVALLVLDGSGADARAARVAGVLLDSRP
LTVWNASGRHTIFRCLFLKPIDLERLAVYVPEENGARREGTGPCKPACASLDPGP
LRVSGEASQTSFHSFVAVPEPTANSVACSLIRVAVDPSDAARDAISRKYTFSN
SGGNVCASAVHTLSPSRCKTAMQEMETIYAGPNAEIVYGSDAARVAPLPTHTGGVGYVA
DAEKTIQGSSAEVRYOLITPOGGAARBDLAFVYTGVAPEPLFVYTRALLSGCTTHL
RLFNPNNGPTTIKRDITVAAAPCPVRLSSADAPRDLVAVSPULGALNSTAFTIPVG
PPGVVASACHEDLNDNGHERMNH"

18520...19749

CDS

/note="orf 11: similar to kaposi's sarcoma-associated
herpesvirus orf 11"

Query Match 100.0%; Score 14020; DB 1; Length 133719;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 14020; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 119700 GCGACGGAAGTCCACTACACCGCTTATGCGGAAACATGGGTCGGGCGCTGCCGAC 119759
|||
Db 119700 GCGACGGAAGTCCACTACACCGCTTATGCGGAAACATGGGTCGGGCGCTGCCGAC 119759
|||
QY 119760 ACCCTCTTCTACCTACTAGACGCTTGTAAATACGACGAAACCGGGGGCTTACTTA 119819
|||
Db 119760 ACCCTCTTCTACTACTAGACGCTTGTAAATACGACGAAACCGGGGGCTTACTTA 119819
|||
QY 119820 AATGTGCTTCTGCTCAAAATTCGCCGAAGGTGGCAACCGACTGCGCGCGCCGCA 119879
|||
Db 119820 AATGTGCTTCTGCTCAAAATTCGCCGAAGGTGGCAACCGACTGCGCGCGCCGCA 119879
|||
QY 119880 GGGTTGCGGCGCAAAACGCGCGCTCCGCCAATCTGGCGGAGCGCGCAC 119939
|||
Db 119880 GGGTTGCGGCGCAAAACGCGCGCTCCGCCAATCTGGCGGAGCGCGCAC 119939
|||
QY 119940 CGAGGCTAAACAGCGGCGGCGCGCCACAGGGAAGGCGGCGCGGCGGCGG 119999
|||
Db 119940 CGAGGCTAAACAGCGGCGGCGCGCCACAGGGAAGGCGGCGGCGGCGGCGG 119999
|||
QY 120000 GGTTCAGATGGCTTTGTGAACAGACTCCACACTGGCTGTGAAGGGCAAGAGTGTCT 120059
|||
Db 120000 GGTTCAGATGGCTTTGTGAACAGACTCCACACTGGCTGTGAAGGGCAAGAGTGTCT 120059
|||
QY 120060 CTTTGTGTAAGCCGCTTTTAAACAGGGTGGGCGCGGATGGCTGCTTGTGTAAGCGGCT 120119
|||
Db 120060 CTTTGTGTAAGCCGCTTTTAAACAGGGTGGGCGCGGATGGCTGCTTGTGTAAGCGGCT 120119
|||
QY 120120 CTAGTTTCCACCTTAAAGCCTTAAAGATTGATTTTCCCTGTTACAGTAATTCGCGACGG 120179
|||
Db 120120 CTAGTTTCCACCTTAAAGCCTTAAAGATTGATTTTCCCTGTTACAGTAATTCGCGACGG 120179
|||
QY 120180 AAAAATCTCCGCGCGGCAAAAGCATAAAAAGCGGCTTGAAGAGATTAGTCTCTAA 120239
|||
Db 120180 AAAAATCTCCGCGCGGCAAAAGCATAAAAAGCGGCTTGAAGAGATTAGTCTCTAA 120239
|||
QY 120240 TCTTGGCGGCTAAATAATAGCAGGCGGCGCGGCTCTTAAGCCGCGGAGGATGTC 120299
|||
Db 120240 TCTTGGCGGCTAAATAATAGCAGGCGGCGGCGGCTCTTAAGCCGCGGAGGATGTC 120299
|||
QY 120300 TGGGACACTCTAGATAGCGATTCAGATTAATAAGGCGGCAAGTGGGAAAGCCTAGCATCG 120359
|||
Db 120300 TGGGACACTCTAGATAGCGATTCAGATTAATAAGGCGGCAAGTGGGAAAGCCTAGCATCG 120359
|||
QY 120360 CCTGTGGGCGCTGGCAACAGACCGATCCAGCTCCCAAGATTAAGTCCGATGCCACCG 120419
|||
Db 120360 CCTGTGGGCGCTGGCAACAGACCGATCCAGCTCCCAAGATTAAGTCCGATGCCACCG 120419
|||
QY 120420 TCACCTCCGTTTGTATGTCCTTACAGAGCGCGTGGATGTTACAAAGAGCGCTTCTGTTG 120479
|||
Db 120420 TCACCTCCGTTTGTATGTCCTTACAGAGCGCGTGGATGTTACAAAGAGCGCTTCTGTTG 120479
|||
QY 120480 CCAAGAGGTTAGAGAGGCGCGGCTGCTGATACAGAGCGGGGTCAATGGTCCCGTGGGCA 120539
|||
Db 120480 CCAAGAGGTTAGAGAGGCGCGGCTGCTGATACAGAGCGGGGTCAATGGTCCCGTGGGCA 120539
|||
QY 120540 CTGGGCGCAACAGAGCATTTGTCAAGGCAAGGTAAAGAAAGCATATTAATCTTACTGTC 120599
|||
Db 120540 CTGGGCGCAACAGAGCATTTGTCAAGGCAAGGTAAAGAAAGCATATTAATCTTACTGTC 120599
|||
QY 120600 GGTCTCAGGAGGCTTAAATAGAAAGCTCGGCTTAAACACAAATCTTCTTGGCCTATAG 120659
|||
Db 120600 GGTCTCAGGAGGCTTAAATAGAAAGCTCGGCTTAAACACAAATCTTCTTGGCCTATAG 120659
|||
QY 120660 TCCGCTCCACACATGGTCCCATGCTTCTGAGTTACGCGCTGTTCCCGGAAAGCGG 120719
|||
Db 120660 TCCGCTCCACACATGGTCCCATGCTTCTGAGTTACGCGCTGTTCCCGGAAAGCGG 120719
|||

QY 120720 CGGACTAGATGCAACGCGGAAGCGGCTGTTCAATTTAAAGTAGTACAGGCGGGGCAATT 120779
|||
Db 120720 CGGACTAGATGCAACGCGGAAGCGGCTGTTCAATTTAAAGTAGTACAGGCGGGGCAATT 120779
|||
QY 120780 TGGCAACCAATGACGCGTTTCCCTGCACTCTGGGTTTACCTGGCAAGCGCCACTGGTTC 120839
|||
Db 120780 TGGCAACCAATGACGCGTTTCCCTGCACTCTGGGTTTACCTGGCAAGCGCCACTGGTTC 120839
|||
QY 120840 TTGGCAAGCGCGGCTGGGAGTATTTTAACTGGAATTTGGCAATCTCTGTCATCGCG 120899
|||
Db 120840 TTGGCAAGCGCGGCTGGGAGTATTTTAACTGGAATTTGGCAATCTCTGTCATCGCG 120899
|||
QY 120900 ACTATGCTGCGCTGGAAGTGGGGGCGGATGGGTGATGTGTTCCACGCGGACGGGCC 120959
|||
Db 120900 ACTATGCTGCGCTGGAAGTGGGGGCGGATGGGTGATGTGTTCCACGCGGACGGGCC 120959
|||
QY 120960 TTTTTCAGGCGCTTGGCGGTTTCCCGGCGCTTGAACAGAACCGGTAAATGCAAAAAGCCGG 121019
|||
Db 120960 TTTTTCAGGCGCTTGGCGGTTTCCCGGCGCTTGAACAGAACCGGTAAATGCAAAAAGCCGG 121019
|||
QY 121020 ATGACGGACTGCGCAGGTGCGTCGCGCAAAACGCGGCGGCTGATGCTTAATGCGGGGA 121079
|||
Db 121020 ATGACGGACTGCGCAGGTGCGTCGCGCAAAACGCGGCGGCTGATGCTTAATGCGGGGA 121079
|||
QY 121080 AACTGTAGGACCTTGGCCAGGCGATACAGTGAATAGGGGTCTGAGTTACAAAAGATGACT 121139
|||
Db 121080 AACTGTAGGACCTTGGCCAGGCGATACAGTGAATAGGGGTCTGAGTTACAAAAGATGACT 121139
|||
QY 121140 CCGTGACACCAAGGCGCGCGCGGCGGAGGGGTCGATCTGGGTCCCAATACCTGACGATTA 121199
|||
Db 121140 CCGTGACACCAAGGCGCGCGCGGCGGAGGGGTCGATCTGGGTCCCAATACCTGACGATTA 121199
|||
QY 121200 AATCTTCTCTGTGGGCGGATTTTCTGAGTACCTCTCTGATGAGGATACGATATG 121259
|||
Db 121200 AATCTTCTCTGTGGGCGGATTTTCTGAGTACCTCTCTGATGAGGATACGATATG 121259
|||
QY 121260 GGAATGGGATATGCGGCGGCGCGGCGGCGGCGGCGGCGGCGGCTGCTGCTGCGCG 121319
|||
Db 121260 GGAATGGGATATGCGGCGGCGCGGCGGCGGCGGCGGCGGCGGCTGCTGCTGCGCG 121319
|||
QY 121320 TCTTCCCGCTTGTCTCTCTTGTGCTTCAAGAGCTTCTGCTGATGAGGATATGATCTC 121379
|||
Db 121320 TCTTCCCGCTTGTCTCTCTTGTGCTTCAAGAGCTTCTGCTGATGAGGATATGATCTC 121379
|||
QY 121380 GTGCATCTGAGACGTAAACAAGAACTCTCCGCGACGCGTGGTGGACCCCAACCCCT 121439
|||
Db 121380 GTGCATCTGAGACGTAAACAAGAACTCTCCGCGACGCGTGGTGGACCCCAACCCCT 121439
|||
QY 121440 ACGGTGTACAGTGGGATGTATGGCCAGAAACGCGGCTCTGGCCAGACGCGCCGCTG 121499
|||
Db 121440 ACGGTGTACAGTGGGATGTATGGCCAGAAACGCGGCTCTGGCCAGACGCGCCGCTG 121499
|||
QY 121500 GGGTGTCTGTGTGGCTCACCGCTGTTGGCTGTTAGGGGATGGGGCTGTTAGGGCTT 121559
|||
Db 121500 GGGTGTCTGTGTGGCTCACCGCTGTTGGCTGTTAGGGGATGGGGCTGTTAGGGCTT 121559
|||
QY 121560 GGGGATTTGGGCTGCCCGGTGAGTGGGCGGGGATTTGCCGAGGGGCGAGGAGCTGGCG 121619
|||
Db 121560 GGGGATTTGGGCTGCCCGGTGAGTGGGCGGGGATTTGCCGAGGGGCGAGGAGCTGGCG 121619
|||
QY 121620 GTTGGCGATTTGGGCGGTTCCAGGTGATTCGGAGGGGGCAAGAGCGTCCGAGGCTCAGGC 121679
|||
Db 121620 GTTGGCGATTTGGGCGGTTCCAGGTGATTCGGAGGGGGCAAGAGCGTCCGAGGCTCAGGC 121679
|||
QY 121680 GGTTCAGGTAGTGTGCTGCTGATGTTGCAAAAACAGCAAGGCTTCTGATTTGGCGGAT 121739
|||
Db 121680 GGTTCAGGTAGTGTGCTGCTGATGTTGCAAAAACAGCAAGGCTTCTGATTTGGCGGAT 121739
|||
QY 121740 GGAATTAAGCAGCAGCGCGGCTGAGTGGGCGGCGGCGGCTGAGGCGGCGGCGGATG 121799
|||
Db 121740 GGAATTAAGCAGCAGCGCGGCTGAGTGGGCGGCGGCGGCTGAGGCGGCGGCGGATG 121799
|||
QY 121800 GGGGCGCAATGCGATGGCGGGGATGCGCGGGAGCACCTGACGTGTTTGAAGTGACAGG 121859
|||

Db	121800	GGGGGCGATGCGATGCGGGGAGTGC	GGGGGAGACCCCTGACGTCTTTGAGTACAGG	121859	
Oy	121860	CCTGAGCTAACACCCGGGCGAGACCCG	CTTGGAGATCCGAACAGATG	121919	
Db	121860	CCTGAGCTAACACCCGGGCGAGACCCG	CTTGGAGATCCGAACAGATG	121919	
Oy	121920	ACGCACTAGACCCCTGATGATGCGACCC	TTG6GATGACCCGCTGATTCGGTG	121979	
Db	121920	ACGCACTAGACCCCTGATGATGCGACCC	TTG6GATGACCCGCTGATTCGGTG	121979	
Oy	121980	GCCGTTGCGTGCATCCGCTGCTGTTCTG	CAACCGCCGACCTTGGGGCCCTGAT	122039	
Db	121980	GCCGTTGCGTGCATCCGCTGCTGTTCTG	CAACCGCCGACCTTGGGGCCCTGAT	122039	
Oy	122040	GTTGTTGAGCGGGGGGCGGAGTGGCGG	CTGGCGCGCTGACAGCCGCCCTTGCG	122099	
Db	122040	GTTGTTGAGCGGGGGGCGGAGTGGCGG	CTGGCGCGCTGACAGCCGCCCTTGCG	122099	
Oy	122100	CGCCTCCCGGCTGTTCTCTAGTGC	CGCGCTCTCCGCAATGTCCTCGAGCACTT	122159	
Db	122100	CGCCTCCCGGCTGTTCTCTAGTGC	CGCGCTCTCCGCAATGTCCTCGAGCACTT	122159	
Oy	122160	CGCAACCCGTGCTCCGATACATAGCGG	AGAGATGTGCGGCTGCCACATGTTGCGG	122219	
Db	122160	CGCAACCCGTGCTCCGATACATAGCGG	AGAGATGTGCGGCTGCCACATGTTGCGG	122219	
Oy	122220	GTTTACTGCTGTAAAAAAGCGAGATT	AGTAGATTGCGCTTCCAGCAGCCGCA	122279	
Db	122220	GTTTACTGCTGTAAAAAAGCGAGATT	AGTAGATTGCGCTTCCAGCAGCCGCA	122279	
Oy	122280	CCTGAGCGCGCGCAGCAGAACCTAT	GTGAGATTGGGATATGCTCCGTAGTGG	122339	
Db	122280	CCTGAGCGCGCGCAGCAGAACCTAT	GTGAGATTGGGATATGCTCCGTAGTGG	122339	
Oy	122340	CGGCTATTGTGATTCCTCCGCGACG	ATTGAGTGGGCGAGAGCGCGTTAA	122399	
Db	122340	CGGCTATTGTGATTCCTCCGCGACG	ATTGAGTGGGCGAGAGCGCGTTAA	122399	
Oy	122400	CGCGAGCAGACCGCAGCGGGGTTT	AGTTAGTTAGTTAAATTCG	122459	
Db	122400	CGCGAGCAGACCGCAGCGGGGTTT	AGTTAGTTAGTTAAATTCG	122459	
Oy	122460	TGCGCGATTTGGTGGAGTGTAAAT	CAACCGCGCGCGCCCTTACCTGTGCG	122519	
Db	122460	TGCGCGATTTGGTGGAGTGTAAAT	CAACCGCGCGCGCCCTTACCTGTGCG	122519	
Oy	122520	CGCGAACCAGGAAAGTCTGTCGCG	CGCAGCGCGCGCGCTGCGAAACCAACGC	122579	
Db	122520	CGCGAACCAGGAAAGTCTGTCGCG	CGCAGCGCGCGCGCTGCGAAACCAACGC	122579	
Oy	122580	CGGCTGATTTGGTGGAGTGTAAAT	CAACCGCGCGCGCCCTTACCTGTGCG	122639	
Db	122580	CGGCTGATTTGGTGGAGTGTAAAT	CAACCGCGCGCGCCCTTACCTGTGCG	122639	
Oy	122640	TGCGCGTGGTGGTCAACCTGCTAA	CCGTAACCTGGAATTTCTGCGCCGCG	122699	
Db	122640	TGCGCGTGGTGGTCAACCTGCTAA	CCGTAACCTGGAATTTCTGCGCCGCG	122699	
Oy	122700	CGCGGAGCCGCGGCTTAACCTTAT	AGTGTGCGAGATCCTGAAACCTGAAACCT	122759	
Db	122700	CGCGGAGCCGCGGCTTAACCTTAT	AGTGTGCGAGATCCTGAAACCTGAAACCT	122759	
Oy	122760	GGCCATATTAACCCAGTATGCGT	GTGCGTGTGCAACCTTTTGAAAAAGATTTA	122819	
Db	122760	GGCCATATTAACCCAGTATGCGT	GTGCGTGTGCAACCTTTTGAAAAAGATTTA	122819	
Oy	122820	TTGCGCGCGGCTTTAAGCAGACAC	CGACCGTGTTCATTTAGTGGAGGAT	122879	
Db	122820	TTGCGCGCGGCTTTAAGCAGACAC	CGACCGTGTTCATTTAGTGGAGGAT	122879	
Oy	122880	TACATTACGCTGCTGCTGGGAGCG	CTTGCACGGTGGTGGCTCTTCAACGCACTA	122939	
Db	122880	TACATTACGCTGCTGCTGGGAGCG	CTTGCACGGTGGTGGCTCTTCAACGCACTA	122939	
Oy	122940	TGCGGCGTCCCGTGCACTCTAC	CGCGCTCCCTGGGCTGCTTTAACGACCCACGA	122999	
Db	122940	TGCGGCGTCCCGTGCACTCTAC	CGCGCTCCCTGGGCTGCTTTAACGACCCACGA	122999	
Oy	123000	CGTCTTATGCTTACCTGCAAAAAC	AGAAATCGCTAGTCCGCTTAACGCGGACATA	123059	
Db	123000	CGTCTTATGCTTACCTGCAAAAAC	AGAAATCGCTAGTCCGCTTAACGCGGACATA	123059	
Oy	123060	TAGTTCCGAAAGCGGCGAGTGT	TGACGCCCCGTTCCCGGTAAGGTTGACATCCGA	123119	
Db	123060	TAGTTCCGAAAGCGGCGAGTGT	TGACGCCCCGTTCCCGGTAAGGTTGACATCCGA	123119	
Oy	123120	ACACAAGTTGACACAGACAGAC	CCCTGATTTTATATGCAACCTTGAGAGAGAGGCTG	123179	
Db	123120	ACACAAGTTGACACAGACAGAC	CCCTGATTTTATATGCAACCTTGAGAGAGAGGCTG	123179	
Oy	123180	CTACCTGCTATCTTAACGGGTT	GGAGTGGGAAAGCTGTGCGGAGACGCGCTGCTGAC	123239	
Db	123180	CTACCTGCTATCTTAACGGGTT	GGAGTGGGAAAGCTGTGCGGAGACGCGCTGCTGAC	123239	
Oy	123240	GCTTACGCTCCCGTCCATGTCG	TACAGTTTACCCCGATTAACCCGACGACGCT	123299	
Db	123240	GCTTACGCTCCCGTCCATGTCG	TACAGTTTACCCCGATTAACCCGACGACGCT	123299	
Oy	123300	CGTCTGTGCGGCGGAGGCGAGT	CCCGACGCTGGTCACTGAGACGCGCGCTG	123359	
Db	123300	CGTCTGTGCGGCGGAGGCGAGT	CCCGACGCTGGTCACTGAGACGCGCGCTG	123359	
Oy	123360	GCTGTGACGCGCAACCTGAAAG	TTTCCCGGCGCAACGCAACCTGGTTGGGCTG	123419	
Db	123360	GCTGTGACGCGCAACCTGAAAG	TTTCCCGGCGCAACGCAACCTGGTTGGGCTG	123419	
Oy	123420	CTGCAACCTTAACGTCGTGAG	ACCCCGAAGACCTTGAGAACGCACTGCTGACTCA	123479	
Db	123420	CTGCAACCTTAACGTCGTGAG	ACCCCGAAGACCTTGAGAACGCACTGCTGACTCA	123479	
Oy	123480	TATAGCGGTTTGGCGCGCGCG	CGCCCTTGAGACCCCTGTTTGATGCCCTGGAAGG	123539	
Db	123480	TATAGCGGTTTGGCGCGCGCG	CGCCCTTGAGACCCCTGTTTGATGCCCTGGAAGG	123539	
Oy	123540	GACGAGCAGCTACGTTGGTGG	GTGGGAGTGGGCGAGCGCGCGCTTAAAGCATTTTAAAC	123599	
Db	123540	GACGAGCAGCTACGTTGGTGG	GTGGGAGTGGGCGAGCGCGCGCTTAAAGCATTTTAAAC	123599	
Oy	123600	GGGTGTTTTTTTGTATAGGT	ATGTGAGCGCGCTGCCCGTCTAGTGTGTTGT	123659	
Db	123600	GGGTGTTTTTTTGTATAGGT	ATGTGAGCGCGCTGCCCGTCTAGTGTGTTGT	123659	
Oy	123660	CCCCAGTAGTGTCTCCATG	ACAAATACAAATTTGAGGCTGCTTTTAAAGGTGCTTCT	123719	
Db	123660	CCCCAGTAGTGTCTCCATG	ACAAATACAAATTTGAGGCTGCTTTTAAAGGTGCTTCT	123719	
Oy	123720	TGTGCGAGGCTTCCGTATAC	GTGATACCGGGGTGTGCGCAGAGAAACCGCGTCCG	123779	
Db	123720	TGTGCGAGGCTTCCGTATAC	GTGATACCGGGGTGTGCGCAGAGAAACCGCGTCCG	123779	
Oy	123780	CTTTATGTCGCTCGCTCC	CCAGAGCAAAAGTGAATG	123839	
Db	123780	CTTTATGTCGCTCGCTCC	CCAGAGCAAAAGTGAATG	123839	
Oy	123840	TTGAGAGAGTGGGCGAGT	GTGCGGTAGCGGCTGTGCAAAAGGCTCACCCGCTCTGTTT	123899	
Db	123840	TTGAGAGAGTGGGCGAGT	GTGCGGTAGCGGCTGTGCAAAAGGCTCACCCGCTCTGTTT	123899	
Oy	123900	TTTTTCTTTTGTGACAAACAA	ATGAGAGCGCTTGAACATTAACCTGCTGATG	123959	
Db	123900	TTTTTCTTTTGTGACAAACAA	ATGAGAGCGCTTGAACATTAACCTGCTGATG	123959	
Oy	123960	GATTTTCTGTCTAATAT	TGCAATAGCTAGTATGAGCAGCAATATGCTTACACC	124019	
Db	123960	GATTTTCTGTCTAATAT	TGCAATAGCTAGTATGAGCAGCAATATGCTTACACC	124019	
Oy	123960	GATTTTCTGTCTAATAT	TGCAATAGCTAGTATGAGCAGCAATATGCTTACACC	124019	

OY	124020	TTAGACACGGAAATCCACCGCTGTGCGCTGACGGTGTTCCTCCACTACCGTTATGCG	124079
Db	124020	TTAGACACGGAAATCCACCGCTGTGCGCTGACGGTGTTCCTCCACTACCGTTATGCG	124079
OY	124080	ATTATATCCTTTTTTATTTTTGCAATTAACGGCTTTGGGAACCGGTGGCTATATAT	124139
Db	124080	ATTATATCCTTTTTTATTTTTGCAATTAACGGCTTTGGGAACCGGTGGCTATATAT	124139
OY	124140	TTTTTAAATTTAAAGCGCTCGCCAACTCTGAGATGTACTATGATGGCTGGTTGTGT	124199
Db	124140	TTTTTAAATTTAAAGCGCTCGCCAACTCTGAGATGTACTATGATGGCTGGTTGTGT	124199
OY	124200	AACATCCCTGTTCTGTGCGCGCTGTTTTTGTTCACGTGGCTGTACTCGCGCACAG	124259
Db	124200	AACATCCCTGTTCTGTGCGCGCTGTTTTTGTTCACGTGGCTGTACTCGCGCACAG	124259
OY	124260	ATGCTACAGCTCGCGACGGACGGATGGAAATCTTTTCTTACTGTACAGATCTT	124319
Db	124260	ATGCTACAGCTCGCGACGGACGGATGGAAATCTTTTCTTACTGTACAGATCTT	124319
OY	124320	GGCGGTACATTTGCTGTGATATCAGCCCTATCAGGTGGCTTATGTTGTGTTTCCGC	124379
Db	124320	GGCGGTACATTTGCTGTGATATCAGCCCTATCAGGTGGCTTATGTTGTGTTTCCGC	124379
OY	124380	CGCCCTGTGGTCAACACGGGGCCCTCCGCTTCTCTGCTGTGTGTCTTTAATCTG	124439
Db	124380	CGCCCTGTGGTCAACACGGGGCCCTCCGCTTCTCTGCTGTGTGTCTTTAATCTG	124439
OY	124440	GGCGTGGGCTGTCTGCGCAACCGGAGCCCTATAGAGGGCCCTGGCTACCCAGAGAC	124499
Db	124440	GGCGTGGGCTGTCTGCGCAACCGGAGCCCTATAGAGGGCCCTGGCTACCCAGAGAC	124499
OY	124500	AGCGAGTGGATATGCTTACGAAAGATCCGGGGAAAGATACCGTAACTGGAAGCTGAAATC	124559
Db	124500	AGCGAGTGGATATGCTTACGAAAGATCCGGGGAAAGATACCGTAACTGGAAGCTGAAATC	124559
OY	124560	AGAACACCAAGCGCATCTGCGGGTTTTTGTTCGGCTTGATGGTGTCTTTTAC	124619
Db	124560	AGAACACCAAGCGCATCTGCGGGTTTTTGTTCGGCTTGATGGTGTCTTTTAC	124619
OY	124620	GGACTTACGTGGTGTATGTTAAAGACAGAGCGGGCCAGAAAGGAGCCGTTAGGGGT	124679
Db	124620	GGACTTACGTGGTGTATGTTAAAGACAGAGCGGGCCAGAAAGGAGCCGTTAGGGGT	124679
OY	124680	GTAATTTGACAGCGTGTGGTGTCTGTTTTAATTTTTTGCCTGCCCTATACACGTGTCAC	124739
Db	124680	GTAATTTGACAGCGTGTGGTGTCTGTTTTAATTTTTTGCCTGCCCTATACACGTGTCAC	124739
OY	124740	TTTTTTGACACCCCTGTGAGACCGGGTTTTCTGGCCGAAAGCTGTACTCAGAGACGTG	124799
Db	124740	TTTTTTGACACCCCTGTGAGACCGGGTTTTCTGGCCGAAAGCTGTACTCAGAGACGTG	124799
OY	124800	ATCAGCGGGCCATGCATATAGTCCCGCTACAGAGCATGTATAGCCGTTCTGCGCA	124859
Db	124800	ATCAGCGGGCCATGCATATAGTCCCGCTACAGAGCATGTATAGCCGTTCTGCGCA	124859
OY	124860	GTCGTGTATCTGCTTGGGTCTCTGTTTAGAGAAAGGTTAGGGATACCTGTCCGTG	124919
Db	124860	GTCGTGTATCTGCTTGGGTCTCTGTTTAGAGAAAGGTTAGGGATACCTGTCCGTG	124919
OY	124920	TTTAGGTGTTTTCCACTTCAGGTAGTTTATAGACACTCAGCGCACTTGGTTGGATT	124979
Db	124920	TTTAGGTGTTTTCCACTTCAGGTAGTTTATAGACACTCAGCGCACTTGGTTGGATT	124979
OY	124980	GTTTGTGTACATTTATTTTCATTTTGTGTACATTTATTTTCATTTAAAGCATGTGACCTG	125039
Db	124980	GTTTGTGTACATTTATTTTCATTTTGTGTACATTTATTTTCATTTAAAGCATGTGACCTG	125039
OY	125040	CAGACCTTACCTGAGCTTACTGTCTGTTTCTTATGACACAGAGAAAGGACTGGAAG	125099
Db	125040	CAGACCTTACCTGAGCTTACTGTCTGTTTCTTATGACACAGAGAAAGGACTGGAAG	125099

QY	125100	GCCACGCCCCACGGGGAAA	CTCATGTGCCAAGCTCGGGGGCGCACGTACCCGCCACTCG	125115
Db	125100	GCCACGCCCCACGGGGAAA	CTCATGTGCCAAGCTCGGGGGCGCACGTACCCGCCACTCG	125115
QY	125160	CAGGGGTTGAAAGCTACAGCGCGGGGTCGACACAGGAGAGCCAGAGTGGGCGCCGTCGGGTGAC	125219	
Db	125160	CAGGGGTTGAAAGCTACAGCGCGGGGTCGACACAGGAGAGCCAGAGTGGGCGCCGTCGGGTGAC	125219	
QY	125220	GTGATGGCGGCCACGGCCGAGTTGGCAGACGGGTTGGCGGGGTAGTGTCTGCGCGAACAATC	125279	
Db	125220	GTGATGGCGGCCACGGCCGAGTTGGCAGACGGGTTGGCGGGGTAGTGTCTGCGCGAACAATC	125279	
QY	125280	CTCGGGGTGGCGCTTGCCTGTGTGTAGTTCAAGGCGCATCGCTGCTGTGTGTGTGAGATGG	125339	
Db	125280	CTCGGGGTGGCGCTTGCCTGTGTGTAGTTCAAGGCGCATCGCTGCTGTGTGTGTGAGATGG	125339	
QY	125340	TACTCATAGAGCTTCGGCGGGGATATCTACGCGCCAGGTACCGGCGCTTGGGCCACCTGGG	125399	
Db	125340	TACTCATAGAGCTTCGGCGGGGATATCTACGCGCCAGGTACCGGCGCTTGGGCCACCTGGG	125399	
QY	125400	AGGACGAGGCGCCCGAAGAACCTTAACATGATGCTGATGGTGTGGGGGATGTGTGAAG	125459	
Db	125400	AGGACGAGGCGCCCGAAGAACCTTAACATGATGCTGATGGTGTGGGGGATGTGTGAAG	125459	
QY	125460	TTTAAACCAGAGCACTCGTGTGTTCCTGATGCGCTTCTCCACAGTGTGATGTCCCACTGG	125519	
Db	125460	TTTAAACCAGAGCACTCGTGTGTTCCTGATGCGCTTCTCCACAGTGTGATGTCCCACTGG	125519	
QY	125520	TCGGGGGTTTGGGTTCGGGGCGGTGTCGTAGAGGGTCTCTTAAGAAGACCGAGCGCCCG	125579	
Db	125520	TCGGGGGTTTGGGTTCGGGGCGGTGTCGTAGAGGGTCTCTTAAGAAGACCGAGCGCCCG	125579	
QY	125580	AGGACCTGGAAACCCAAACTCCCGCGAGCACTAGTGAATAATGTATCCGCTGGCGGAAAG	125639	
Db	125580	AGGACCTGGAAACCCAAACTCCCGCGAGCACTAGTGAATAATGTATCCGCTGGCGGAAAG	125639	
QY	125640	GCCATPAAGCCCCCATATGACACCCAGGGTGTGTGAGAAGACCCATGATCGCGATCGGGCC	125699	
Db	125640	GCCATPAAGCCCCCATATGACACCCAGGGTGTGTGAGAAGACCCATGATCGCGATCGGGCC	125699	
QY	125700	CCCACGTAGCTGTCTTTCGATGGCCACGGTTCACAGATGGTCAGACCGGGAATCCCGGG	125759	
Db	125700	CCCACGTAGCTGTCTTTCGATGGCCACGGTTCACAGATGGTCAGACCGGGAATCCCGGG	125759	
QY	125760	AGGATGTTTCCCTCTCTTAAGTGTGTGTGAGAGACGGCGCGACGTGCAACCCGACGTTTG	125819	
Db	125760	AGGATGTTTCCCTCTCTCTTAAGTGTGTGTGAGAGACGGCGCGACGTGCAACCCGACGTTTG	125819	
QY	125820	GTGAAGCGCGCCATCATCGCGCCCTGGGAGCGGGGCGACCGGGGGTGAACAAAGCGCGCACT	125879	
Db	125820	GTGAAGCGCGCCATCATCGCGCCCTGGGAGCGGGGCGACCGGGGGTGAACAAAGCGCGCACT	125879	
QY	125880	GCTGGCGGCTGAGCGCGCTTGCATAAACAAGTCAAGTTCCTGTTTGTGCAAACTTGCGGG	125939	
Db	125880	GCTGGCGGCTGAGCGCGCTTGCATAAACAAGTCAAGTTCCTGTTTGTGCAAACTTGCGGG	125939	
QY	125940	AGTGGGCCAGAGTGTGTGTGTGTGACACCGGTAGTCTTTCGTGAGAGTTTCGTGCGGGCG	125999	
Db	125940	AGTGGGCCAGAGTGTGTGTGTGTGACACCGGTAGTCTTTCGTGAGAGTTTCGTGCGGGCG	125999	
QY	126000	GTGAAGCTGGGCCCCCATATGATACCACTGTTGCTCCGAAGAAGAGGTCCAGTTTGGCGCC	126059	
Db	126000	GTGAAGCTGGGCCCCCATATGATACCACTGTTGCTCCGAAGAAGAGGTCCAGTTTGGCGCC	126059	
QY	126060	ACCGAAGTGAAGGTCGTGAATAGACTTCATGCTGTTGTGTGAGATGACAGTCTTCTTC	126119	
Db	126060	ACCGAAGTGAAGGTCGTGAATAGACTTCATGCTGTTGTGTGAGATGACAGTCTTCTTC	126119	
QY	126120	GACAGACCTCTCTGACCCACAGGTGCGGACACAGGTGCGCGGAGTCAAAAGTTTGGCAC	126179	
Db	126120	GACAGACCTCTCTGACCCACAGGTGCGGACACAGGTGCGCGGAGTCAAAAGTTTGGCAC	126179	
QY	126180	GCCTGGCGCACTCTGTCGAGTGTGTGGGCTTGATTTGCAAGATGACGCCCGGGGTTTGG	126239	

Db	126180			126239
Qy	126240	GACACGACCACTGACAGGGGCTTTCTCTGACGGGATGGGAATCTGTAGCCCTCGTTTA		126239
Db	126240	GACACGACCACTGACAGGGGCGTTTCTCTGACGGGATGGGAATCTGTAGCCCTCGTTTA		126239
Qy	126300	CCGGCCAGGGCATCTGTGATAGGGGTAAACCACTGCTCTCCGTGCTGACGTGTGGCCG		126339
Db	126300	CCGGCCAGGGCATCTGTGATAGGGGTAAACCACTGCTCTCCGTGCTGACGTGTGGCCG		126339
Qy	126360	GACACCAACGACCCGGGAGAGAGCGGCTGTGTGATGTAAGATGGGTGGCAGGTGT		126419
Db	126360	GACACCAACGACCCCGGAGAGAGCGGCTGTGTGATGTAAGATGGGTGGCAGGTGT		126419
Qy	126420	GTCGCTGAACGTCGGGTAGGGGTGGAGCTCGGCAAGAGACAGGTGCTCAAGGTCGAT		126479
Db	126420	GTCGCTGAACGTCGGGTAGGGGTGGAGCTCGGCAAGAGACAGGTGCTCAAGGTCGAT		126479
Qy	126480	CCCTGGGTGAGGTGGCGGACGGGGAGAGACACAGCACTGATGAGTTACCGGTGGCTTC		126539
Db	126480	CCCTGGGTGAGGTGGCGGACGGGGAGAGACACAGCACTGATGAGTTACCGGTGGCTTC		126539
Qy	126540	AGGTCAAGTGTGACGCGTGTGCTGAGCACTCACTCGGCGGGGGCGGCGATGACGAT		126599
Db	126540	AGGTCAAGTGTGACGCGTGTGCTGAGCACTCACTCGGCGGGGGCGGCGATGACGAT		126599
Qy	126600	GCGTTAAACGGCACGGGGGCTACCGCTGTGATGCTGTTGGGTGGCGCTGATCACTTCTCC		126659
Db	126600	GCGTTAAACGGCACGGGGGCTACCGCTGTGATGCTGTTGGGTGGCGCTGATCACTTCTCC		126659
Qy	126660	GACAGGACGGGGGTGCTGCGGCGGACGATGAGGCGCAATGTGCTCAAGTCCCTGCAT		126719
Db	126660	GACAGGACGGGGGTGCTGCGGCGGACGATGAGGCGCAATGTGCTCAAGTCCCTGCAT		126719
Qy	126720	AGTTCCTTGACGAGAAACAGTGTGCTGTGACAGAGCGCGGTGTGCTCCGGGTTTC		126779
Db	126720	AGTTCCTTGACGAGAAACAGTGTGCTGTGACAGAGCGCGGTGTGCTCCGGGTTTC		126779
Qy	126780	CAACCGACCGACGCGCTGACGCTGATGTGCTTAAGACGCGCACGTCGCTAGCATGATG		126839
Db	126780	CAACCGACCGACGCGCTGACGCTGATGTGCTTAAGACGCGCACGTCGCTAGCATGATG		126839
Qy	126840	TTGGTGAACCGCTGCGAGATGGGTATCTCGCGCCCACTGCGCGCTTGAATGCCATCTTG		126899
Db	126840	TTGGTGAACCGCTGCGAGATGGGTATCTCGCGCCCACTGCGCGCTTGAATGCCATCTTG		126899
Qy	126900	TATGCGTGTTCATTAAGGACAGCACTGTGCGACCCAGCGGTTCGCCCCGCGCTCG		126959
Db	126900	TATGCGTGTTCATTAAGGACAGCACTGTGCGACCCAGCGGTTCGCCCCGCGCTCG		126959
Qy	126960	GTCACCCAGGTTTCTGGGCTAAACAGGCGTGTGCTGCTGCTGCTGCTGATCGGCTGG		127019
Db	126960	GTCACCCAGGTTTCTGGGCTAAACAGGCGTGTGCTGCTGCTGCTGCTGATCGGCTGG		127019
Qy	127020	GGGCGATATATGGGACCCCGCGCATCTGTCCGTTAAACACGACGATGTTGAATAAG		127079
Db	127020	GGGCGATATATATGGGACCCCGCGCATCTGTCCGTTAAACACGACGATGTTGAATAAG		127079
Qy	127080	TGTGATCTGACAGAGGCGCGGCCCAAGGGGTCCCACTTGCAGTGTGTGAGGACAGATCCG		127139
Db	127080	TGTGATCTGACAGAGGCGCGGCCCAAGGGGTCCCACTTGCAGTGTGTGAGGACAGATCCG		127139
Qy	127140	TTGGAAGCATGTGTCAGAGTGTGCGGTGACAAACCTTTTGTGCAACCGGTGGAACATCCG		127199
Db	127140	TTGGAAGCATGTGTCAGAGTGTGCGGTGACAAACCTTTTGTGCAACCGGTGGAACATCCG		127199
Qy	127200	AGAAGCTGATGACACGAGGCGCAGGCGAATAGGCGCCAGTGTGCGGACGAGGTGCG		127259
Db	127200	AGAAGCTGATGACACGAGGCGCAGGCGAATAGGCGCCAGTGTGCGGACGAGGTGCG		127259
Qy	127260	TGTTGCGCACCATCTCAGGTTTCTTGGGGCGACCAAGCATTTGAGGAAGAAAGGGCTGC		127319
Db	127260	TGTTGCGCACCATCTCAGGTTTCTTGGGGCGACCAAGCATTTGAGGAAGAAAGGGCTGC		127319
Db	127260	TGTTGCGCACCATCTCAGGTTTCTTGGGGCGACCAAGCATTTGAGGAAGAAAGGGCTGC		127319
Qy	127320	TCGTGAAACCCAAAGTTGCGATGACTTGGCGGATGTTGGCTGTGTGATGCGCACGCT		127379
Db	127320	TCGTGAAACCCAAAGTTGCGATGACTTGGCGGATGTTGGCTGTGTGATGCGCACGCT		127379
Qy	127380	CCCGGTTCCACAGCTCCAGGTGCTTCACGAATGATTCGAAGCTTGTGGAGGTTTCC		127439
Db	127380	CCCGGTTCCACAGCTCCAGGTGCTTCACGAATGATTCGAAGCTTGTGGAGGTTTCC		127439
Qy	127440	CCAAAGGAGGGAAGGCACTCCGCAATGGGTGCGGCGCTCTGATGATGATCAACGGG		127499
Db	127440	CCAAAGGAGGGAAGGCACTCCGCAATGGGTGCGGCGCTCTGATGATGATCAACGGG		127499
Qy	127500	CCCGGTTCCGAGCTCCGTCGCGGGGAGAGCGGCAAAAGCACGACGAGGACAGCTTG		127559
Db	127500	CCCGGTTCCGAGCTCCGTCGCGGGGAGAGCGGCAAAAGCACGACGAGGACAGCTTG		127559
Qy	127560	AGAACTTGTATCTAGATGTCGTTACAGGTTTCCGCTGATGTCGTGGCGGGGTC		127619
Db	127560	AGAACTTGTATCTAGATGTCGTTACAGGTTTCCGCTGATGTCGTGGCGGGGTC		127619
Qy	127620	AGTTGGCTCAGAAATGTTGTGGAGAGCTGAGAGACAAAGAGGCGCAGCGCCCGGAG		127679
Db	127620	AGTTGGCTCAGAAATGTTGTGGAGAGCTGAGAGACAAAGAGGCGCAGCGCCCGGAG		127679
Qy	127680	ACCAGGCTCCAGGTGGCGGATGACAGAGCGGGCTCATGGCGGATTAATGTGTGTA		127739
Db	127680	ACCAGGCTCCAGGTGGCGGATGACAGAGCGGGCTCATGGCGGATTAATGTGTGTA		127739
Qy	127740	AATAGGGCCCTTCGAAATCTGTAAGCCAGCGCAACGTTGGGTGGATGGCGGTAATA		127799
Db	127740	AATAGGGCCCTTCGAAATCTGTAAGCCAGCGCAACGTTGGGTGGATGGCGGTAATA		127799
Qy	127800	CCTGGGCGCTCCGAGGTTAAGGAGCGGCTGTGCTGATGCGCTCAACGAGGTTCAAAA		127859
Db	127800	CCTGGGCGCTCCGAGGTTAAGGAGCGGCTGTGCTGATGCGCTCAACGAGGTTCAAAA		127859
Qy	127860	GACCCAGACAGATGATAGGCTGACTGAATAAAGCACTCTGAGGAATGTATGCTTGA		127919
Db	127860	GACCCAGACAGATGATAGGCTGACTGAATAAAGCACTCTGAGGAATGTATGCTTGA		127919
Qy	127920	GGCAGGACGATTAACGAGATGTTGGTATTAACGTTCCGCTGCTGTGTGGGCGCTG		127979
Db	127920	GGCAGGACGATTAACGAGATGTTGGTATTAACGTTCCGCTGCTGTGTGGGCGCTG		127979
Qy	127980	TGGACGTTTTAAGAAACCCACGAGGACGAGCGCTGCGGTCGCGCACCTCTGGCAG		128039
Db	127980	TGGACGTTTTAAGAAACCCACGAGGACGAGCGCTGCGGTCGCGCACCTCTGGCAG		128039
Qy	128040	TGGAGTGTGCTGTTGTGTTAATAGCTGTGTGGGCTGCGCGAGAAATGCGCCACTGAC		128099
Db	128040	TGGAGTGTGCTGTTGTGTTAATAGCTGTGTGGGCTGCGCGAGAAATGCGCCACTGAC		128099
Qy	128100	GGCGTAGTGGGCTAAATCCACACAGGGCGGATGTGATTTCCGCCCGGGGACACGCTG		128159
Db	128100	GGCGTAGTGGGCTAAATCCACACAGGGCGGATGTGATTTCCGCCCGGGGACACGCTG		128159
Qy	128160	GCATGGAACAATAATGTTTGGAGGCACTGCACTGTGTGAATAGGCGCTGTGCAAGTGT		128219
Db	128160	GCATGGAACAATAATGTTTGGAGGCACTGCACTGTGTGAATAGGCGCTGTGCAAGTGT		128219
Qy	128220	GTAATATGATGAGCATATGTGGGTTACGTTTCCGACGGGAGCGCTGGAAACAGCACTG		128279
Db	128220	GTAATATGATGAGCATATGTGGGTTACGTTTCCGACGGGAGCGCTGGAAACAGCACTG		128279
Qy	128280	TAGCTCTGCGGGGCGATGAGCGGGCTATCTGGAACCGTTAGCGTTGAGAGGCC		128339
Db	128280	TAGCTCTGCGGGGCGATGAGCGGGCTATCTGGAACCGTTAGCGTTGAGAGGCC		128339
Qy	128340	TGCACGGCCAGCGGTAATATGTTCCTGTTTGAACGGGAGCATCACCGGCGCATATTGGG		128399
Db	128340	TGCACGGCCAGCGGTAATATGTTCCTGTTTGAACGGGAGCATCACCGGCGCATATTGGG		128399
Qy	128399	TGCACGGCCAGCGGTAATATGTTCCTGTTTGAACGGGAGCATCACCGGCGCATATTGGG		128399
Db	128399	TGCACGGCCAGCGGTAATATGTTCCTGTTTGAACGGGAGCATCACCGGCGCATATTGGG		128399

QY 128400 TCTCTCGGGCAACGGTCTCCAGGCGGTGATGGCAATGTCAACCGGAGCTGGCCCTGC 128459
| | | | |
Db 128400 TCTCTCGGGCAACGGTCTCCAGGCGGTGATGGCAATGTCAACCGGAGCTGGCCCTGC 128459
QY 128460 ACGCGCACTCATATTTCTACTAGTGTGCCAAGGTGACGGCGCCCAAGGGGGGT 128519
| | | | |
Db 128460 ACGCGCACTCATATTTCTACTAGTGTGCCAAGGTGACGGCGCCCAAGGGGGGT 128519
QY 128520 ACCCGATCGGGCGCAACCGTCTCGTCCAGCTCAGATGTCTGCCACCTCTAACCCG 128579
| | | | |
Db 128520 ACCCGATCGGGCGCAACCGTCTCGTCCAGCTCAGATGTCTGCCACCTCTAACCCG 128579
QY 128580 AACGTTCTATCGAGCGCGCTGTCTCTAAGGCACTGCACTATTTCCGTAGATCTTGTA 128639
| | | | |
Db 128580 AACGTTCTATCGAGCGCGCTGTCTCTAAGGCACTGCACTATTTCCGTAGATCTTGTA 128639
QY 128640 GGTGGCGCATCAGTCTGTGGCCATAGGGCAAGGATATAGTATGATGGCCCTGGAGTGC 128699
| | | | |
Db 128640 GGTGGCGCATCAGTCTGTGGCCATAGGGCAAGGATATAGTATGATGGCCCTGGAGTGC 128699
QY 128700 GCCGACCGATTTCCAGAGGTGATATTAACGAGGCGCCGAAGATGCCAGATACG 128759
| | | | |
Db 128700 GCCGACCGATTTCCAGAGGTGATATTAACGAGGCGCCGAAGATGCCAGATACG 128759
QY 128760 CCCAGCGTGGGTCGTCATCGTCTGTCAAAAGTTATCAGAGGCGGTTCACAGCCAA 128819
| | | | |
Db 128760 CCCAGCGTGGGTCGTCATCGTCTGTCAAAAGTTATCAGAGGCGGTTCACAGCCAA 128819
QY 128820 AGTAAATTTCTACTAAGCACTGTCTGGCACAAGGCCCAAACTTTCTGCGTCCGA 128879
| | | | |
Db 128820 AGTAAATTTCTACTAAGCACTGTCTGGCACAAGGCCCAAACTTTCTGCGTCCGA 128879
QY 128880 TTGTCTATGAATAAACCTCTCTCTGTGACATAAGGGCTGCACGGCCCGCAGAGGTTC 128939
| | | | |
Db 128880 TTGTCTATGAATAAACCTCTCTCTGTGACATAAGGGCTGCACGGCCCGCAGAGGTTC 128939
QY 128940 GTGCGTTGGGCACTATTTGCTAAGTACCGCGGCAAAAGCAAGGCGGTGGGACTTTAA 128999
| | | | |
Db 128940 GTGCGTTGGGCACTATTTGCTAAGTACCGCGGCAAAAGCAAGGCGGTGGGACTTTAA 128999
QY 129000 TACGGCGTATAGGGTGTAGTATGCGGTGGGCGCCGCTCATGTTCATAGTGCATTTCA 129059
| | | | |
Db 129000 TACGGCGTATAGGGTGTAGTATGCGGTGGGCGCCGCTCATGTTCATAGTGCATTTCA 129059
QY 129060 ATATTATTTATGTTAGTTTGGGCACTTGGGATGTTACATTATTAACCTTCCCATGT 129119
| | | | |
Db 129060 ATATTATTTATGTTAGTTTGGGCACTTGGGATGTTACATTATTAACCTTCCCATGT 129119
QY 129120 CACAGTAATCATTGACAGATCCCTTCTTAACATCAACAACTTTCCGGGTGTGAGG 129179
| | | | |
Db 129120 CACAGTAATCATTGACAGATCCCTTCTTAACATCAACAACTTTCCGGGTGTGAGG 129179
QY 129180 TTACAGTAAGGGTGGGAGGGAATTAAGTGGCGAACCAGCAATACGTCGGGGGC 129239
| | | | |
Db 129180 TTACAGTAAGGGTGGGAGGGAATTAAGTGGCGAACCAGCAATACGTCGGGGGC 129239
QY 129180 TTACAGTAAGGGTGGGAGGGAATTAAGTGGCGAACCAGCAATACGTCGGGGGC 129239
| | | | |
Db 129180 TTACAGTAAGGGTGGGAGGGAATTAAGTGGCGAACCAGCAATACGTCGGGGGC 129239
QY 129240 GGGAGTGGGAGCGCTGTAACCCGAGATGTCACCTTACGCTTGTAGGCGATGCAACA 129299
| | | | |
Db 129240 GGGAGTGGGAGCGCTGTAACCCGAGATGTCACCTTACGCTTGTAGGCGATGCAACA 129299
QY 129300 CCTCCGAAGTGTCTCTGTGGATGTTTGTGATTAAGTAAACGAAAGTGTGGAG 129359
| | | | |
Db 129300 CCTCCGAAGTGTCTCTGTGGATGTTTGTGATTAAGTAAACGAAAGTGTGGAG 129359
QY 129360 AAAGTAACTTATAGATGACCTCTCTGCGCGGTGGCGGTGACAGCTGTGTTGAT 129419
| | | | |
Db 129360 AAAGTAACTTATAGATGACCTCTCTGCGCGGTGGCGGTGACAGCTGTGTTGAT 129419
QY 129420 GAATGAACATTCCTCTGGGGCTCTGAGGGTGGTGGGTGAGTCTCACTAAGGCGGCCA 129479
| | | | |
Db 129420 GAATGAACATTCCTCTGGGGCTCTGAGGGTGGTGGGTGAGTCTCACTAAGGCGGCCA 129479

QY 129480 ACTCAACACTAACTTCCTCCGTTTCAGACCGGTGAGCGGTTTCGTGTAGCGTCTTGTCG 129539
| | | | |
Db 129480 ACTCAACACTAACTTCCTCCGTTTCAGACCGGTGAGCGGTTTCGTGTAGCGTCTTGTCG 129539
QY 129540 AGGGGGTGGCTTAACCCCTTGTGTGTGTAACAATCCAGTAACCCGTAATTCACGCGG 129599
| | | | |
Db 129540 AGGGGGTGGCTTAACCCCTTGTGTGTGTAACAATCCAGTAACCCGTAATTCACGCGG 129599
QY 129600 TCAGGGCGATTTGTAACAAACCTTAACAGCATATTAAGCTTTCACAAAGCATTTTGGTA 129659
| | | | |
Db 129600 TCAGGGCGATTTGTAACAAACCTTAACAGCATATTAAGCTTTCACAAAGCATTTTGGTA 129659
QY 129660 ACAATTTGTAATTAATTAAGCCCAAGTTTATACAAAGCGAATCTACTTACCGATTAATA 129719
| | | | |
Db 129660 ACAATTTGTAATTAATTAAGCCCAAGTTTATACAAAGCGAATCTACTTACCGATTAATA 129719
QY 129720 AATGCAACCGCAAGAGATTAACACTGACTGATTTCTGTTCGAATGGTTGCAATTTAAG 129779
| | | | |
Db 129720 AATGCAACCGCAAGAGATTAACACTGACTGATTTCTGTTCGAATGGTTGCAATTTAAG 129779
QY 129780 AATGAGAGTAATTTGGCCCGCTGAGAAATGCCGGAATTAAGGGCGGTATTTTACAT 129839
| | | | |
Db 129780 AATGAGAGTAATTTGGCCCGCTGAGAAATGCCGGAATTAAGGGCGGTATTTTACAT 129839
QY 129840 GTGCTACAGGGTAGAAAACCTTGTAGGTTTCAGTTGAGTCACCTGCGCACGTAACCCGC 129899
| | | | |
Db 129840 GTGCTACAGGGTAGAAAACCTTGTAGGTTTCAGTTGAGTCACCTGCGCACGTAACCCGC 129899
QY 129900 CTAGAGTGTGTCACGCGGTGTGTGTCAGAGAAATGATCTCTTAATTTTAACTTAAGG 129959
| | | | |
Db 129900 CTAGAGTGTGTCACGCGGTGTGTGTCAGAGAAATGATCTCTTAATTTTAACTTAAGG 129959
QY 129960 GGTTCCTGTAATTAATTTAAGTTATGATGATGATGATGATGATGATGATGATGATGAT 130019
| | | | |
Db 129960 GGTTCCTGTAATTAATTTAAGTTATGATGATGATGATGATGATGATGATGATGATGAT 130019
QY 130020 ACTCCAAAAGATACTCGATTAATGCGGTATATGTGAAGTTTGCAACAAATGCAAGCGGT 130079
| | | | |
Db 130020 ACTCCAAAAGATACTCGATTAATGCGGTATATGTGAAGTTTGCAACAAATGCAAGCGGT 130079
QY 130080 GAGTAGGCCCAAGAAAATGATTAACCTATATGAGGAAATTTTATAGTACGTTTGCTA 130139
| | | | |
Db 130080 GAGTAGGCCCAAGAAAATGATTAACCTATATGAGGAAATTTTATAGTACGTTTGCTA 130139
QY 130140 ACTGCAAAATTAATTTTAATTAATTAATTTATATTCATGATGCAAGTTAATTTGTCG 130199
| | | | |
Db 130140 ACTGCAAAATTAATTTTAATTAATTAATTTATATTCATGATGCAAGTTAATTTGTCG 130199
QY 130200 TGGTGTCTTCTGAATTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAAT 130259
| | | | |
Db 130200 TGGTGTCTTCTGAATTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAAT 130259
QY 130260 GCTGCCCTTGCACATTAACCAATAGGCAATGTTTCAATGTAATGTAATGTAATGTAATGTAAT 130319
| | | | |
Db 130260 GCTGCCCTTGCACATTAACCAATAGGCAATGTTTCAATGTAATGTAATGTAATGTAATGTAAT 130319
QY 130320 AAGTGCACGACAGATTCACCAATAGCTATTAACCAAGATGTAATGTAATGTAATGTAAT 130379
| | | | |
Db 130320 AAGTGCACGACAGATTCACCAATAGCTATTAACCAAGATGTAATGTAATGTAATGTAATGTAAT 130379
QY 130380 AAGTATTAACATTAACCAATTAACCAATTAACCAATTAACCAATTAACCAATTAACCAAT 130439
| | | | |
Db 130380 AAGTATTAACATTAACCAATTAACCAATTAACCAATTAACCAATTAACCAATTAACCAAT 130439
QY 130440 AGTATGATTAATAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA 130499
| | | | |
Db 130440 AGTATGATTAATAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA 130499
QY 130500 CCAACAGTGTCTAAATTAACCAATTAACCAATTAACCAATTAACCAATTAACCAATTAACCAAT 130559
| | | | |
Db 130500 CCAACAGTGTCTAAATTAACCAATTAACCAATTAACCAATTAACCAATTAACCAATTAACCAAT 130559
QY 130560 TTCAAGTAATTAACCAATTTGTGTATACCTGCTAAATTTGCAACCAAGATCAATTTATTC 130619
| | | | |

QY	132780	CTCCGCGCGCCGGGAGGGGGGCGCGGGAGCCCGGGGCGCTCGGGGGGGCCGGCGGGG	132839
Dp	132780	TCCTCGGCGCCCGGAGGGGGGGCGGGGAGCCCGGGGCGCTCGGGGGGGCCGGCGGGG	132839
QY	132840	GCGCGACCGAAGGGCCCGGGAGAACGGGGGAGTCGGGAAAACCGAGAGGGAGCGGGGAGCA	132899
Dp	132840	GCGGAGCCGAGAGGGCCCCGGGAGAACGGGGGAGTCGGGAAAACCGAGAGGGAGCGGGGAGCA	132899
QY	132900	GGGAGCGGCGTGTGCGCTGCTTGTGAGACACGGGGTAGCGGGCTGCTGCTGCTGCGTGCC	132959
Dp	132900	GGGGAGCGGCGTGTGCGCTGCTTGTGAGACACGGGGTAGCGGGCTGCTGCTGCTGCGTGCC	132959
QY	132960	TGCTTGTGAGAGGGGACAGTAGGCGCTGCTTCGCTGGCGCTGCTTGTCTGAGAGGGACAGTA	133019
Dp	132960	TGCTTGTGAGAGGGGACAGTAGGCGCGTGTGCTGCTGGCGCTGCTTGTCTGAGAGGGACAGTA	133019
QY	133020	GGCGCTGCTTGTGAGAGGGAGACAGTAGAGCGCTGCTTGTGCTGCGCTGCTGCTGAGAGGAGC	133079
Dp	133020	GGCGCTGCTTGTGAGAGGGAGACAGTAGAGCGCTGCTTGTGCTGCGCTGCTGCTGAGAGGAGC	133079
QY	133080	AGTAGGCGCTGCTGGCGTTGCTAGTAGAGGCTGCTCGCTGGCGCTGCTTGTGCTGCTGCGGCC	133139
Dp	133080	AGTAGGCGCTGCTGGCGTTGCTAGTAGAGGCGTGCCTGCGCTGCTTGTGCTGCTGCGGCC	133139
QY	133140	TGCTTGTGCTGCTCGCTGGCGCTGCTTGTGCTGCTGCGCTGCTTGTGCTGCTGCGCGCC	133199
Dp	133140	TGCTTGTGCTGCTCGCTGGCGCTGCTTGTGCTGCTGCGCTGCTTGTGCTGCTGCGCGCC	133199
QY	133200	TGCTTGTGCTGCTGCGCTGGCGCTGCTTGTGCTGCTGCGCTGCTTGTGCTGCTGCGCGGCC	133259
Dp	133200	TGCTTGTGCTGCTGCGCTGGCGCTGCTTGTGCTGCTGCGCTGCTTGTGCTGCTGCGCGGCC	133259
QY	133260	TGCTTGTGAGAGGGGACAGTAGAGGCTGCTTGTGCTAAAGGGAGCGTAGCGCTGCTGAT	133319
Dp	133260	TGCTTGTGAGAGGGGACAGTAGAGGCTGCTTGTGCTAAAGGGAGCGTAGCGCTGCTGAT	133319
QY	133320	GGCTTGTAGTAGAGGGCTGCTGGGCGGCTAGTAGAGGCTGCTGGGCGGCTAGTAGAGGCTGCT	133379
Dp	133320	GGCTTGTAGTAGAGGGCTGCTGGGCGGCTAGTAGAGGCTGCTGGGCGGCTAGTAGAGGCTGCT	133379
QY	133380	GGGCTGTAGTAGAGGGCTGCTGGGCGCTAGTAGAGGCTGCTGCGGCTGCTAGTAGAGGCTGCT	133439
Dp	133380	GGGCTGTAGTAGAGGGCTGCTGGGCGCTAGTAGAGGCTGCTGCGGCTGCTAGTAGAGGCTGCT	133439
QY	133440	GGGCTGTAGTAGAGGGCTGCTGGGCGCTAGTAGAGGCTGCTGCGGCTGCTAGTAGAGGCTGCT	133499
Dp	133440	GGGCTGTAGTAGAGGGCTGCTGGGCGCTAGTAGAGGCTGCTGCGGCTGCTAGTAGAGGCTGCT	133499
QY	133500	GGGCTGTAGTAGAGGGCTGCTGGGCGCTAGTAGAGGCTGCTGCGGCTGCTAGTAGAGGCTGCT	133559
Dp	133500	GGGCTGTAGTAGAGGGCTGCTGGGCGCTAGTAGAGGCTGCTGCGGCTGCTAGTAGAGGCTGCT	133559
QY	133560	TGCTTGTGAGGGGCGGCTTGTGCTAGTAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	133619
Dp	133560	TGCTTGTGAGGGGCGGCTTGTGCTAGTAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	133619
QY	133620	GCTGCGGCGCAGCTGCTGTCGAGAGGCGTCCGAGGGCCAGACGAGGACAGGAGGACCGCGGCC	133679
Dp	133620	GCTGCGGCGCAGCTGCTGTCGAGAGGCGTCCGAGGGCCAGACGAGGACAGGAGGACCGCGGCC	133679
QY	133680	CTTCTTCCCGCGCGGACCGCGGGGACCGCGCGCCAGATCT	133719
Dp	133680	CTTCTTCCCGCGCGGACCGCGGGGACCGCGCGCCAGATCT	133719

RESULT 2	AF210726	LOCUS	DEFINITION
	AF210726	130733 bp	DNA linear VRL 27-MAR-2000
		Macaca mulatta rhadinovirus 26-95 long unique region L-DNA, complete sequence.	

ACCESSION	AF210726
VERSION	AF210726.1 GI:73299900

KEYWORDS	
SOURCE	Macaca mulatta rhadinovirus 26-95
ORGANISM	Macaca mulatta rhadinovirus 26-95
	Viruses; dsDNA viruses, no RNA stage; Herpesviridae; Gammaherpesvirinae; Rhadinovirus.
REFERENCE	1 (bases 1 to 130733)
AUTHORS	Alexander, L., Denekamp, L., Knapp, A., Auerbach, M. R., Damania, B. and Desrosiers, R. C.
TITLE	The primary sequence of rhesus monkey rhadinovirus isolate 26-95: sequence similarities to Kaposi's sarcoma-associated herpesvirus and rhesus monkey rhadinovirus isolate 17577
JOURNAL	J. Virol. 74 (7), 3388-3398 (2000)
MEDLINE	20137370
PUBMED	10708456
REFERENCE	2 (bases 1 to 130733)
AUTHORS	Alexander, L., Denekamp, L. M., Knapp, A., Auerbach, M., Czajak, S., Damania, B. and Desrosiers, R. C.
TITLE	Direct Submission
JOURNAL	Submitted (02-DEC-1999) Microbiology, New England Regional Primate Research Center, One Pinehill Dr., Southborough, MA 01772, USA
FEATURES	location/Qualifiers
SOURCE	1..130733

gene	4213. .7611
	/gene="ORF06"
CDS	4213. .7611

```

/protein_id="AAE59980.1"
/db_xref="GI:7329991"
/translation="MFVLFMLHLPDSVSELLPAKITSPTWCPRPFGDTYLLTCGCT
STARQRORSTQRNNMLTNGNSNFGVLSVTPPATISIDRACQTKTTSNNIDFVPS
SRRLTLOENCSGSSGYLYGANTNRYLCYSGGANTLRYNVLNLTAAINGNTNNIHFEV
LTKKGTGYTCGCAFIENEGFVSTIIVFTSFTEKPNIDPNSHKNATQIIOOTASA
OHEKXVYVSFVSGFVLTGLTALSLIMCLFIRCNENSESTNSASOTLSIOSSH
NORSMQNECSHRTYRNRAHGEIEELPNQHTSDSCCOLYILEVNVAVDQGEKMTI
NEVMQYDDVYVENIEQTSIEDNEVEMDSDTINPAPNTYSGLIEVDVEVFNLELN
QTHGLELLENENIEHMLNNEIYDMLE"
/gene="ORF02"
/complement(1852..2418)
/gene="ORF02"
/complement(1852..2418)
/codon_start=1
/product="DHR"
/protein_id="AAE59981.1"
/db_xref="GI:7329992"
/translation="MDIAAGCAVDAEOLGIGKNGTMPMPYLKENMVFQKMTSTSV
VEKXVYVINGKRTWESIPKKRPLRVNRINILISRELREPHGSHFLARTLDDAPNRY
QYKLEQQLTNNVYVIGSKSYSESLNKCPLKLYTIMESFDDCVFPFSINFTETML
SELPKGNIDNEENIGIKYKFOYELNENK"
/gene="ORF04"
/2595..3782
/2595..3782
/gene="ORF04"
/codon_start=1
/product="complement binding protein"
/protein_id="AAE59982.1"
/db_xref="GI:7329993"
/translation="MWMPITLTCFICOVILVDSKDEENVTCLPKPPDRFPAWTKRANQE
NVAQGRVRELICRPGYKLOAANYVCLSGMTPTPNAECRRKGNPEDIINGEYII
TSDNAKFNQSNITRYKCNNGYLLIATVTCTKLYSDNLVMDQRPAPCTIECKCPK
DIENKGYVYQDEIVNLELITFCNDFSLGKATTTCTMTNGTWSSVPRCCQITCSA
PAIDHGLTLVGSRRYKHOQSVTIGDEDFTLGNHMCCEVSLNMPPLPTCVINKT
DPTSPVSPGRKEDMPPEPNKSHESETTTETPKTQTHKSETSPSPKAPNPEHTKP
TPPEGISKQTTNRPKASQNPRIAPMSSMKKRHVIVLVLFASVASLFLVLAALVCC
FLK"
/4213..7611
/gene="ORF06"
/4213..7611

```

```
/gene="ORF06"  
/codon_start=1  
/product="ssDBP"  
/protein_id="AAF59983.1"  
/db_xref="GI:7329994"  
/translation="MASKNAGAPLEEDNOSGRAPICAGGVYVAKODEPFAASITL  
NRPGSGVSPILITXGTLVEHEPFLTYKAAKKKADPTTLAKVYCFHREVYFPAASIL  
FRPVDTGTLNELEEARALBGTQTEPGPHSTIWNPLECPQLPDKDMFLGVVTE  
GFEKRLMRGCLVPVAFQTOVQIAGROAFKPLVLEDELFAPHGHRMPREYKIDVAVL  
YDSLITIAQLRLKDYAVIAHAEKQFMDHYKIAKIVAKQCFSTLPKTTDSSSH  
IVDSVAEIALSYGCMFLECPDACEILNYDSMPIDFGDCDEARVALNESEAOAV  
HVAQGLFAANSVLITKVKOAPRGKGDVNVNPFLOHGLFNEATIKENSSEAF  
KGVSNALDSSPTPHLAAVASSPHILATCYMOFLOHKKSTQOAFMAYVYCT  
AANSEKTLCHGNTPATCLNTLFLKMDRPAVTPQRRDYPYVGTAGTPTNDEILG  
NFASFRDEEDGNPADEHPKTYWQLQTVIEKLSAIGTEDHNVNLTINIOSFLR  
VFKGIDSIVDEVPKFNYSMTKNNEFNEHYKSVHILQFCNVYQWAPCAVPLNLY  
KSLMIIODICLPKMIYEDONPAMGLISEMLKMHROTLPNTNKAACLDGVLTCG  
LKIVHRMFCDFPTDAGSNGMLAPFKMOVILARAMVYVPSIKIKNNIIFESNTAGSE  
AVQSGFYKPTGTRDTPYVAGPYMKFLNSLHRLPPDKTALYLHKISQNTKPYLK  
DVDPDELAELQTVIYKINSLEAFETNLDVDPDSLMTARKILNKAALRACQIOPAT  
TLHCLTPVLQTIIDAEYPHVIGSAAIAPVAYLAEIKRITALTVQTTARQVPAATGL  
RPVITVPMVVKYTGANGNNNPHCGNIGYFAGGVGNLWPESSPEFKTGVSAMLK  
RHVMATPLIDRLIKRAGQITSTFEAESVRSVOALLKEDKNPLKLSVLEILRHLG  
KGCODLSSEVQYILGDCMLDEVLTFLDNIAQSVPMTEADGALIEDRQDADDLQ  
FVSDSDIATASCQPEEQDLPRTPSAGALLAKKKRINALLSDLD."  
7636..9696  
/gene="ORF07"  
7636..9696  
/gene="ORF07"  
/codon_start=1  
/product="transport protein"  
/protein_id="AAF59984.1"  
/db_xref="GI:7329995"  
/translation="MARLALYLAQLSALAVDSLVIYFADPRSIDGARILKTKTOIEN  
LNRDLPLLEONSVEVTSLSLEVEHLINDKLELIGELERSLROYSREHEPFLHFR  
PECHYSTVYPOFGGLGIYNMCLINDVELLCRGYFVFCIGANGESLDEFLHFR  
LSTLRGISPIPHDLVYVPCVOCILREYIPNPGSSILAIVADHNIKCKYVRAE  
PIHGLFETELSQDLKATYKRSADTOHGRSSADOLRESSLAIDHNIKFKYSSIME  
LSNLITVMAQGTGLQGTENECOSMARLTHEADHMERHALITPKLSATHYDSEDRP  
PIESLFCGGLFNSIDDTINALSRDCSVYFEQQAQNTVMRKQNELFTLNSILRQGA  
GSKRPATPESEPTTVAATAASDVIAKDAQREKYMKVAKNGEKLKECLOTOGAVL  
ANALCMRYMGAVGAEGASELVNHLRLRRFALPWEARCSDOILFENSKYIKNSLYS  
ORLSREHVEITLQFYGLITGLTPROSLDFPGPANVLAOCFEAAGMLPHKMLVSEM  
IWPQIOKPDWIDQTFNRPQOLPEGDINAVQCSANCFIEILVLSALYRTMEKLRIF  
SLAREKLSISMVKGILTGLTLYTEDAPLVLLISQNGIMFKDLIALYHLHQLSDG  
HDDN"  
9683..12172  
/gene="ORF08"  
9683..12172  
/gene="ORF08"  
/codon_start=1  
/product="orf08"  
/protein_id="AAF59985.1"  
/db_xref="GI:7329996"  
/translation="MMITNRRRLRLRAMVVIILGTAIVENVTTPKGAATTAAPKPPG  
STPPPPPPRAEAPKFRVCSASATGELFRNLKCTGCTGCTKHOBELIAPVKKNY  
PHITVRIRKRVAVTSVYRGMTFAVTKQEVIRPVQIETINHDITYOCFSSNRVN  
VNGIVNTYTDDEINQVFLQPVGLINDIRYSQPLAYTTPGMPQIYVKTVCNC  
EIVIMIRASAPYSGYFVIALDQTVESFCHNDSTCSVAETENGLAGHEALVNTYID  
FATRPPTETREYFADSGEYIVSKAEDEKFSVACILTKTKTPRAIQTHESAYHFVAN  
DVTAFPTSPLEVANFTGYSCIDDEVLOKLTINDTIKTHHNGSVAOYKTEQGEFL  
LIMQPIPLISLVDEMRGLNGTTPAPRATTSYVRSVYNNECATDNLAAPROGFAY  
DKLRASINKVLEELSRAMCREQVRODTVMYELSKINPISVATATIGRVSKAFEGDAL  
SVTDCVAVDAQSAVSIHKSILRTSTPGMCSRPPVFRNLSTTLKRGQGLPNEEILTD  
NOVACEKTECHYEYIASNVYTYKDYVKEKINTESELTCTFALNISEFTENIDRV  
IELYSRAEKLSGSVDFIETMEFREYNYTORLAGLREDLDTIDNRRLADSEIY  
ADLDGVRGTVVAVASVITLFGSIVSGINIKSPFGMLMIIIVAVVILVPLANRR  
TNATAQAPITMIYPIDIDMKOPSGSKVDQBJKNILAGHQLQOEERRRLDQQSAPS  
LFRASDGLKRRFRGYKPLENEAOEYEMK"  
12290..15334  
/gene="ORF09"  
12290..15334  
/gene="ORF09"  
CDS
```

```
/codon_start=1  
/product="polymerase"  
/protein_id="AAF59986.1"  
/db_xref="GI:7329997"  
/translation="MDFENPYLGRPRGPRSHRSTDAAPAGAGAVOPPPDVCRILPA  
CLRTPGAGMIPVITIPPEPYENGARSDVLLAERSMWTARDKRPVAPDQDOSTIF  
HAYVDETTVADMDCAEYPSRFQDIDISGVLLGLETEGTSVCVNVFQOYFYFA  
KVPGAGVITHILOQALKNTRAKRACGSESTRVNNRIKLTQVYAHAPREITLSSGML  
STSLDRVACGCEYFESVNDVAREFVLDHGTGTCWYSCAATRILRLAARDRTALEED  
CSMDLSVQARSDMPPRIVAFPIECTGEAGFPCTARGDAVLIQISCVETTREAGP  
NPINILSVSGCDIPIDTVLEPPEMDVSPFAMIRDEFVDFLGTGINSFDPPLYL  
ITRASOYVNLNRYETIKTGSIFEVEHPREGGGGFMRSYKIRIAGIYVYIDMYOVR  
EKLSDYKILDTYAROCIGKKEEDYSKDIPLRSGSGRAGVSGCYVMSYVLMODL  
LKMIMHVEISEIAKIAKIQARVYLTDGQOLRVPSCLLEAARENFTLPPTPGGOG  
YQCARVINPILGTFDEPVLVYDRASLPSIIQANNLCSTYIRGRDLHNLNLPDOY  
ETVPLSGGPVHFHRHRESLLGRLTVLEKRRARIRRTIACDPSLKITLIDQOLA  
IKVCMNVAGFTGVASGLPLCINIETVTLGRMLEKSKSYALTEDETRTLRGRE  
VTARHGAERFVYVDGDSLFACQYSAEVSAFCDDLAARITADLPPPIKLEAKET  
FKCLLLTKRREYIGVILNDKVMGVGDILRKTACKFOERCRAIIDLVDHPYKAA  
RLCKRPHHAYEESGLPAGFIKYEIVNLSYLDLRNSVYPIEOLTFESTELSRPCDYK  
TTNPLHVAIVOKLSRCEBELPOVHDRIPTYVYVDAPSKSLALEHPDYVRHQIPVAV  
DLVYDKLVHGSAANLILQLFGNNAUTVAILNPLNVPKLPs"  
15429..16679  
/gene="ORF10"  
15429..16679  
/gene="ORF10"  
/codon_start=1  
/product="orf10"  
/protein_id="AAF59987.1"  
/db_xref="GI:7329998"  
/translation="MLVNELSVVIGDMVEVFRGRFSFVNLTIRLOTENKHCYAVARVL  
PESIDILHOFARFAGIVYRLKELPPESSCVALLPLDGGADARVAPGVLDSSRP  
LTVVNASGRHTIRFCLFLKPIIDLERAVTYVEEGNARGSEGPAPKPCARESP  
LRVGEASQTSHPHFVAEPFANSVACLSLIRLIDVRRPSSDAHHDARIISKYVTFNS  
SGGVNCKASVHTLSPSRCKTQMEIIVAPGPMEIYVGQSPVLPHTGTGVRVGA  
DAEKTIOGSSAEVRVOLIFQOGAARLDLIVGVAPEPLFVTPVTLISGCTTHL  
RLFNPNGPTIKRDTLVAAAPCPVVALSSADBARDLVASPTGALISINAFIIPVG  
FPVYVSAECHYSILSDNCGHERMNH"  
16688..17917  
/gene="ORF11"  
16688..17917  
/gene="ORF11"  
/codon_start=1  
/product="orf11"  
/protein_id="AAF59988.1"  
/db_xref="GI:7329999"  
/translation="MGTPVRFREFREWQTSILVNGTSPYSLVMAATIHGCVLILVNR  
SELCTVTERSPCLPACPSIGRLVGRFPGFAPASATLGRGRTVYFAGHRDNPDLIV  
PAVERADRREILRVHAPQOTTRVRSRYGLKVFVAIVTVVRPGVFLHFPQDVRPIALTD  
Query Match 54.6% Score 7651; DB 1; Length 130733;  
Best Local Similarity 99.7% Pred. No. 0; Mismatches 25; Indels 4; Gaps 3;  
Matches 9321; Conservative 0;  
Db QY 119709 GTCCACTAACGCGTTATGCGGAACATGGTCCGTCGCGGCTCCGACACCTCTTC 119768  
|||||  
Db 117489 GTCCACTAACGCGTTATGCGGAACATGGTCCGTCGCGGCTCCGACACCTCTTC 117548  
|||||  
QY 119769 TACCTACACTAGAGCGTTTGAATAATCAGACGAACCGCGGCGTTACTTAAATGTGCT 119828  
|||||  
Db 117549 TACCTACACTAGAGCGTTTGAATAATCAGACGAACCGCGGCGTTACTTAAATGTGCGT 117608  
|||||  
QY 119829 CTTCGCTAAATTCCTCCGCAAGGTGTCGCAACCGACTCGCGCGGCGCGGAGGCGTTGGCG 119888  
|||||  
Db 117609 CTTCGCTAAATTCCTCCGCAAGGTGTCGCAACCGACTCGCGCGGCGCGGAGGCGTTGGCG 117668  
|||||  
QY 119889 CCGAAGCCGACAGGCGCTCCGCAATCTGGCGGAGGCGGCGGACGCGACCGAGAGCTTAA 119948  
|||||  
Db 117669 CCGAAGCCGACAGGCGCTCCGCAATCTGGCGGAGGCGGCGGACGCGACCGAGAGCTTAA 117728  
|||||  
QY 119949 ACAGCGCGCAGCGGCGCGCCACACAGGAGGAGGCGGAGCAGCGCGGCTGCGCGGCTTACAGA 120008  
|||||  
Db 117729 ACAGCGCGCAGCGGCGCGCCACACAGGAGGAGGCGGAGCAGCGCGGCTGCGCGGCTTACAGA 117788  
|||||
```


QY 120009 TGGCTTTGTGAACAGACTCCACACCTGGCTGTGAAGGCAAGAGACTGCTCTTTGTAA 120068
|||||
Db 117789 TGGCTTTGTGAACAGACTCCACACCTGGCTGTGAAGGCAAGAGACTGCTCTTTGTAA 117848
QY 120069 ACCCGCTTTTAAACAGGGTGGCCGATGGCTCGTGTGTAAAGAGCGCTCTAGTTCC 120128
|||||
Db 117849 ACCCGCTTTTAAACAGGGTGGCCGATGGCTCGTGTGTAAAGAGCGCTCTAGTTCC 117908
QY 120129 ACCCTAAAGCCTTAAGGATGTAATTTTCTGTTCAGTAATCCCGCAGGAAATTCCT 120188
|||||
Db 117909 ACCCTAAAGCCTTAAGGATGTAATTTTCTGTTCAGTAATCCCGCAGGAAATTCCT 117968
QY 120189 CCGCGCGCAAAAGCATAAAGGCGCCCTTGAAGAGATTCAAGTCTCTAATCTTCCG 120248
|||||
Db 117969 CCGCGCGCAAAAGCATAAAGGCGCCCTTGAAGAGATTCAAGTCTCTAATCTTCCG 118028
QY 120249 CTAAAAATAGACAGCGCGCCCGACGCTGTGAACCGCGAGCGGGGATGTGCGACCT 120308
|||||
Db 118029 CTAAAAATAGACAGCGCGCCCGACGCTGTGAACCGCGAGCGGGGATGTGCGACCT 118088
QY 120309 CTAGATAGGATCCAGATACTAAGCGGCGAGTGGGAAACGGTAGATCCGCTGGTGG 120368
|||||
Db 118089 CTAGATAGGATCCAGATACTAAGCGGCGAGTGGGAAACGGTAGATCCGCTGGTGG 118148
QY 120369 CCTGGCAACAGACCGCATCCACGTCGCCAAGATACTGCATGCCACGTCACCTCCG 120428
|||||
Db 118149 CCTGGCAACAGACCGCATCCACGTCGCCAAGATACTGCATGCCACGTCACCTCCG 118208
QY 120429 TTTGTATCGTCCCATAGACAGCGCGGTGAGTTTCAAGAGACGCTTGTGGCCAGAGGT 120488
|||||
Db 118209 TTTGTATCGTCCCATAGACAGCGCGGTGAGTTTCAAGAGACGCTTGTGGCCAGAGGT 118268
QY 120489 TAGAGAGGCGCGGCTCTGTACAGGAGGCGGTCATGTCGCCGTTGGGCACTGGGCGCA 120548
|||||
Db 118269 TAGAGAGGCGCGGCTCTGTGTACAGGAGGCGGTCATGTCGCCGTTGGGCGCACTGGGCGCA 118328
QY 120549 CAGAAAGCCTATTGTCAAGGCAAGGTAAAGAAAGCGATATAGTCTACTGCGGCTCAAG 120608
|||||
Db 118329 CAGAAAGCCTATTGTCAAGGCAAGGTAAAGAAAGCGATATAGTCTACTGCGGCTCAAG 118388
QY 120609 AAGCTTAATACGACAGCTCCGCGCTTAAACACAAATCTTGTGGCTATATGTCGCTCA 120668
|||||
Db 118389 AAGCTTAATACGACAGCTCCGCGCTTAAACACAAATCTTGTGGCTATATGTCGCTCA 118448
QY 120669 CACTGCTCCATGCTTTCAGAGTTCAGGCGCTGTCGCCGAAAGGCGGAGCTAGA 120728
|||||
Db 118449 CACTGCTCCATGCTTTCAGAGTTCAGGCGCTGTCGCCGAAAGGCGGAGCTAGA 118508
QY 120729 TGCACGCGGAGAGCGGCTTTCATTTAAGGTAGTCAAGCGGCGCAATTTGCCAACA 120788
|||||
Db 118509 TGCACGCGGAGAGCGGCTTTCATTTAAGGTAGTCAAGCGGCGCAATTTGCCAACA 118568
QY 120789 GTGAGCGCTTTCCTGCAAGTCTGGGCTTTCACCTGCGAAGCGCACTGTTTGGAGCC 120848
|||||
Db 118569 GTGAGCGCTTTCCTGCAAGTCTGGGCTTTCACCTGCGAAGCGCACTGTTTGGAGCC 118628
QY 120849 GGGCGGTGGGGAATTTTAAAGTCTGAATTTGCGAGTCTCTGTCATTTGGCACTATGCTG 120908
|||||
Db 118629 GGGCGGTGGGGAATTTTAAAGTCTGAATTTGCGAGTCTCTGTCATTTGGCACTATGCTG 118688
QY 120909 GCTTGGAAATGGGAGGCGGATGGGTATGTCGTTCCACGCGGAGCGGCTTTTGGAG 120968
|||||
Db 118689 GCTTGGAAATGGGAGGCGGATGGGTATGTCGTTCCACGCGGAGCGGCTTTTGGAG 118748
QY 120969 GCTTGGCGGCTTCCGCGCTTTGACAGAACACCGTATATCAAAAAAGCTCGGATGACGGA 121028
|||||
Db 118749 GCTTGGCGGCTTCCGCGCTTTGACAGAACACCGTATATCAAAAAAGCTCGGATGACGGA 118808
QY 121029 CTGGCAGGTGCGTCCGCGCAAAACGCGAGCTGAGATGCTCTAATGGCGGAAACTGTAG 121088
|||||
Db 118809 CTGGCAGGTGCGTCCGCGCAAAACGCGAGCTGAGATGCTCTAATGGCGGAAACTGTAG 118868

QY 121089 CACTTCCAGGCGATACAGTGAATAGGGGTCTGACTTACAAAGATGACTCCGTGACAC 121148
|||||
Db 118869 CACTTCCAGGCGATACAGTGAATAGGGGTCTGACTTACAAAGATGACTCCGTGACAC 118928
QY 121149 CACGGGCGCGCGAGAGGGGCTGATCTGGGTCCCAATACCTGACGATTAATCTTCTC 121208
|||||
Db 118929 CACGGGCGCGCGAGAGGGGCTGATCTGGGTCCCAATACCTGACGATTAATCTTCTC 118988
QY 121209 TGTGGCGGTATTTTGTGGGTACCTTCTCTGATGAGGAGATACGTTATGGGAATGGG 121268
|||||
Db 118989 TGTGGCGGTATTTTGTGGGTACCTTCTCTGATGAGGAGATACGTTATGGGAATGGG 119048
QY 121269 TATCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTGTGCTGCTCCGCTCCGCC 121328
|||||
Db 119049 TATCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTGTGCTGCTCCGCTCCGCC 119108
QY 121329 TCTTGTCTCTGTTGTCTTTTCAAGAGCTTGTCTCTGTGGAGTTGTGACTCTGCAATCTG 121388
|||||
Db 119109 TCTTGTCTCTGTTGTCTTTCAAGAGCTTGTCTCTGTGGAGTTGTGACTCTGCAATCTG 119168
QY 121389 AGACGTAAACAAGAACTCCTCCGCGACGCGGTGGTGGAGCCCAACCCCTACGATG 121448
|||||
Db 119169 AGACGTAAACAAGAACTCCTCCGCGACGCGGTGGTGGAGCCCAACCCCTACGATG 119228
QY 121449 GAGTGGATGTATAGCCAGAGAAACGGGGGTCTGTGGCCGAGACGCGCCGCTGGGTGTCT 121508
|||||
Db 119229 GAGTGGATGTATAGCCAGAGAAACGGGGGTCTGTGGCCGAGACGCGCCGCTGGGTGTCT 119288
QY 121509 GTGTGGCTACCGCCCTGTTTGTGCTTTAGGGAGATGGGGCTGTGAGGCGTTGGCATTTGG 121568
|||||
Db 119289 GTGTGGCTACCGCCCTGTTTGTGCTTTAGGGAGATGGGGCTGTGAGGCGTTGGCATTTGG 119348
QY 121569 GGTGTGCTCCGCTGATGTCGGCGCGGGGATTTGGGAGGGGGCGAGACGTCGCGTGGCGAT 121628
|||||
Db 119349 GGTGTGCTCCGCTGATGTCGGCGCGGGGATTTGGGAGGGGGCGAGACGTCGCGTGGCGAT 119408
QY 121629 TGTGGCGGTTCAGAGTATCGGAGAGGGGGCAAGAGAGCTGAGGCGGTTCAAGT 121688
|||||
Db 119409 TGTGGCGGTTCAGAGTATCGGAGAGGGGGCAAGAGAGCTGAGGCGGTTCAAGT 119468
QY 121689 GAGTCTGTGGCGATGTTTGCATAAAGACAGAGAGCTGCTGATTTGGGCGATTTATGCT 121748
|||||
Db 119469 GAGTCTGTGGCGCGACGTTGCAAAAGACAGAGAGCTGCTGATTTGGGCGATTTATGCT 119528
QY 121749 GACGACGCGCGTACAGTGTAGTGGGCGCGGGGTGTGACGCGGGGTGATGTTGGGCGGA 121808
|||||
Db 119529 GACGACGCGCGTACAGTGTAGTGGGCGCGGGGTGTGACGCGGGGTGATGTTGGGCGGA 119588
QY 121809 TGCATGCGGGGATCCCGGGAGCAACCTGACGCTGTTTGAAGTGCACAGCCCTGAAGCT 121868
|||||
Db 119589 TGCATGCGGGGATCCCGGGAGCAACCTGATGTGTTTGAAGTGCACAGCCCTGAAGCT 119648
QY 121869 AACACCGCGCGAGACCCGCTTGGCGAGCGGCTTGAAGATCCCAACAGATGACGACTCA 121928
|||||
Db 119649 AACACCGCGCGAGACCCGCTTGGCGAGCGGCTTGAAGATCCCAACAGATGACGACTCA 119708
QY 121929 GACCTGACCCGATGATGGCGACCTTGGGAGTACCGGCTGATTCGGGCGGCTTTCG 121988
|||||
Db 119709 GACCTGACCCGATGATGGCGACCTTGGGAGTACCGGCTGATTCGGGCGGCTTTCG 119768
QY 121989 GTGTCCGATCCGTCGCTTGTTCGCAACGCGCCGCACTTGGCGCCCTGATGTTGTGGA 122048
|||||
Db 119769 GTGTCCGATCCGTCGCTTGTTCGCAACGCGCCGCACTTGGCGCCCTGATGTTGTGGA 119828
QY 122049 GCGGGGGCGCGGGGTGC -GGC -GGCTGGCGCGCGCTGCCACGCCCCCTGCGCGCTCC 122106
|||||
Db 119829 GCGGGGGCGCGGGGTGCAGGCAAGCTGGCGCGCGCGCCAG - -GCCGCCCTGCGCGCGCTCC 119886
QY 122107 CCGGCTGTTCTAGTGGCGCGCGCTTCCGCAATGTCCCGCAGAGAACTTCCGAAC 122166
|||||
Db 119887 CCGGCTGTTCTAGTGGCGCGCGCTTCCGCAATGTCCCGCAGAGAACTTCCGAAC 119946
QY 122167 CGTGTCCGATTAATGCGGAGAGATGTTGCCGCGCTGCCCAACATGTTCCGCGTTACT 122226

D	11947	CGTGTCCCGAATGATGCGCGAAGATGTTGCCGGCTGCCCAATATGTCGGGTTTACG	12006	D	121027	GTCCCGCTGTCCATGTCCGTACAGTTTACCCCGGATTAACCGACGACGTCTGTCT	121086
Q	12227	GCCTGTAAAAACGGCAGATTAACTAGATTGCCCTTTCCACGACCCGACACCTGAGC	12286	Q	123307	CGGGCCGAGGCGACGTCCCGCACCCGTCGTAACGTGACACGGCGCGCCGAGCTGTGC	123866
D	12007	GCCTGTAAAAACGGCAGATTAACTAGATTGCCCTTTCCACGACCCGACACCTGAGC	12006	D	121087	CGGGCCGAGGCGACGTCCCGCACCCGTCGTAACGTGACACGGCGCGCCGAGCTGTGC	121146
Q	12287	GCGGCAGCAGCACTATGTTTATGTCGATGTCGATATGTCGCTAGGTGGCGGCTA	12346	Q	123367	AGCGAAGCTGAAGTGTTCCTCCCGGCCAACGGAACAACCCGTGTGTGGGTGTGTCAC	123426
D	120067	GCGGCAGCAGCAACTATGTTTATGTCGATGTCGATATGTCGCTAGGTGGCGGCTA	120126	D	121147	AGCGAAGCTGAAGTGTTCCTCCCGGCCAACGGAACAACCCGTGTGTGGGTGTGTCAC	121206
Q	12347	TTTTGATCTGCGCGCAGCCGATTAACCGTTAGGTGGCGCAGAGCCCGTTAACCGCAGC	122406	Q	123427	GTAACTGCGGTGAGACCCGGAAGACCTTGAGAACGCGACGTGCTGTACATATAGC	123486
D	120127	TTTTGATCTGCGCGCAGCCGATTAACCGTTAGGTGGCGCAGAGCCCGTTAACCGCAGC	120186	D	121207	GTAACTGCGGTGAGACCCGGAAGACCTTGAGAACGCGACGTGCTGTACATATAGC	121266
Q	122407	GAGACCGCAGCGGGGTTTATGTTGCTTACTATTAACGTTTAAATACCTGTGGCCCA	122466	Q	123487	GGTTTGGCGGGCGGGCCCGCTGAGACCCGCTGTTTTCGATATCCCTGGAAGGACAGC	123548
D	120187	GAGACCGCAGCGGGGTTTATGTTGCTTACTATTAACGTTTAAATACCTGTGGCCCA	120246	D	121267	GGTTTGGCGGGCGGGCCCGCTGAGACCCGCTGTTTTCGATATCCCTGGAAGGACAGC	121328
Q	122467	TATTTGGGTGCGAGTGTAACTACGCGCGCCGCGCCCGCTTACCTTGTCCGCGCGAA	122526	Q	123547	CACCTAGTGTGGGTGTGTGGCAGCGCGCCGCTTTTAGGCATTTTTTTAACGGGTGT	123606
D	120247	TATTTGGGTGCGAGTGTAACTACGCGCGCCGCGCCCGCTTACCTTGTCCGCGCGAA	120306	D	121327	CACCTAGTGTGGGTGTGTGGCAGCGCGCCGCTTTTAGGCATTTTTTTAACGGGTGT	121386
Q	122527	CCGGGAAAGTCTGTTCGCCCGCGCAGCGCGCGCTGCGGAAACCAAGCCGCTTGA	122586	Q	123607	TTTTTGTATAGTCTATGTAGCGCGCGGTGTCCCGCTGTCTAGTGTGTTTCCACGT	123666
D	120307	CCGGGAAAGTCTGTTCGCCCGCGCAGCGCGCGCTGCGGAAACCAAGCCGCTTGA	120366	D	121387	TTTTTGTATAGTCTATGTAGCGCGCGGTGTCCCGCTGTCTAGTGTGTTTCCACGT	121446
Q	122587	ATTTCGGGGGCGGTGGGCTTGGTGTAGTATTCACACAGATGCGATGTGGGCGGT	122646	Q	123667	GAGTGTCTCCATGACAAATTAACAATTTGAGGCTGGCTTTTATAGGTTGTTTGTGCGA	123726
D	120367	ATTTCGGGGGCGGTGGGCTTGGTGTAGTATTCACACAGATGCGATGTGGGCGGT	120426	D	121447	GAGTGTCTCCATGACAAATTAACAATTTGAGGCTGGCTTTTATAGGTTGTTTGTGCGA	121506
Q	122647	GGTGTCAACGTCATTTGTTAAACCCGTAATCTGGAATTCCTTGTCCGCGCGCGTGA	122706	Q	123727	CGCTTCTGTGTAACTGCTATACACCGGGGTGTGCGCAGAAACCGGCTTCCCTTATG	123786
D	120427	GGTGTCAACGTCATTTGTTAAACCCGTAATCTGGAATTCCTTGTCCGCGCGCGTGA	120486	D	121507	CGCTTCTGTGTAACTGCTATACACCGGGGTGTGCGCAGAAACCGGCTTCCCTTATG	121566
Q	122707	GGCGGGCCCTTAAGCCCTTATAGTGTGTGACAGGATCCGTAACCTGGAAGCGGGCATA	122766	Q	123787	TCCGCTGCCCTCCAGAGCGAAAGTGAAGATGTTCTCTGGGCGTTTGGCTTGAAG	123846
D	120487	GGCGGGCCCTTAAGCCCTTATAGTGTGTGACAGGATCCGTAACCTGGAAGCGGGCATA	120546	D	121567	TCCGCTGCCCTCCAGAGCGAAAGTGAAGATGTTCTCTGGGCGTTTGGCTTGAAG	121626
Q	122767	TAAACCCCAATGAGCGTGTGCGTGGTGGCAACCTTTTGTGAAAAAGATTTATTCGCGC	122826	Q	123847	AGTCGGGAGATGTGCGGTAGCGGCTGTGCAANAAGCTCACCCGCTTCTGTTTTTCT	123906
D	120547	TAAACCCCAATGAGCGTGTGCGTGGTGGCAACCTTTTGTGAAAAAGATTTATTCGCGC	120606	D	121627	AGTCGGGAGATGTGCGGTAGCGGCTGTGCAANAAGCTCACCCGCTTCTGTTTTTCT	121686
Q	122827	CGGGTGTAAAGACCAACACGACCGCTGTTTCAATTTATGCGGGAGAGATTAACATTA	122886	Q	123907	TTTTTGTAGACAAACAATGAGCGCTTGAACCAATTAACCTGATGGAATTTTC	123966
D	120607	CGGGTGTAAAGACCAACACGACCGCTGTTTCAATTTATGCGGGAGAGATTAACATTA	120666	D	121687	TTTTTGTAGACAAACAATGAGCGCTTGAACCAATTAACCTGATGGAATTTTC	121746
Q	122887	ACGCTGCTGTGGGAGAGCTTGGCAAGCTGCGGTGCGCTTCAAAAGCACTATGGGCG	122946	Q	123967	TGTCTAACTATTTGCAATGACTACAGTAACTATGACGCAATATGTCTTACACCTAGACA	124026
D	120667	ACGCTGCTGTGGGAGAGCTTGGCAAGCTGCGGTGCGCTTCAAAAGCACTATGGGCG	120726	D	121747	TGTCTAACTATTTGCAATGACTACAGTAACTATGACGCAATATGTCTTACACCTAGACA	121806
Q	122947	GTCCCGCTGCACTTACCGCGTCCCTGCGGTGCTGTAAACGACCCACGACGTTCTT	123006	Q	124027	CGGAATCCACGCTGTGTGGCTGACGGTGGTTTTTCCACCTACCGTTATGCAATATAT	124086
D	120727	GTCCCGCTGCACTTACCGCGTCCCTGCGGTGCTGTAAACGACCCACGACGTTCTT	120786	D	121807	CGGAATCCACGCTGTGTGGCTGACGGTGGTTTTTCCACCTACCGTTATGCAATATAT	121866
Q	123007	ATGCTTACCTGGGCAAAACAGGAATGCGCTAGTCCGTTAACTGAGGCGACATATATGTC	123066	Q	124087	CGTTTATTTATTTTGTGCAATGACGCTGTTTGGCAACGCGTGTGTCATATATTTT	124146
D	120787	ATGCTTACCTGGGCAAAACAGGAATGCGCTAGTCCGTTAACTGAGGCGACATATATGTC	120846	D	121867	CGTTTATTTATTTTGTGCAATGACGCTGTTTGGCAACGCGTGTGTCATATATTTT	121926
Q	123067	GAAGCGGGCAGCGTGTGTTACGCCCCCGTTTCGCGGTAGAGGTTTACATTTCCGAAACGAAG	123126	Q	124147	AATTTTAAAGCGCTCGCAACTCTGTGATGTACTGATGCGTGGTGTGTTGTAACCTCC	124206
D	120847	GAAGCGGGCAGCGGTGTTACGCCCCCGTTTCGCGGTAGAGGTTTACATTTCCGAAACGAAG	120906	D	121927	AATTTTAAAGCGCTCGCAACTCTGTGATGTACTGATGCGTGGTGTGTTGTAACCTCC	121986
Q	123127	TTTGAACGAAACGACCCCTGAAGTTTATTAATGCAACCTGAGAGAGAGGGGTCTACCTG	123186	Q	124207	TGTTTCTGTGGCGGCTGTTTGTTCAGCGGTGCGGTGTGACGCGCGCACAGATGCTCA	124266
D	120907	TTTGAACGAAACGACCCCTGAAGTTTATTAATGCAACCTGAGAGAGAGGGGTCTACCTG	120966	D	121987	TGTTTCTGTGGCGGCTGTTTGTTCAGCGGTGCGGTGTGACGCGCGCACAGATGCTCA	122046
Q	123187	TGTATCTTTTAAAGCGGTTTGAGTGGGAAAGCTGTGCGGAAACCCCTGCTTGAAGGTTTAC	123246	Q	124267	CGTCGCGACGCTGCAAGGTGGAATCTTTTCTTTTACCGTACACGTACTTTGGCGTGT	124326
D	120967	TGTATCTTTTAAAGCGGTTTGAGTGGGAAAGCTGTGCGGAAACCCCTGCTTGAAGGTTTAC	121026	D	122047	CGTCGCGACGCTGCAAGGTGGAATCTTTTCTTTTACGTACAGTACTTTGGCGTGT	122106
Q	123247	GTCCCGCTGTCCATGTGCTGACAGTTTAAACCCCGCATTAACCGACGACGTCTGTCTGT	123306	Q	124327	ACATTTGTGTGTATACGCTTATTCAGGTGCTGTGTAGTGTGTGTTTCCCGCGCGCGT	124386
D	121027	GTCCCGCTGTCCATGTGCTGACAGTTTAAACCCCGCATTAACCGACGACGTCTGTCTGT	121086	D	122107	ACATTTGTGTGTATACGCTTATTCAGGTGCTGTGTAGTGTGTGTTTCCCGCGCGCGT	122166

QY 124387 GGGTCAGACGCGGGGCTCCGGCTTCTGCGGTGTGTCTTTAATCGTGGCGTGG 124446
|||||
Db 124167 GGGTCAGACGCGGGGCTCCGGCTTCTGCGGTGTGTCTTTAATCGTGGCGTGG 122226
QY 124447 CGGTGTCTGCAACGCGGAGCTTATAGAGCGGCTCGGTCAACCAAGAGACGAGCT 124506
|||||
Db 122227 CGGTGTCTGCAACGCGGAGCTTATAGAGCGGCTCGGTCAACCAAGAGAGCT 122286
QY 124507 GGATATGCTACGAGATGCGGGGGAATACGCTCAACTGGAAGCTGAGAAATCAGAACCA 124566
|||||
Db 122287 GGATATGCTACGAGATGCGGGGGAATACGCTCAACTGGAAGCTGAGAAATCAGAACCA 122346
QY 124567 CCAGCGGATCTCGGGGTTTTGGTTCGGTTGGGGTGATGAGTCTTTTACGAGCTTA 124626
|||||
Db 122347 CCAGCGGATCTCGGGGTTTTGGTTCGGTTGGGGTGATGAGTCTTTTACGAGCTTA 122406
QY 124627 CGGTGTGTATGTTAAAGACGACAGCTGCGCAAGAAAGGAGCGCTTAAAGGTTAATGG 124686
|||||
Db 122407 CGGTGTGTATGTTAAAGACGACAGCTGCGCAAGAAAGGAGCGCTTAAAGGTTAATGG 122466
QY 124687 TGACGGTGGTGGTGTGTTTTAAATTTTGGCTGCGCTATCACCTGTGCACTTTTGG 124746
|||||
Db 122467 TGACGGTGGTGGTGTGTTTTAAATTTTGGCTGCGCTATCACCTGTGCACTTTTGG 122526
QY 124747 ACACCTGTGAGAGACCGGTTTTCTGGCGAAACGTCTACCTCAAGGAGAGTATACGC 124806
|||||
Db 122527 ACACCTGTGAGAGACCGGTTTTCTGGCGAAACGTCTACCTCAAGGAGAGTATACGC 122586
QY 124807 TGCCCATGCACATATCTCTCTCTACAGAGCATGTATAGCGGCTTCTGCCAGTCTGT 124866
|||||
Db 122587 TGCCCATGCACATATCTCTCTCTACAGAGCATGTATAGCGGCTTCTGCCAGTCTGT 122646
QY 124867 ATTCTGCTGTGGGTCTGTCTGTATAGAGAAAGGTTAGGGAATACCTGCTCGGTAAAGT 124926
|||||
Db 122647 ATTCTGCTGTGGGTCTGTCTGTATAGAGAAAGGTTAGGGAATACCTGCTCGGTAAAGT 122706
QY 124927 GTTTTTCACTTCAGGTATGTTATGAGACACTCAGCGACTTGGTTGGATTGTTGG 124986
|||||
Db 122707 GTTTTTCACTTCAGGTATGTTATGAGACACTCAGCGACTTGGTTGGATTGTTGG 122766
QY 124987 TACATTTATTTTATTTTGTGTACATTTATTTTCAATTAAGCATCTGACCTCAGACCT 125046
|||||
Db 122767 TACATTTATTTTATTTTGTGTACATTTATTTTCAATTAAGCATCTGACCTCAGACCT 122826
QY 125047 TACCTACGTTTCTGCTGTCTTATGACACAGAGAAACAGGAGCTGGAAGCCACGC 125106
|||||
Db 122827 TACCTACGTTTCTGCTGTCTTATGACACAGAGAAACAGGAGCTGGAAGCCACGC 122886
QY 125107 CCCACGGGAAACTGTATGTCCGCAAGCTCGGGGCGACGTACGCCCACTGCGAGGGGT 125166
|||||
Db 122887 CCCACGGGAAACTGTATGTCCGCAAGCTCGGGGCGACGTACGCCCACTGCGAGGGGT 122946
QY 125167 GGAACGTCAAGCGGGGGGTGACAGGAGGCGCAGGTGGCGCCGTCGGGTGACGTGATGG 125226
|||||
Db 122947 GGAACGTCAAGCGGGGGGTGACAGGAGGCGCAGGTGGCGCCGTCGGGTGACGTGATGG 123006
QY 125227 CGGCAACGGGCGAGTTGGGAGAGGGGTGGGTGGGTAGTGTGCGGAAATCTCGGGGT 125286
|||||
Db 123007 CGGCAACGGGCGAGTTGGGAGAGGGGTGGGTGGGTAGTGTGCGGAAATCTCGGGGT 123066
QY 125287 CGGCGTTGGCCGTGTGTAGTTTACAGGCGATGCGCTGCTGTTAGATGTGTACTCCA 125346
|||||
Db 123067 CGGCGTTGGCCGTGTGTGTAGTTTACAGGCGATGCGCTGCTGTTAGATGTGTACTCCA 123126
QY 125347 TGCGGTGCGCGGGGTATCTCAGCCCAAGGTACCGGCGCTTGGCCCACTGGAGAGCA 125406
|||||
Db 123127 TGCGGTGCGCGGGGTATCTCAGCCCAAGGTACCGGCGCTTGGCCCACTGGAGAGCA 123186
QY 125407 GGGCCGGAAGAACCTTAACATGATGTGATGTTGTTGGGGGATGTGAGTTAGCC 125466
|||||
Db 123187 GGGCCGGAAGAACCTTAACATGATGTGATGTTGTTGGGGGATGTGAGTTAGCC 123246

QY 125467 AGAGGCACTGTGGTTCCCTGATGCTTCTCTCCAGGTGATGTCCCACTGTGGGGG 125526
|||||
Db 123247 AGAGGCACTGTGGTTCCCTGATGCTTCTCTCCAGGTGATGTCCCACTGTGGGGG 123306
QY 125527 TTTTGGGTCCGGGCTGTGCTGAGGGGTCTCTTAAGAAACCGAGCGGCCCAAGAGCT 125586
|||||
Db 123307 TTTTGGGTCCGGGCTGTGCTGAGGGGTCTCTTAAGAAACCGAGCGGCCCAAGAGCT 123366
QY 125587 GGAACCCAAACTCCCGCAGCATAGTGAATATATCCGCTCGCGGGAAGAGCCCTTA 125646
|||||
Db 123367 GGAACCCAAACTCCCGCAGCATAGTGAATATATCCGCTCGCGGGAAGAGCCCTTA 123426
QY 125647 GGGCCCCATAGACCCAGGGCTGTGGAAGAACCATGATCGGCATCGGGCCCCACGT 125706
|||||
Db 123427 GGGCCCCATAGACCCAGGGCTGTGGAAGAACCATGATCGGCATCGGGCCCCACGT 123486
QY 125707 AGCTGTCTTGATATGCCACGCTTCCACCATGTGTACAGACCGGAGAAATCCCGGAGATGT 125766
|||||
Db 123487 AGCTGTCTTGATATGCCACGCTTCCACCATGTGTACAGACCGGAGAAATCCCGGAGATGT 123546
QY 125767 TCCCTCCTTAAGTGTGCTCGGTGAGACGGCGCGACGTGCAACCCGAGCTTGTGAAG 125826
|||||
Db 123547 TCCCTCCTTAAGTGTGCTCGGTGAGACGGCGCGACGTGCAACCCGAGCTTGTGAAG 123606
QY 125827 CGGCAATCAGCGCCCTGGGAAGCGGGCACCGGGGGTGACCAAGCGGCACTGTGGCG 125886
|||||
Db 123607 CGGCAATCAGCGCCCTGGGAAGCGGGCACCGGGGGTGACCAAGCGGCACTGTGGCG 123666
QY 125887 GCTCTCAGCGCGTTTGCAACAGATCAGTTTCTGTTCTGCAAACTCGCGCAGTGGC 125946
|||||
Db 123667 GCTCTCAGCGCGTTTGCAACAGATCAGTTTCTGTTCTGCAAACTCGCGCAGTGGC 123726
QY 125947 CCAAGTTGTGTTGGTTTGCACCGAGTCTTCTGTGTAGATTTCTGCGGGCGGTGAAG 126006
|||||
Db 123727 CCAAGTTGTGTTGGTTTGCACCGAGTCTTCTGTGTAGATTTCTGCGGGCGGTGAAG 123786
QY 126007 TGGGCCCCATGATGATCACTGTTCGTCGAGAAACGAGGTCAAGTTTGGCCACGAG 126066
|||||
Db 123787 TGGGCCCCATGATGATCACTGTTCGTCGAGAAACGAGGTCAAGTTTGGCCACGAG 123846
QY 126067 TGAAGGTCTGTGAATAGATTTCAATCGTTTGTGTGTAGATGAGATTTCTTCTGACAGAC 126126
|||||
Db 123847 TGAAGGTCTGTGAATAGATTTCAATCGTTTGTGTGTAGATGAGATTTCTTCTGACAGAC 123906
QY 126127 CTTCTGACCCAGGTTCCGCAACAGGTTGCGCGCGAGTCAAAATTTTGGCACGCCCTGGC 126186
|||||
Db 123907 CTTCTGACCCAGGTTCCGCAACAGGTTGCGCGCGAGTCAAAATTTTGGCACGCCCTGGC 123966
QY 126187 GCACTTCTGTGACGTGCTGGGGCTGATTTGAAAGATGACGCCGGGGTTTGGACACA 126246
|||||
Db 123967 GCACTTCTGTGACGTGCTGGGGCTGATTTGAAAGATGACGCCGGGGTTTGGACACA 124026
QY 126247 GCACTTCTGTGACGTGCTGCTGTGACGGATGCGAATCTGTAGGCTTCGGTTACCGCCA 126306
|||||
Db 124027 GCACTTCTGTGACGTGCTGCTGTGACGGATGCGAATCTGTAGGCTTCGGTTACCGCCA 124086
QY 126307 GGGCACTGTGATAGCGGTAAACACATGTGCTCGGTGAGAGTGTGGCGGACACA 126366
|||||
Db 124087 GGGCACTGTGATAGCGGTAAACACATGTGCTCGGTGAGAGTGTGGCGGACACA 124146
QY 126367 CCAGACCCCGGAGAGAGGCGCTGTGTAGATGAGAGTTGGCCAGGTGTGCGCT 126426
|||||
Db 124147 CCAGACCCCGGAGAGAGGCGCTGTGTAGATGAGAGTTGGCCAGGTGTGCGCT 124206
QY 126427 GAACTTCGGTTAGGGTGTGACTGTGGCAAGAGACACAGGTCTCAAAAGTTGATTCCTGGG 126486
|||||
Db 124207 GAACTTCGGTTAGGGTGTGACTGTGGCAAGAGACACAGGTCTCAAAAGTTGATTCCTGGG 124266
QY 126487 TCAAGTGGCGGACGGGGAAGGAACACGACGATGAGTTAACGGTGGGCTTACAGTCAG 126546
|||||
Db 124267 TCAAGTGGCGGACGGGGAAGGAACACGACGATGAGTTAACGGTGGGCTTACAGTCAG 124326
QY 126547 GTGTGAACGGGTTCCTGAGACACTTCACTCGGCGGTGGCTGTGATGACACTGTCTTAA 126606

QY	128767	CTGGGTCCGTCATCCGTCGTTGTCAAAGTTATTCAGAGGGCGGTGTTACAAAGCCAAAGTAAAA	128822
Db	126547	CTGGGTCCGTCATCCGTCGTTGTCAAAGTTATTCAGATGGCGGTGTTACAAAGCCAAAGTAAAA	126606
OY	128837	ATTCACTAAAGCAGCTGTTCTGCGACAAAGGCCCAAAACACTTTTGGCTCCGAATTTGTCAT	128886
Db	126607	ATTCACTAAAGCAGCTGATCTTGGCAGACAGGCCCAAAACACTTTTGGCTCCGAATTTGTCAT	126666
OY	128887	GAATTAAGACCTCTCTTCTTGAGCTAAAGGGCTGACAGGCCCAAGCAGAGGGTTCTGCGCTT	128948
Db	126657	GAATTAAGACCTCTCTTCTTGAGCTAAAGGGCTGACAGGCCCAAGCAGAGGGTTCTGCGCTT	126722
OY	128947	GGGCGATATTGCTTAAGTCTACCGCGCCCAAAAGCAAGCGGGTGGGACTTTAATAGCGCG	129006
Db	126727	GGGCGATATTGCTTAAGTCTACCGCGCCCAAAAGCAAGCGGGTGGGACTTTAATAGCGCG	126786
OY	129007	TATAGGGGTTGTTAGGTATGCGGTGGGAGCGCGTCCATGTTACATGAGACT	129056
Db	126787	TATAGGGGTTGTTAGGTATGCGGTGGGAGCGCGTCCATGTTACATGAGACT	126836
RESULT 3	AF210726/c		
LOCUS	AF210726	130733 bp	DNA linear VRL 27-MAR-2000
DEFINITION	Macaca mulatta rhadinovirus 26-95 long unique region 1-DNA.		
ACCESSION	AF210726		
VERSION	AF210726.1		
KEYWORDS	GI:7329990		
SOURCE			
ORGANISM	Macaca mulatta rhadinovirus 26-95		
REFERENCE	1 (bases 1 to 130733)		
AUTHORS	Alexander, L., Denekamp, L., Knapp, A., Auerbach, M. R., Damania, B. and Destroiers, R. C.		
TITLE	The primary sequence of rhesus monkey rhadinovirus isolate 26-95: sequence similarities to Kaposi's sarcoma-associated herpesvirus and rhesus monkey rhadinovirus isolate 15757		
JOURNAL	J. Virol. 74 (7), 3388-3398 (2000)		
MEDLINE	20173730		
PUBMED	10708456		
REFERENCE	2 (bases 1 to 130733)		
AUTHORS	Alexander, L., Denekamp, L. M., Knapp, A., Auerbach, M., Czajak, S., Damania, B. and Destroiers, R. C.		
TITLE	Direct Submission		
JOURNAL	Submitted (02-DEC-1999) Microbiology, New England Regional Primate Research Center, One Pinehill Dr, Southborough, MA 01772, USA		
FEATURES	Location/Qualifiers		
SOURCE	1..130733		
	/organism="Macaca mulatta rhadinovirus 26-95"		
	/mol_type="genomic DNA"		
	/isolate="Macaca mulatta rhadinovirus isolate 26-95"		
	/db_xref="taxon:119193"		
	513..1784		
	/gene="R1"		
	513..1784		
	/gene="R1"		
	/codon_start=1		
	/product="ORF1"		
	/protein_id="AAF59980.1"		
	/db_xref="GI:7329991"		
	/translation="MEVLIEMILQVSVELLPAKLTSPVPTWCPRPHGDFITLNCRT		
	SPARORSQWRNNLTMGMSFYGLGVATVPATNTSDRACTKTTTBSRNNIDFRS		
	SRRLQERCSSTGYTANNTRYLRCTSGANVTLRNVFHLNSTAVANGTNNITFV		
	LTEKGVGYECSAFIGNEKVFQTLINVEFTSFTEKPTNIDPNESHNKTKQIQDTASV		
	QHPENYVVFSPVFSIGVLTGIAISLIMQLFTIRCNSESSSTNSASQTSYIQPSH		
	NORSNTNECSRHYTRNAHOESIELLPNOSTSPDSCCOLVLELVKNVAVDGOENT		
	NEVMQODVVAVENIEQTSYEDNVEHMDVSDTINPNPNYSGLILEVDVIFYNELEN		
	OYHGILLENLDHNEYNHNLAKMIEIDYDLE"		
	complement(1852..2418)		
	/gene="ORF02"		
gene			

CDS
complement(1852..2418)
/gene="ORF02"
/codon_start=1
/product="DHFR"
/protein_id="AAF59981.1"
/db_xref="gi:7329992"
/translation="MDIIVNCIVAVDEOLGIGKNGTWPMPVILRNEMVPOKMTSPSV
VGEKNVIMGKRTWSPSEKKRPLVNRINILSLELAEPPHGAFLARTLDDAFNPR
OKIKLEQNLNFWAIGKSVESVLAQCKPLKLYITRIMESDCEVPPSINFETYM
SELPEKDNFVENGIKYKQVYKKNFNK"
2595..3782
/gene="ORF04"
2595..3782
/gene="ORF04"
/codon_start=1
/product="complement binding protein"
/protein_id="AAF59982.1"
/db_xref="gi:7329993"
/translation="MFVPIPLTCICQYILVDSKDEGVYCLAPFPDRNWKTAQNE
NVAVTRELICRGEYKQLQANVYECLSNGTWTPNAECRRKCSNPEDILNKEVIT
TDSDAFNGSNITKTCNGYLLGATVRCILKLYDSNLVDMQAPATCELEKKQAP
DIENKYYVQGEFNYLETTIFETCKNDESLGNTLTCTMTGMSSTPCCQQTGSA
PIHDGSLSSRYKRGKSGOATYCEGGFGLFNHMKOTCSLAMPNLPICVINT
DPTSEVSGPKKBDGEMTPPENPKSHSEETTTTETPKOTGHSTSPKPYNPTETK
TTPENGISKQTTTNRKAPSQNPPVIAPEMKNKHVVLVLFASVSLVLAALICG
FLK"
4213..7611
/gene="ORF06"
4213..7611
/gene="ORF06"
/codon_start=1
/product="ssdBp"
/protein_id="AAF59983.1"
/db_xref="gi:7329994"
/translation="MAKSGNAGQPLEDNGSRAPIGAGGYVAYSKODPPEASITLG
NRSSGYSPLIYGLVYEHNEPETYAAKAKYDTTLTAKYCFPIREYVFNINSL
RPVYDGLNLECEARNALFGYTFIEPGPHSIWNLCEPOLPDDENMLGVYVE
GKEKELMGCGLPVAFFQVQVOVQIAGROAKVPLVDEDLFAPHGHRMRFYHFKDASV
YDSLSTIAQALRIKDYAVIHAIEKOFMODHYIAKIVQAKOFSTLPTKTDGSHM
IYDSVFAASLYSGCMFLPECPODAEELNYSMPILFQDQSPEARVNALERMSAEQAV
HYAGOLFVAASLYLTKYKOKAPRGOKGDVAVNSPFLQHLGFLNLEATTIKENSGAF
KGVPRNALDGSSFTPYHLAYAASBPHLLALCYTMOLFQHKHSTQOAPRMNYVCT
KANSEGTGCHGNTPATLNTLFTLKORPRAVTPPOKRDYVVTGTAGTINDSLTFL
NEASRRDEEDGNPADDEHPKTYTWOLCQTVPEKLSAIGITEHDHNVNLTNTISLR
VEKGIDSIVDEGVMEKFNYSKNNFNEHEKSVHILQFCQNYWOAPCAVEFLNYL
KSLMTIDICLPYCMATIEODNPAGILPSEMLKHEPOTLTNTFKACLDGVLTTGEE
LKIVHRMDFPEFDIDAGSNGLMAPEKQVRIARMMVPSIKIRNTIESNAGESE
AVOSGFVAPETGRDITYVAGPYMKFLNSLHRLAEPRDTKTAALYMKHISQTKPULK
DVPDELELVSVKYNLSLAFETVNLVDVDSLSTARIKLNALILRAGQIOFVAT
TLHCTLPVLOTIDAEYEPHYLGSALIAIPVAYLAEIRBTLATVOTKARPOVATGKL
RVLIVYAVPNKYTVGNNNVNFHCGNIGYAGAGVGNVNLPESSPQKYSYMLKRL
RHVMWTPIIDRIKRAAGCOTISTFEASVKSRSVALLDEKQNPMLKLSVILEIRHIG
KCCQOLDSSEDOYVIGDCYMLTDEYLPFLNDINAGSVCPWTEDAGCALIEDQADDDQ
FVDSDDIATASQPEEOLPTPSAGALLGAKRKRIINALSDLL"
7636..9696
/gene="ORF07"
7636..9696
/gene="ORF07"
/codon_start=1
/product="transport protein"
/protein_id="AAF59984.1"
/db_xref="gi:7329995"
/translation="MARLEALVQLSALAVDSLVIFFADPRSIDGARILKTKQIENL
INRDLITLIRENSYESTLSLEVEHLKINLEDKLGELESRLORSYRSHEFFELTFL
PCRHHSYVTFQFYGGGLIDVNMKILINDYELLCRIGSYPCFICANERALSGLDVLIT
LSTLKGISFTIPPLDLYVTSVPCVQCLREIELVPMQSSLLVADVADRHCIDCKVVRNE
PLHGLEFNSQGLKTKRRSDATQOGRSSADOLRESLSALIDOHNI PKVYSVNSL
LSNLYNNAAGQLOGTQENECOSMARLLTHEADMHERRALITPKLATHYDCEFRPD
PLESFCGGLSFSDITINALSPDCSYVFOQAVYTNVMRKONELFRLNLSILGOSGA
GSKARATSEPTTVAATTAASDVTKAOYKREQYMKVADGKRTKTECLOQOAVILV
ANALCMRWGCVAYGEASELVNHLRRRPAALRPEARCRSDOLLFENSKITKSLYS
QSLSEHEHETIDTQFGLTGRDQLFGPANNVLAQCFEAGMI.PHKMKVYSEEM
IMPQLOPKDWIDTQFNREYOLPEBGLNVAQNSACFIRELVSAVALNRWMEKTLRE

SLAREKLSISNLDVKGGLTSGLYTYEDQAPLVLSQNTGWIIFKDLIYALLYHHLQSLDSC
HDDN"
9683. .12172
/gene="ORF08"
9683. .12172
/gene="ORF08"
/codon_start=1
/product="ORF08"
/protein_id="AAF59985.1"
/db_xref="GI:7329996"
/translation="MAMTRRRRLRLRAWVILAIIGTAGVGNTPPKAGTATKPPPC
STPPPPPPAPPAEAFKFRVCSASATGELFRPNLEGGTCDKTHQDELLWVFNKNIY
PHIKVRKRRKRVASVTVYRCMTETATGCKEVRIPVQYETINMHDITTYOCSSRRV
VNGVINYTDQDFINQVFLQPVESGLDINIDRFESQPVLYTPGMFPIYRRTTVNC
EIVIMIASABEPISEYFALDIVEPSPCHNDSTCSVAEKTEENGLGVRALNTYIVD
FATRPPTETREVFADSGEYVSMKADEKSAVCALTLEKTPPRAIOGTHASVHFVAN
DYATFTPTSEVANEFTGYSCLDEVIQKINDTIKTLSDHVTYNGSOXYKEGELF
LLMOPLAPLSLIDEMRGNGTTPAPATTSVSRVRSRNEQATMDLAPLOLQAFY
DKLRASINKVLELELSRACRQGVPTTYMWEISKINPISVMTAITGRVSAKFVSDAI
SVTDCVAVDQASVSIHKSRLSTPGWCISRPVTRFELNSTTLEFGQLGPRNEILLTD
NOVEACKETCEHYFIASNVTVYKDYVVKINISEITGLTFALNLSFENIDERY
IELYSRAEKKLSGSVFDEITFMREYNYTORIAGLRDLMTIDILNRDLARDLSEIV
ADLDGVKRTVVNVAASVITLFGSIVSGFINFKSPFGGMLMVLVAVVLVYFALNR
TNATAQAPIRMIVPIDIKMOPSGGKVQDEQIKNIIAGHQLOQEEERRRLDQGRAPS
LEFRASDLKRRFRGKRLNDEADQYEMSK"

12290. .13334
/gene="ORF09"
12290. .13334
/gene="ORF09"
/codon_start=1
/product="polymerase"
/protein_id="AAF59986.1"
/db_xref="GI:7329997"
/translation="MDFNPYILGPPRPHSHRGTDAPAPAGACVAPPDVCRLIPA
CLRRPAGAGMIIPVITPPPTFENGARGDVLILANRSMTATDRKVPAPDDQDSITF
HAYDVETVTAADRCAPVPSRFPNDIISGTVIKLGGTEGCTSCVAVPRQOYFVA
KVPACINTVTHILOAKNTAGRAAGFESTRYNKKITLTYYAEHPVETILSSSML
STLSRLVACGCEVFESNVDAVRFLDHGFTTEGWCARVTPRLARDAWATALEFD
CSMEDLSVOADRSWMPYRIAVADIECTEGAGFPATDGDVAIDISCVYTTREGAP
NPPIILFSVGTCDIPDIDVLEPSEYDMLVSFFAMIDFEVDELTGNIINFDPIYL
ITRASOVNRLNREYTKIKTGSIFEVHEPRGGGGFMRSVSKIKAGIVPIDMVOCV
EKLSDYKLDIVAROCIGGKREDSYKIDIPRLSPSGGAKSVYVMSVYIMDL
LKMPIHVEISEIAKLAKIQRVLYTDGQURLFSCLEAARENFILPVLPPEOCG
YOGATVINPIGFIDEPVLVDFASLYPSIIQAHNLCTYIMHGDPLHLHPDPDDY
ETFLVSGGPHVHKHKRRESLLGRLLVLEKRRRIKRTLAACDPSLKITLDKQGLA
IKVNCNAVYGTGVASGLLPCINIAETVLEKRTLEMSKSYEALTEEDTRETREGRE
VTARHGAFFRVYVGDPSLFTACDGSAAEVAFCDDLAARTADLPPLIKLEAKT
FKCILLITKRRYIGVILDKMWKGVDLIRTKACKFOEORAILDILVHPPEYAA
RLUCRRPHAYVEBGLPAGFTIKYIEVLAASITDLNSVYPIEQLTFSTELSPVCDYK
TINLPHLAVYOKLASRCELPOVHDRITPYEVVDAGSLKSLDAEHPDYVROHQIPVAV
DLYEDKLVHGAANILQCLFENNADTTVALYNLVNVPYKLFs"

15429. .16679
/gene="ORF10"
15429. .16679
/gene="ORF10"
/codon_start=1
/product="ORF10"
/protein_id="AAF59987.1"
/db_xref="GI:7329998"
/translation="MLVNELSVLIGDMVEVTFHGRFSPVNLTRLOTFEKHGGVAVRIL
PESLDQLHQHFAFGLVYTRLEKELPPFSCVALIAPLDSGDADARAPAGVYLDSSRP
LTVWNASGRIHTIRFCLELFLPITIDERAVTVYFVGENGARSGETKPKCAIESLGGP
LRVSEASQTSPIHFAVLPPTANSVACISLRLQVRPSSDAARDARISRYVFN
SGWVNCASVHTLSPSRCTAQMEEITVAPGDNAEITVIGSGSPVLPHTGGRGVYVA
DAEKTIQPGSSAEVAVOLIFQOAGARGDLAFIVGVADEPLVVTPTALLISGCTHLL
RLFNNGCPPTIKRDTLYAAAPCVVRLSSADAPRLVAVSPDIALSINAFTIPVC
FPGVVSACHTVSLDNGVHERMNH"

16688. .17917
/gene="ORF11"
16688. .17917
/gene="ORF11"
/codon_start=1
/product="ORF11"

Query Match 1.2%; Score 172; DB 1; Length 130733;
Best Local Similarity 100.0%; Pred. No. 3.1e-89;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 131523 TTGTGTTTGGTTCGTGGCGGATGATGTTGGAACATTCGTGTTTGTGATGTTAGGCC 131582
|||||
Db 130332 TTGTGTTTGTTCGTTGGCGGATGATGTTGGAACATTCGTGTTTGTGATGTTAGGCC 130273
|||||

QY 131583 AAACGTGGAAAACATTAAGAGTTGTTATGAATAATTTTGTGTAACAAACCATGTT 131642
|||||

Db 130272 AAACGTGGAAAACATTAAGAGTTGTTATGAATAATTTTGTGTAACAAACCATGTT 130213
|||||

QY 131643 TTAGCTCCCAAGAACATTAATAATGTTTATAGAACATGCCATGACAG 131694
|||||

Db 130212 TTAGTCCCAAGAACATTAATAATGTTTATAGAACATGCCATGACAG 130161
|||||

RESULT 4
CHV1G/C 2007 bp DNA linear VRL 29-AUG-1995
LOCUS Caprine herpesvirus type 1 gene for glycoprotein gC.
DEFINITION 249225
ACCESSION 249225.1 GI:804975
VERSION 249225.1 GI:804975
KEYWORDS glycoprotein gC.
SOURCE Caprine herpesvirus 1 (CPHV-1)
ORGANISM Caprine herpesvirus 1
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae;
1 (bases 1 to 2007)
REFERENCE Hecht P., Engels M., Loeffe E. and Ackermann M.
AUTHORS Comparison of the glycoprotein gC genes of bovine and caprine
TITLE herpesviruses
JOURNAL (in) Schwyzer M., Ackermann M., Bertoni G., Kocherhaus R.,
McCullough K., Engels M., Willek R. and Zanoni R. (Eds.);
IMMUNOLOGY OF VIRAL INFECTIONS. PROC. 3RD CONGRESS EUROP. SOC.
VER. VIROL.: 147-152;
Fondation Marcel Merieux, Lyon (1995)
2 (bases 1 to 2007)
REFERENCE Engels M.
AUTHORS Direct Submission
TITLE Submitted (09-MAY-1995) Monika Engels, Institute of Virology,
JOURNAL Faculty of Veterinary Medicine, University of Zurich,
Winterthurerstr. 266a, Zurich, CH-8057, Switzerland
FEATURES
source Location/Qualifiers
1. .2007
/organism="Caprine herpesvirus 1"
/mol_type="genomic DNA"
/db_xref="taxon:39944"
258. .264
TATA_signal
331. .1896
/function="virus attachment"
/codon_start=1
/product="glycoprotein gC"
/protein_id="CAA89200.1"
/db_xref="GI:804976"
/db_xref="SPTREMBL:Q66044"
/translation="MAPLGRAMLLALVCAWALGAGAGAGAHASPPPPAPPEGSEEG
DDARETIPATGTGQDVASDTPPAPEPATDPSASAPADIGATPNNDSPDPG
AEBDAEEDGAEERDDDEAPRACRPPRSPKPPGRMMCLCDHMAAPYA
DPLVYNGCVAAADAAAAGPARLEIMFLTRGRRSSGDAESVRNPPRAGPALLIAIEN
CTVAYRDARAGGATILFPAPTPDRRLPLTRISLTATBEVYTRWRRTAGADLKTYVT
THRPDVAIAPRPTLRGAGHSAECCAAYITPPKSTRLEWRNRTVDFQARDEFENS
EAGLSRTSVVTLDEAGADSHPPNLRCSVFSQSLMNRREMAPVLAIVDPPBELRA
FEGEAVCEAVCEVERNTLRMAVADGAAAPATAATLAGVCAERGLVNLVSRLSG
ADGPVAVTCTAAGYBEPLPEPSVETIYDASPSAAAGPILISGVVCAALGAAGVLL
VYACIRCARPRRL"

polyA_signal
1947. .1954

BASE COUNT 238 a 767 c 752 g 250 t
ORIGIN
Query Match 0.1%; Score 20; DB 1; Length 2007;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 132803 CCGGGCCCGGGCCGCTCG 132822
|||||
Db 709 CCGGGCCCGGGCCGCTCG 690
RESULT 5 5077 bp DNA linear VRL 28-AUG-2000
KS082242 Kaposi's sarcoma-associated herpesvirus chemokine receptor homolog
LOCUS gene, complete cds and large viron protein gene, partial cds.
DEFINITION
ACCESSION U82242 GI:9931979
VERSION
KEYWORDS
SOURCE
ORGANISM Human herpesvirus 8 (Kaposi's sarcoma-associated herpesvirus -
Human herpesvirus 8)
Human herpesvirus 8
VIRUSES: dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Rhadinovirus.
REFERENCE 1 (bases 1 to 5077)
AUTHORS Guo,H.G., Browning,P., Nicholas,J., Hayward,G.S., Tschachler,E.,
Jiang,Y.W., Sadowska,M., Raffeld,M., Colombini,S., Gallo,R.C. and
Reltz,M.S.
TITLE Characterization of a chemokine receptor-related gene in human
JOURNAL virology 228 (2), 371-378 (1997)
MEDLINE 97223350
PUBMED 9123844
REFERENCE 2 (bases 1 to 5077)
AUTHORS Guo,H.G., Browning,P., Nicholas,J., Hayward,G.S., Tschachler,E.,
Jiang,Y.W., Sadowska,M., Raffeld,M., Colombini,S., Gallo,R.C. and
Reltz,M.S.
TITLE Direct Submission
JOURNAL Submitted (13-DEC-1996) Inst. of Human Virology, University of
Maryland, Baltimore, 725 W. Lombard St., Baltimore, MD 21201, USA
REFERENCE 3 (bases 1 to 5077)
AUTHORS Guo,H.G., Browning,P., Nicholas,J., Hayward,G.S., Tschachler,E.,
Jiang,Y.W., Sadowska,M., Raffeld,M., Colombini,S., Gallo,R.C. and
Reltz,M.S.
TITLE Direct Submission
JOURNAL Submitted (28-AUG-2000) Inst. of Human Virology, University of
Maryland, Baltimore, 725 W. Lombard St., Baltimore, MD 21201, USA
REMARK Sequence update by submitter
COMMENT On Aug 28, 2000 this sequence version replaced gi:1930013.
FEATURES
SOURCE Location/Qualifiers
1. 5077
/organism="Human herpesvirus 8"
/mol_type="genomic DNA"
/db_xref="taxon:37296"
44. 1072
/note="ORF74"
/codon_start=1
/product="chemokine receptor homolog"
/protein_id="AAB51506.1"
/db_xref="GI:1930014"
/translation="MAAEFLITFLDDESNENLTANSGYDYSNFSLEVSVCBMTTV
VPTWNGIISLILINLVNGLVYIFCKHRSRAGAIDILIGLCLSLISLLA
EVLMEFLPNIIISGLCEIFPYLYLIDFISVVCGLVRLIVASTRSPKOSL
GWLTSAALISALVSGDACRHSRVDPYKQMCENGNMADRRLRYRTSYTA
GFLPLALILFLFALTCVVRKRLQARRVGVIVAVLFEFECFPHVNLNLDTL
LRRRWIDSCYTRGLINVLAVISLQALYSAAVPLIYSCGLSKQRMVGLQSLRQ
SFMSGART"
complement(1223..>5077)
/note="ORF 75"
/codon_start=1
/product="large viron protein"
/protein_id="AAB51507.2"

/db_xref="GI:9931980"
/translation="DLTADAEAFVSFYTSTRTGLTLVPGTGAGYLLMTIFRRPPTSR
EERERDVEIOTVLAVSLPGLGYPHVIRSPRSERSEVSGPYNNHRTTSTEL
GVILRELGLOMAVEVGRHLYSKITOTLTLEPPOTIRAFOTQDILVRYGLEVRPG
POPYARPHIEDVITMOAVMISLGDILPLAYOASTGNNVNFVIFPGRTMRMRH
NCARQARFIEHVAIVHVSVOGRIGLNLHSTLPPGGCTGALGTGATGALP
RAHSFRIRIFAKDQOAEMLQAGVPTLGGFLKVRRTIATPGNALVCSISTTJSKE
CISLRMIPOOTVCLGFEPTDGPDPYPNLYROSSNAVR1LETLVORLACPIE
SGLNRSHPAPVVRHLOIAPRTGLTELPVSPREVRHLBPADAGDAVEAAVHE
FLANYCSLVAVVAESGAVPGDLETLEVIQARACAOITYLGRSTRDQRIYD
DLGCTTRVSVSDPPSPSWLALSDGVNCSGPEVDWGLATGISTHQLRHAT
VGSKFEFTFRHMDRCNSGLIAQOAGVPLDIPVSDYHLVHSSMLAEVAPVPTVEA
ITPSMANILHDKDEFTWVKAIPOLLPVPMAGQAMAGEQAKMATVSGATVATE
ALTNLMSEPVSKLODVLVTGAVAMPDHQAGLLOCELPACKEGCELVALSISAA
SSPILSRHVRITQOQEVLPENSVFTSMARKSRRVTPDPVREGALVYLV
NOSGLINGSTFEHNFASRHPILPNSTVSLMLVKYLSKRLIYSGHIGGGGL
PSATEMLAGRGQLSLPHPNPLELNVSTPGALVEPOVHLSEVLARADRCVA
HPLGTVPREGGNVTVLQNETVVEFTLSLOYSWTFSDEMNVLVPLPLDNDH
RKDGRLEHHLGSLRAMCLGSLRLFCPTSPRVAALVLPSSAPYALMALQNTGF
EVATVVEELKRGQSLSGSLITCLRTGCOASYASARGVIALCNDPTCASTLTEL
NRPTFSICGGEVGFOLVNLGVYGRSSSPYTGPPPMQAVNLEFNVSKLYDSH
LNTQIPONTKSVFRLRGVLPMSAGEVILGVYEDDALEYILRQGEITLYHGNA
ADETLPRHYPNRTGNTVAGLTFSSGRRHALIIDPSLHFMQOMQHVPPDLTPLSH
SPWMAAQOSIYLMVSKKINDH"
BASE COUNT 997 a 1418 c 1524 g 1138 t
ORIGIN
Query Match 0.1%; Score 20; DB 1; Length 5077;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 126300 CCGGCCAGGCCCATCTCGAT 126319
|||||
Db 2481 CCGGCCAGGCCCATCTCGAT 2500
RESULT 6 6671 bp DNA linear VRL 16-FEB-2003
AY189899
LOCUS Pseudorabies virus strain Ea UL15 (UL15), UL17 (UL17), UL16 (UL16),
and UL14 (UL14) genes, complete cds; and UL13 (UL13) gene, partial
cds.
ACCESSION AY189899
VERSION AY189899.1 GI:28395421
KEYWORDS
SOURCE Pseudorabies virus
ORGANISM Pseudorabies virus
VIRUSES: dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Varicellovirus.
REFERENCE 1 (bases 1 to 6671)
AUTHORS Xiao,S.B., Zhang,H., Fang,L.R., Niu,C.S., Ma,X.R. and Chen,H.C.
TITLE Sequences analysis and identification of splice site of
JOURNAL 1 UL15, UL16 and UL17
2 (bases 1 to 6671)
REFERENCE 2 (bases 1 to 6671)
AUTHORS Xiao,S.B., Zhang,H., Fang,L.R., Niu,C.S., Ma,X.R. and Chen,H.C.
TITLE Direct Submission
JOURNAL Submitted (03-DEC-2002) Lab of Animal Virology, College of Animal
Science and Veterinary Medicine, Huazhong Agricultural University,
Wuhan, Hubei 430070, P.R. China
FEATURES
SOURCE Location/Qualifiers
1. 6671
/organism="Pseudorabies virus"
/mol_type="genomic DNA"
/strain="Ea"
/db_xref="taxon:10345"
complement(324..5469)
/gene="UL15"
complement(join(324..1466,4351..5469))
/gene="UL15"
/note="DNA packaging"
/codon_start=1

/product="U15"
/protein_id="AA038880.1"
/db_xref="GI:28395422"
/translation="MFGLDATRRYADLKKRREASERDCAEARFFNEAIAAPORHQ
TVPAVGTLHNCESARIFAGLARAALGAAVADPALARAEALEFAAYDEGRL
AFHRAAYTSAMAVDAMRSNGAFROLRPVNFALISRPSPDATTALGTGACAGT
GADDDGDEKEDDGGAAEKRGAGVAPGRPEDEDAEERKSGSGGGGGTGGGAK
GGGGGGGGGTLELFQKMLHNAVFLATVLLGSHAERATVLLAEDTPLESEDAV
RHFROAVTVLVKRGENTVTPDGARSTVIVASSHNTGIRGODPNLTFDEANFIR
LRMCRRADRVHDKENITVTPDGARSTVIVASSHNTGIRGODPNLTFDEANFIR
PDVOTILGPMNOASCKIIFVSTNTGASTISFLNLTGMDLNTVYTCDEHMRV
AHTDPTACSCVYLKPFVTMDAARTTAERLLPDSFMETLGGAVAREAPVTLRAA
GERLLYRPSSTANRLLAGTILHYVDPAFTANARFGGVAVYGSYRSNIVLELH
FFRLALGASADEIRACVRCCLARYLALHGDASFARVAVSGNSQDSVAVLGMAR
ELAEELRAARVAVADPVPVYFHGAPGAGAVYPPFLQOKOTPAFDEFVKONGAV
MASOELVSVTGARADPVEYLNAOLGNVETASGGEHVEFTGKRGACADIALVALV
AVHSLTPDGLFA"
1517. 3316
/gene="U17"
1517. 3316
/gene="U17"
/codon_start=1
/product="U17"
/protein_id="AA038881.1"
/db_xref="GI:28395423"
/translation="WDAHIANTKQOMTFEPALVHVIVPDLRRAGVPLAPRAH
AOTRYHSGVCEPWPVSFAGHVOTGAVESVLTLPLOKARGGGLFVSLPLAGAFD
GTTAVALLVGAELIFETVDELTPARTRVVNDERLELCROFANARARVPEVAAA
GGHIDALLPAPAATIDEGEOLTRGGEDEPAPAHADORELITLVRADDELVAAPHV
RSHVSGLMOGALRRGGDGGSGALAEAAAPAPAPRAAGAGDGGGAMRELLTTP
ODRPLTALDMDIAGYALAGGDAPAHVRRPRLVARRHOTETETVYVAAEHSTTA
WGRGRPASEPLARVLAECERHVEHPALAELELVRHSHALAVPLGEEPELP
VFDAFAELVLEFRFNACVRLAGVRESVREPMMROIIEAIRPBRBEALVDVAGR
APALIDAEARLLETQPARREVDSGLTAAALARAAGVTFESGGLGVLEFDY
YSAGEVIRTRAPPAVAVPATRCGFACRFACRGLPGRSVAYLGVASRDRLAL
VYLPGEFEPALRLWEPALVDPVLERLCRV"
3343. 4329
/gene="U16"
3343. 4329
/gene="U16"
/codon_start=1
/product="U16"
/protein_id="AA038882.1"
/db_xref="GI:28395424"
/translation="WEVAALITEDFAANRLRSDSRKVYAALGVYAAVLAAPGAA
TVDAVYVLTREPRLAQRHVVVLLNDAALVAAYVTTLRSGGELVRLITGDA
SLEALPADLCPVAPVPAVSRLDDAAEPVSAAPARRCECVLAPGAMWSDRITFL
OMDPALLALCPAGMRARHLAGVLAGLISPRDDGGSCRCRECVHDVALNATPHPDGA
GAACICAPCLMRDOKREIRASDSGLFRVFLDPAVRYRMIPRRKIVYASGLGL
DARGRHVYVNDAGRVLVLDPDASHALVCGCFLRALCDPPSRALPELINDY"
5468. 5947
/gene="U14"
5468. 5947
/gene="U14"
/codon_start=1
/product="U14"
/protein_id="AA038883.1"
/db_xref="GI:28395425"
/translation="MFASDRRERVRVLAEFORSEVFKARTVELLRGRADKKNPFEVR
AFMAKQARVDVERHLRLAARYESVEOKARALQAVRQAAVRAVGLDRRRRTADPA
FALDAADDAIYAGEURLDAAALDDMAAGGDPDEDEGEADGALLTOMLEEAAEA"
5917. 5671
/gene="U13"
5917. 5671
/gene="U13"
/note="protein kinase"
/codon_start=1
/product="U13"
/protein_id="AA038884.1"
/db_xref="GI:28395426"
/translation="MAAGGGGGSRTALAPPVIRHGTSAFCGGDGDGBASVTLGRAG
PREAVYLIPRPGDLAVPDDLOVATFDLTGDPVAVAGAGSYGSLVAVYATTLRAGF
GHEAVMTLLAEATRSAGVRYVRLVGLSAPLRQLVFRAYEEDMDAYRKSULTARBGH

BASE COUNT 795 a 2443 c 2573 g 860 t
ORIGIN
Query Match 0.1%: Score 20; DB 1; Length 6671;
Best Local Similarity 100.0%: Pred. No. 2.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 122692 CCGCCGCGCGGTGAGCCGC 122711
Db 3695 CCGCCGCGCGGTGAGCCGC 3714
RESULT 7
KSU40394/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
source
1. 8481
/organism="Human herpesvirus 8"
/mol_type="genomic DNA"
/specific_host="Homo sapiens"
/db_xref="taxon:37296"
/clone="Lambda SGL-1"
/note="provisionally designated HHV8; Isolated from an
AIDS-related body cavity based lymphoma"
83. 4009
/note="ORF 75; tegument protein; similar to ORF 75 of
Saimiriine herpesvirus 1; Swiss-Prot Accession Number
P11282 and to tegument protein of Epstein-Barr virus
(strain B95-8); Swiss-Prot Accession Number P03179"
/codon_start=1
/product="membrane antigen p140 homolog"
/protein_id="AB04748.1"
/db_xref="GI:4154095"
/translation="MAYDVTGLMLESDDLTADEAFVNFYSRTGTLTLVPGTGGYL
LWITRRPPTSEERSEKDEIVQVLAIVSLPGVPIRIRSVPRGSEFVSFGYGP
LMHRRPTLTSTELAVLOELGQEMARVVGRLVSKITQTLLEPDPQPIRAFTQNTD
LVPTGLEVPBPQVAPARPHIEDVIMQAVMISLGGDLPLAVQASTQDNVNAVRYV

Query Match	0.1%;	Score 20;	DB 1;	Length 28559;
Best Local Similarity	100.0%;	Pred. No. 2.5;		
Matches 20;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY 126300 CCGGCCGAGGGCCATCTCGAT 126319				
Db 16548 CCGGCCGAGGGCCATCTCGAT 16567				
RESULT 9				
LOCUS 293872				
DEFINITION	U93872	133661 bp	DNA	linear VRL 09-JUL-2001
		Kaposi's sarcoma-associated herpesvirus glycoprotein M, DNA replication protein, glycoprotein, DNA replication protein, FLICE inhibitory protein and v-cyclin genes, complete cds, and tegument protein gene, partial cds.		
ACCESSION	U93872			
VERSION	U93872.2	GI:14627174		
KEYWORDS	Human herpesvirus 8 (Kaposi's sarcoma-associated herpesvirus - Human herpesvirus 8)			
SOURCE	Human herpesvirus 8			
ORGANISM	Viruses; dsDNA viruses, no RNA stage; Herpesviridae; Gammaherpesvirinae; Rhadinovirus.			
REFERENCE	1 (bases 29032 to 30108; 117733 to 118431)			
AUTHORS	Zhong, W., Wang, X., Herndler, B., and Ganem, D.			
TITLE	Restricted expression of Kaposi sarcoma-associated herpesvirus (human herpesvirus 8) genes in Kaposi sarcoma			

CDS	/note="ORF 09, DNA polymerase homolog"		
	/codon_start=1		
	/protein_id="AAB62593.1"		
	/db_xref="gi:2246468"		
	/translation="MDPEPPIIDTPRGGRPRNTVROPTEPSPVPSPTKRCRLIPAC QTPGARGVAVDTPEPTPTFOGPKRGVEFAGTSGIWKTRGQARNAMSLIHVVD IYETVTVADRCEDVPSFQTDIPSGTVLKLILGRILAGASCVAVRQRCYFYLAQ GVNLIVHQALQALQAFGASCSFSTEPYRKILRAYDQAVAKITLSSSPMRTIS DRLTTCCEVESNVDAIRREVLDHGEFTFGMCSPNAPATQARDSTLEFPSCME DLKFIPTETMPPTIISFDIEGCKGEPNADDEMIIOISCVLHVGDKRYTRM LLGLGTCDPLPGVEVPEPSEYDMIAFLSMRLRYNVEITIGYNIANDPYIARAT OYVDFKLODFTKITGVSVEYHVRGSGDGGKPMRSOSKVAISGIVPDMIOVCREKL SLSYKLDITVAKQCLGRQKDISYKDIPLERKSGPDGAKVNCVIDSVLMDLLR FQTHVEISEIAKLAKIPTRVLTGQOQIRVSCLEAAATGYILPYKGVADGYOG AVTISPSPGFDDPVLVDFASLYPSIIQAINLCYSTLIPDSLHLHPKSPDYETF VLSGPGVHYVKKKRESILAKLTVMILAKREIKRTLASCTDPALKTIDKOLAIVY TCNAVGETVAGSGILPCINIAETVTLQGRMERLSQAFVAISPERIAGLRPIDV SPDARKVITYDTSLSLTCCMGFMDSVSDPAEELATITTTTLFRSPKLEAEITFC LLILTKRYVGLSDDKYLMMKGVLDLIRKTACRQVQESSVOLDILRPPVAAAKLI SGAQDMVYREGLEGFEVKIIOVLNASHRELCERSVPLDKLTFTTELSRPADYKTON LPHLVYOKLQARQELPQIHRIPIYVDFVAGSLRSLSLAHPYVQKHGRVAVDLY FDKLVHAVANTIIOCLFQNNMSATVAMLYNFIIDIVTFPTP"		
	14500..15756		
	/note="ORF 10, herpesvirus saimiri ORF 10 homolog, conserved in other gamma-herpesviruses"		
	/codon_start=1		
	/protein_id="AAB62594.1"		
	/db_xref="gi:2246469"		
/translation="MGTETAFILGDWEITVSNCFCTCSILTCGLPYRSSGDTPLRLIP			
Query Match	0.1%;	Score 20; DB 1; Length 133661;	
Best Local Similarity	100.0%;	Pred. No. 2.7;	
Matches 20; Conservative	0;	Mismatches 0; Indels 0; Gaps 0;	
Db	132104	CCGGCCAGGCGCATCTCGAT 126319	
LOCUS	KSU75698 137508 bp DNA linear VRL 03-MAY-1997		
DEFINITION	Kaposi's sarcoma-associated herpesvirus long unique region, 80		
ACCESSION	U75698		
VERSION	U75698.1		
KEYWORDS	GI:2065526		
SOURCE	Human herpesvirus 8 (Kaposi's sarcoma-associated herpesvirus - Human herpesvirus 8)		
ORGANISM	Human herpesvirus 8		
REFERENCE	Viruses; dsDNA viruses, no RNA stage; Herpesviridae; Gammaherpesvirinae; Rhadinovirus.		
AUTHORS	1 (bases 47193 to 47522; 133099 to 133729)		
TITLE	Identification of herpesvirus-like DNA sequences in AIDS-associated Kaposi's sarcoma		
JOURNAL	Science 266 (5192), 1865-1869 (1994)		
MEDLINE	95090463		
PUBMED	7997879		
REFERENCE	2 (bases 35021 to 55726)		
AUTHORS	Moore,P.S., Gao,S.J., Dominguez,G., Cesarman,E., Lungu,O., Knowles,D.M., Garber,R., Pellett,P.E., McGeoch,D.J. and Chang,Y.		
TITLE	Primary characterization of a herpesvirus agent associated with Kaposi's sarcoma		

CDS	J. Virol. 70 (1), 549-558 (1996)		
	MEDLINE 9609469		
	PUBMED 8523568		
	REFERENCE 3 (bases 28661 to 29741; 117919 to 118101)		
	AUTHORS Zhong,W., Wang,H., Herndler,B. and Ganem,D.		
	TITLE Restricted expression of Kaposi sarcoma-associated herpesvirus (human herpesvirus 8) genes in Kaposi sarcoma		
	JOURNAL Proc. Natl. Acad. Sci. U.S.A. 93 (13), 6641-6646 (1996)		
	MEDLINE 96270595		
	PUBMED 8692871		
	REFERENCE 4 (bases 122794 to 123567; 123809 to 127297; 129372 to 130400; 130551 to 134441)		
AUTHORS Cesarman,E., Nador,R.G., Bai,F., Bohenzky,R.A., Russo,J.J., Moore,P.S., Chang,Y. and Knowles,D.M.			
TITLE Kaposi's sarcoma-associated herpesvirus contains G protein-coupled receptor and cyclin D homologs which are expressed in Kaposi's sarcoma and malignant lymphoma			
JOURNAL J. Virol. 70 (11), 8218-8223 (1996)			
MEDLINE 97048116			
PUBMED 8892957			
REFERENCE 5 (bases 1 to 137508)			
AUTHORS Moore,P.S., Boshoff,C., Weiss,R.A. and Chang,Y.			
TITLE Molecular mimicry of human cytokine and cytokine response pathway genes by KSHV			
JOURNAL Science 274 (5293), 1739-1744 (1996)			
MEDLINE 97094384			
PUBMED 8939871			
REFERENCE 6 (bases 1 to 137508)			
AUTHORS Russo,J.J., Bohenzky,R.A., Chien,M.-C., Chen,J., Yan,M., Maddalena,D., Parry,J.P., Peruzzi,D., Edelman,I.S., Chang,Y. and Moore,P.S.			
TITLE Nucleotide sequence of the Kaposi sarcoma-associated herpesvirus (HHV8)			
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 93 (25), 14862-14867 (1996)			
MEDLINE 97121480			
PUBMED 8962146			
REFERENCE 7 (bases 1 to 137508)			
AUTHORS Russo,J.J., Bohenzky,R.A., Chien,M.-C., Chen,J., Yan,M., Maddalena,D., Parry,J.P., Peruzzi,D., Edelman,I.S., Chang,Y. and Moore,P.S.			
TITLE Direct Submission			
JOURNAL Submitted (17-OCT-1996) Dept of Pathology/Genome Center/Division of Epidemiology, Columbia University, 650 West 168th Street, New York, NY 10032, USA			
REFERENCE 8 (bases 1 to 137508)			
AUTHORS Russo,J.J., Bohenzky,R.A., Chien,M.-C., Chen,J., Yan,M., Maddalena,D., Parry,J.P., Peruzzi,D., Edelman,I.S., Chang,Y. and Moore,P.S.			
TITLE Direct Submission			
JOURNAL Submitted (02-MAY-1997) Dept of Pathology/Genome Center/Division of Epidemiology, Columbia University, 650 West 168th Street, New York, NY 10032, USA			
REMARK Sequence update by submitter			
COMMENT On May 3, 1997 this sequence version replaced gi:1718251.			
FEATURES			
SOURCE			
1..137508			
/organism="Human herpesvirus 8"			
/mol_type="genomic DNA"			
/db_xref="taxon:37296"			
/cell_line="BC-1; virally infected primary effusion lymphoma derived cell line"			
/note="sequence derived from overlapping lambda phage and cosmid clones isolated from libraries; A prototype sequence for the terminal repeat (TR) unit is deposited under GenBank Accession Number U75699. The left junction variant TR sequence unit immediately preceding base pair 1 of the LUR is deposited under Genbank Accession Number U75700. The remaining LUR sequence extending from this sequence to the right TR unit is not available due to difficulties in cloning and sequencing of this region"			
1..137508			
/note="long unique region LUR"			
105..974			

/note="ORF K1"
/codon_start=1
/protein_id="AAC57081.1"
/db_xref="GI:1718252"
/translation="MELVYVCSLAVCFRGLISLSLSSRLCPGVSTPYTLTCLNSA
SLPLISVYCNNTRLRLTERVILDTIACNFCVSGHOSITWTRADPVLDTLCAQ
PSATVYGOHVLTLCSTSGNNYVHMLPNGRNTVSOTKYNTFLMSDEGCTLVGK
LSRLSNRCLCFMARCANITPETHVSVSTSGRTSTNSVLIIHATRDVYVVEA
KSTHFIEVHFLVFMFLVALIGTMCGLCTIIFAHQKQKQDSKVTQQDQDYSLHD
LCTEDYTOPDVW"

1142..2794
/note="ORF 4: The HVS ORF 4 homolog has alternatively
spliced messages encoding membrane bound and secreted
proteins; complement binding protein vCBP homolog"
/codon_start=1
/protein_id="AAC57082.1"
/db_xref="GI:1718253"

/translation="MAFLRQTLMLTFTWVIGDNEKCSQKLTIGYRLKMSRDGIA
VGEYVELRCRSGTYTARNITATCLOGTWEPTATCNKSCPNPELIONGVTFHG
ODALKGANISYVCEGFLVREYVRCMIGASGOMASSSPCEKEKCHRPKIKN
GDPRKPOXYENDAVFECNEGTVLGVPHSICAVNNTWNTSMPTCELACGKFPST
HGPRKGFSLYTHKQSVTFACNDGFLRGSPTITCNTEMDPLCKVLEDIDDDNN
SNBRRLHPTNPKRNGNVFORSNYTEPTPKPETHRTAATCDTNCBPRLPTSEFN
EYTSWTITKQLEDEKTIQPNTHITSALTSMKAKNFTKNTNSTDHLHASTPTSD
DAPTSIPSVQTPNVTNMAPRTLTLSTHIEGPNSTSEKATSSLSHNSKMDTGI
YTLNKTQPLSPNKTNSQASSTKPRVETHNKTISNPAISLSDADVPQRPREPTL
PLPRPASKNRLEKQVLIGLTLVALTCGLITLHFHYLFR"

3210..6611
/note="ORF 6: ss DNA binding protein ssDBP homolog; EBV
BALF5 homolog"
/codon_start=1
/protein_id="AAC57083.1"
/db_xref="GI:1718254"

/translation="MALKGPQRLTEENIGSAPRPGCYLYAVLTNHPICEASILNG
YBRAKFSPLHLGLTVESDFPLNKAANKIDATTAASKLTSIHEAIFYHNTHLFQ
PLTQGLKLEKCSRELFGSTFVEQHQKGLTWSEAPQELCAEITMAVITVTFG
KERLYGKLVLPVSQTPVHIGHOAFKIPLEDDEDFRQAEKLFNPNDSITSLH
DSIFGTGIAQALRYKADVTYIOASEROFVDQYKIPLVYAGDPOCARCTDSTLMV
IDSLVAELGMSYGLSFTIEGPODCEVLTNPFIENCEPDRRLALEVHMEOLH
ICAQLFAANSVYTLFRVAKLPQKNORGDANVTSLPHGICYSIATYKENGASAFK
GVYVSLDSSSYTLQHLAYASSFSPLHARMCYTLDFLPHKNTNSQSYNVYVSTA
APSQMCDLQGGCPAVICINTLFYRMKDRPEVLSNKRQDYVITAGYVNDLEILGN
FATFEREEGNVEDAPRYWQLOQNTKTEKASNGISEGVALTLLVIDIPSEVYK
FNGIDSTVAELKFTNCMKIKNNYFNRENTKSVHNLQACNVYQAPCPVEFLTYK
SLTIVIODICLTCMAYEODNPAYGIVPSMLKMHOTMMTNKGCACPDGATGGEL
KITVHOSMPCDLEDTDAIGMFAPOVRIAMAMVPTIKIKRILFENSTGSES
IQAGFMKPAQSQDSYTVGCPYMKETLNAKLTLEPSTKTSALYIMHIGOTKRPILPG
VGEHLELCNTVYKASSQAFEEINVLDPDLTSTYAKTIKNSILIRACQTOFYAT
LSCLSPTQLVPAEEYPHVLGVLSSPEYRAKVGASVTIVOSTLKOAVSTNGRLR
PIITVPLVYVYKYSNGNTNVEHCANLGYFSGCVGRNRLPESVPKKNVSSMLRR
HYIMTPLVRLVRYVINGINSPEEAIVKRSYQNVLEDRNPLPRTVYVELYKPRM
SSGASLTREDVYIYIGPVAIVGDEVLSLTSTVQACVPMVAEVSADVIQDIDDCLO
FYGPREPCLIGOGSVYELFPSPGVSLTYGKKRKLASLSDLT"

6628..8715
/note="ORF 7: transport protein homolog; EBV BALF3
homolog"

/codon_start=1
/protein_id="AAC57084.1"
/db_xref="GI:1718255"

/translation="MAKELAAVYADYSALAMDCLISYADPATLDTKSLALTGKQS
LHQTLLPLLRONAHCSGLSELEHFMKTMMLWBRWCEALANLOKSIPIESCMT
OHTSNRSVFNFGYMALEKLKSLINDEIVEFKRSLVAYICGSSASLEGLEVEF
VQKLRISVFPNDLYVNLPCLEECLOCLTPNOSTSLOAMPDACISICTPAGE
PVKGLFENELKQIGLOTPEISPTPCOSIRRODELRSSIAMVGHHTFGEYTRVL
EISNLTYSSGSHDATCDGDRCSHLASLFTHADMHKRRVYDAGLCEGEGYTKHFD
CFRPDSLETLFCGGLFSVEDTIESLQKDCSFAFYQVANTYALQKONEGYTSLKDL
AAGOLIGKCSSTESCSSEARQLVGGKGPBEYLRARQELILQKVARGPKRLKDC
IRHOGHILSQTGLRLMGSVIYNASALQNHFLRAQFISLPMODLTVCPTFEENS
YIKNSYICORLGRHEVEILTEFYKLITGPKLSRPHLPSPRPVATLCEAGMGLPH
OKMVSSEMIWPSIEPKDMTEPNQFSPENDINILQKRAMVYITAEIVSYELVYRT
WERELKITLTPGSSPGFERKPAGLTTGLTLTFETSPALVLDKTKGWLKFDLYALY
HILQISNHNDSOV"

CDS

/note="ORF 8: glycoprotein B gb homolog; EBV BALF4
homolog"
/codon_start=1
/protein_id="AAC57085.1"
/db_xref="GI:1718256"
/translation="MTPRSRLATGLVILLVCFCAQAANSRGDTFOTSSPPRPGSS
KAPTKGEESGKSVDFYOFRCASISITGELFRFMLEGCPCTKQYHOEGILLVYK
KNVPIHFKVRYRYKATSTVYRGLESITRKVYELPRPLYEISHDSTYQCS
MKVNVGVENTFDRDDVNTVYLOPEGLTDNIOGFEQSPVYIARPGMPGLYVRT
TYNCEIVDMTARSABRYNYEVSISGTVREYSPKCYMESSGSTPSKNGISQVVLNH
TVYVTSDRGTSPTPQNRIVETATYATLMSASEKTTAVCPALMKTPRSIOTTHDS
FHVVAEITATFTAPLTPVANEFTDYSLTSDINTLMSKAKLASTHVPNGTVQYFH
TTGGLVLMQPMASINLTHAOGSGNPTSPSPSAPMTTSARRRRSASTAAAGG
GSDNLSYLOLFAVDKLRDGINOVLELSRAMCROVRDNLMLWELSKINPTSVTA
IYGRVPSAKVEGDAISVTECINOVSSVNHKSLRPNKQVCYARPLVEKFLNSML
FTGOLARNEIITNNQVEKCDTCGEYETTRRETYVYDAATRLINTDSTLMPF
IALNLSFQINIDKALIELYSASAKRASSFDELEMPRENTYTHRLAGLELDNLT
DMKKEFRDLSEIVADLGIKTVVNAVSSVVLGSLVYGTINFTKHPGLGMLTI
IVAIILITFMLSRRNTTIAQAPVKMIYPDVDRAPPSGAPPREIKNLLGMHOLQ
QEBRKADDLKSTPSVFORFANGLRQLRGYKPLQSLDISPETGE"

CDS

/note="ORF 9: DNA polymerase homolog; EBV BALF5 homolog"
/codon_start=1
/protein_id="AAC57086.1"
/db_xref="GI:1718257"
/translation="MDFNFPIDPTRGPRNTVROPTPSQSPVPESTRYCRLIPAC
OTRPGVAVAVDTFTPTPYOQGRGVFAGFEGFSIMKTRGOARNAPMHLFEHYD
IYVETTYTADRCGEVPSFORDIIPSGTVIKLIRTDLGASVCVNVRORCXYTLAPQ
GVNLHVLOOALDAGFGRASCSTGTEPRVKILIRATIDQYAVOKITLSSPMRTLS
DRLTGCEVEFESNVDAIRREVLDHGFSTFGWYECSPARTQAROWTELEPDCSME

Query Match 0.1%; Score 20; DB 1; Length 137508;
Best local Similarity 100.0%; Pred. No. 2,7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 126300 CCGGCCAGGGCCATCTCGAT 126319
DB 131809 CCGGCCAGGGCCATCTCGAT 131828

RESULT 11
EHV020824
LOCUS EHV020824 184427 bp DNA linear VRL 02-FEB-1996
DEFINITION Equine herpesvirus 2, complete genome.
ACCESSION U20824
VERSION U20824.1 GI:695172
KEYWORDS
SOURCE
ORGANISM Equine herpesvirus 2
Equine herpesvirus 2
Gammaherpesvirinae.
Gammaherpesvirinae.

REFERENCE 1 (bases 1 to 184427)
Telford,E.A., Watson,M.S., Aird,H.C., Perry,J. and Davison,A.J.
The DNA sequence of equine herpesvirus 2
J. Mol. Biol. 249 (3), 520-528 (1995)
JOURNAL MEDLINE 95302501
PUBMED 77833207

REFERENCE 2 (bases 1 to 184427)
Telford,E.A.R.
Direct Submission
Submitted (09-FEB-1995) Elizabeth A.R. Telford, Institute of
Virology, MRC Virology Unit, University of Glasgow, Church Street,
Glasgow G11 5TR, United Kingdom

FEATURES
source
1..184427
/organism="Equine herpesvirus 2"
/mol_type="genomic DNA"
/strain="86/67"
/db_xref="taxon:133899"

repeat_region 1..17553
repeat_region 9248..10399
CDS
/rpt_type=direct
/note="ORF E1"

```
/codon_start=1
/product="G protein-coupled receptor"
/protein_id="AAC13788.1"
/db_xref="GI:695173"
/translation="MATTSAITVNTSSLATMTNTFTSLTSLVTTIASLPSTNSS
EDYDDLDVDYDESAPCYSDPTRLAAQVPAALYLVFPGELGNTLLVYIVRYK
IKNTITLMLNLATLSDLFLTLTFPMNHITGMHYDMTFPGLSLCLGVCMSLSXSY
FCITLLVDRLAVAVATLRLRFVTCGIVTCGTFGLAGLSLPEFFRHODDNG
RVQCDPYPEKSTWMMRAHAKVIMSLIPLIMAVCYVIIIRLLRPSKKRYA
IRLIFVIMVAFVFWPYNIVLSTFHAFLNLQCALSNLMDALLITKTVAAVTHCC
INPIYAFVGEKFRRLHYHFHTYVAIYLCYIPLSGDGEKGGPTRI"
polyA_signal
10494..10499
/note="ORF E1"
10660..10665
/note="ORF E1"
12533..13114
/note="ORF E1"
14197..14541
/note="ORF E2"
18810..19733
/note="ORF E2: product has hydrophobic N-terminus"
/codon_start=1
/protein_id="AAC13789.1"
/db_xref="GI:695174"
/translation="MIIIGLVLSLASTASAIQAMMPQVITGHEGRPLSYCHYAK
NPSKPMIMMLIKTEGSAFRTGIVPRKGPVYTKSSSGGVFTVDSLHMAADGRA
CMVQENDPKDESQSDYHNTATNIVLETPRRSLIGPOLPTTAGRSTQISQTPG
LSSQESRVSVAVRKGVKVVYSSSLHVECPGATAGINTISAVLEFKVGEATQAVT
ISTSLTTLTDLSPVIEGTQAKWCGVNATKEDSGEVMCMIGMDFPEEGEGSGDEDFSG
VDFPKITVTEPEGDEDDDLTYTSSEBEKK"
polyA_signal
19761..19766
/note="ORF E2"
19784..19789
/note="ORF E2"
20320..20844
/note="ORF E3: product has N- and C- hydrophobic domains
and 6 N-linked glycosylation sites"
/codon_start=1
/protein_id="AAC13790.1"
/db_xref="GI:695175"
/translation="MATEVQPAALVVLGCGVATPTPSKSTLIYNSQNTYPSIE
NGOSLYTSGDAGGPGCTLSRDVAIPMMQALLLEH.IRQOOLRRPLVLDAGEAGRP
GEGEATPTIPK.IILAVSEFHTLMSLHSIKOHNAVIM.CNLSGSPASFCRPGIGFTPLG
DPGERDLKFAVRVPALAHKADALAKLPEMFREHSDVLTGHRGAIKIRNFENG
LGYRLIYAPTSAFVIDEDVSSNGKRGPFYGVVGVGSIISGASELDDLYEAGFGM
GNVLGLHGVYSGEDDPALQOELYESHMLAQRGSGAPILLGFAVMDGSAAPDMGPA
SRPSFTGATASITSRKACLSPIVRGGASVPMIGDFPQRPQARAGATAHSDGRRLA
SILAAVOTFINVAGRAVLSTQSGRLBETMAKITAACGVMLKTYTSLDPEAVSEL
SHFSPGNASNMRSILSKFLNVEAOVYLLVYVPPRNQOLIEGKFTGCGVSLGLHL
ARAKIYLYDRSDPYCOGGRYLCLFMHKRPALPIDRMCGTASYRPTAPSRPYN
SDAPSPDAREVLGILRHPTVGCKNTYVKHVDRCASRGVQOOGVGLDPLVDVSM
VYVPSAGPSPSMPTWMPPOVDFDCLIHEDGVSGYCSALGKSNVFEPPYBAGK
MAIASEVLSIALAPIAREDTYVNLSTAMPILKQAQGVFTLLIRKRCFCDAVSCN
VTSASSRRAGGDPREGADIKSFVASAEVYTPCAEWKLLPDLKEASVLIPLPASP
GKAFAASYQOVRQKRYTSPVNI.SGAYTLKRLCAHVAHLAKRLAVSGHVGQGLM
AALAMAMAGMRSLDVEYVRLDGPMLFSETPGVALLEVLPSASAVAYLSKYL
LCYRVGTGKTEKRMFRIITRGDOVLLCEDEEVEARSHVNERERGGFENHAY
EGYPEREAREALATPRLI.NRPNKHKHVAVALILPGCYPLAALDALDEPFDALAS
HLDLAHVTIDVCGILFVAGVNTSDTKSDMLTSALVHSRNPCTIRDLRSKDTFSLG
VGSMACTRLFEGDMAVSPALDSRDIRCVPAVSCFESRWLVFINQSDPAFETLRG
SILPCMAQGTILHGAPSPCECLRLVLSGSAAMEYSGDSVAGMAPAPVAPETLLPV
AGICSRDGRHLVTLHDITASYIYLMQMPHVKSNIP.IAVSPMKQVFEYDLHAHVTAHSH"
CDS
25639..26190
/note="ORF E4"
```

```
/codon_start=1
/protein_id="AAC13792.1"
/db_xref="GI:695177"
/translation="MVPSSREFFEEMDRVLENEAKUSLITNLKNVEAQTLDMAKPEV
LTREALALAMVDECKEYTHQLEIWMQVAVSEAPTTSAINSLGIIIRTHQOGD
NFRGLISLSPASCFLEVLVQSDRCISVFASLAKFYVESQNLIMLAYSGLSAGLRE
PFRSMYLPALOKKMLRFYEFK"
CDS
26436..29873
/note="ORF E6"
/codon_start=1
/protein_id="AAC13793.1"
/product="single-stranded DNA binding protein"
/db_xref="GI:695178"
/translation="MNSNRAAGVEENQVQASVGPCEVYLYPQSTPPEEASLIG
NLHAGVEFSLP.LLSGLTVEADFHVNNAKAKLDPTVSYKASATIREVYFPMAC
FKPIFAGGLEGLCAASRQLFGVAEFERAGARPELADLGLHLPGEASHLGVVY
TESFERLYRQGLVAVSLOISVQVEGDEAKVBLVYGELEFPAKSPCEBNLRFYHAG
SRVLEAHYTSIAOLARVDVPLIGALEROSFDQKLPKYECREFPATGHGACD
CSLTIYVAETELAVSYGLSFLVEYQSTALISYDKMPTPEGCEPTPOVRYALQFNA
KQAVHVSOLFSGNSVYLTLARVQKQASNRGGGGENVYSPFMHGACIAPENQKNG
LPSPGPVAPASALSGSNSLHLAYASPSQMLAKHCITYLQFAHQKSSNNGVNP
VYGTAAANTPMCELRCGCPASCVAVTLEYRLDRPPVAVASVRDPVYVVGAVYNDL
DIAGNFANYRDKDESNQSEEREKFTYQVOTVQLERLSEGEDEGDVDAIHNIG
SELKVFELIDGIVGEVAFRTNSMKNNVNRRESILH.IHIVQVCVWYQPCPEVL
NLVYRCVLAAYODICLPQMYAEQENAVGVSPQEMIKMYOTLMTNFKNSCIDKGYL
TGTEKYVYHNDPQDFPDVDSAAAGEVSCQTVYRISALMARVWKIKRRIIEFNS
PGTESIOAFAHGTDPKDGCVSGPYMFHLSITHSQLEPPGAKISPLTLMHTEKROL
PVFNPVRESVETELANVEQNSRLHGETSIIDVVEYFNTYAKRLNNAELRACGQTO
FYATTIHCLPDKIQTVPAEEYPAHLAGRVADVEYLGAAELVLPVVOCHRSNICE
VGKCRPIYTLPLNKKYTGTVGNSQIFQCANLGYFIRGVYKNLIPDAGSRKQGVST
SMRKRHFMPLSDHLRLRSYQAAVAVEIGVARRVOQLISDNDPHV.IHDVLOLY
KSLSECRSVSEVSEIYEMGOXYTFADQVSRRLORLSDIGGDSMEANALVLSGEEDP
LGELFEFEKVDACELCHPQODEFALAPQAAAPQYSSSSVAGKKRANVTLGDLG"
29997..32183
/function="role in capsid maturation/DNA packaging"
/note="ORF E7"
/codon_start=1
/protein_id="AAC13794.1"
/db_xref="GI:695179"
/translation="MARLEAVVAVQVEDLAELVSLGLYCDPSSIDKRCVANSKKVK
LCESLIPCLRLQNDTECSPLSELOHLQNLQNTREMLQVITDLSDDPSSEFEALHPS
RLBEGPCRHARHVRVPEYGAETKYSLSLNDVVEFRRLNSVYFCLEPABEALALGE
TVALFGLRGRVSPIDPADAVYSVPCASCFPEAAMLPOGSEVYSLMLAAVNCVHRC
VPSPDVCVCFENELRHIGADARAARGGSGEVRGDEEDDEDEEDRQDQGA
GDGAALRYLTSSLSVLAGHTIFEEEDRRLAEISNLVYSSAARCGYCGTARATSS
HMAKLIFAHEARMHRSRAWLGRGAPSHFDARPSLES.LFCGGFNS.IDDITIALQKD
CSATFLKKSNTOTLLOOQNELVRLNEVLNCGADEGACAKAEIA.AEAPLKPYGAS
CDPRLVSDARERDLYLKLTRDGLRLRITDICTETHGVSDTSLRYWGSALYASGA
RLVNHFLPERQFVGIMADILPAGGAFAENSKYIKNALHGQRLENHDS.IVAFYRL
ITGPLSIONSHFVPYDQVVALAYCIDAAGAMHOKRLVITEMPGIESKDWIDCNENF
YSIETGDNLTQKTLNITIRAVYLSISLNVNWKSSLSLSATFLRGCLAESAGEL
GEGVLYTEGTAPLVAVDSKGYVFKDLYTLTYLHLDSGRKQASV"
polyA_signal
30114..30119
/note="ORF E3, E4 and E6"
32195..34819
/note="ORF E8"
/codon_start=1
/product="glycoprotein B"
/protein_id="AAC13795.1"
/db_xref="GI:695180"
/translation="MGVGGGGRVILCLMCVAALLCGVAQVEVAETTPPEATHRPEV
AENRANPILPERYGCASPGGELFERPLESCNTEKDKHIEGIALIKYNIYVYF
NVKRYKIMSTITTYKGSBDATINQTHRSVAVLYPQMDHYQOESANQVWEGH
VNITYYDRQMWETFLKRAQDLSLITRYQSPRYATPRLNLSYTTITTYKCEVTE
MSASMKREFFEVYVSGDTIMSPSLIKENGTEPER.IKRPNS.IQLNLYAVTKYVGL
GOANARAEFFA.IFEDYSLSMKATENSSYCOLILMKGNSIAIQOHSNLF.IANDYT
ASFSTPEENAFNEDEPKC.IANNQOEELKATVEKTHRNGAKYKXSTL.IYV
OPLIOLIDHNAKLTNTATASPTSPYSPRRRDTYSVGGGNGDNGNSTKEES
VAAQOVFAIYNKSKINRYGELSRAMCRQYARSLAMWTLSKINPYSWALYGRP
VSAOLIGVAVNSQCI.SVDQSVFVHKMKAPGABDLCTIRPVGKFTINGSEL.PAQ
LGPNEVTEIYELYSKTEKRLSNVFDIENQMWYKRYDYYVSTL.LTDLPTLHMTTN
LSIVENIDFKVILEYLSKRYENLQNFQETNRYNYTQNLRLKRDSDISIDHGRD
SFIOITLGDIMQDLCTIGKVVYVNVASGVESLGS.IVSGVISPFFKMPFGMLIYLIAG
```

CDS

polYA_signal
CDS

VVVVYLFMTSRISYSAPIRMLYGVGERAAQEGAHVSESDIQRNLTMGHQPOQROR
AEEEARREEVKGKRTLFVYIRDSATSVLRRRGGGCGYRLQDGSDDDEGYEPLRRQ
DGGYDDVDVEAGADTGV"
34855..34860
/note="ORF 07 and 08"
35089..38115
/note="ORF 09"
/codon_start=1
/product="DNA polymerase replicative subunit"
/protein_id="AAC13796.1"
/db_xref="GI:695181"

/translaction="MSFMYLYVKRTFLKKAAPSRTKEYTRIIIPCKFTPGAAGVVP
HSTLDPVCFVGGKREPIILYGDGSRSLMSAGGCGGTGAGHPTVALFHHVYDIE
TVYGDRCDFVGFQFDIIPSGTVLKLRTSDRSVCVNVROELIYFVRYEGIK
LDFLIOGCSRENENFSGRYREKTSKRVLCREVCVAREVYVPAASSOGFVLDLAGL
TAGACVFETNVDAARFTIINDGSENGFPAASCAAPROGASARSDTELEFYCAGD
LEPHARADMPGCVNYLSPDIECGENGFPASDEDMILDISVYKMSGSGEAPRYVL
LNLGCEETEGEVYOCPSBLDLILYFTIRADVEFTGIVINSFDEYVIDRATQ
VYNLNLKEFTRVRSISIEVHKPKNSAGMRAVSKVAGVPIDMYOVCRLKLS
NYKLDIVAGECVGAKKEDVSYKEIPIHLFRGPGGARLGLCYVKSALVLDLRYEMT
HVEISEIAKIPTRRVLTGQOIVNFSGLDVAEGYILFVDRHADDEGYOGATV
IDPSPEVMPVLYVDFASLYPTIIQAHNLCYSTMIPODLICLPHLPGDYEFPFLA
SGPVHFVKKHKAIVSLATLNLWLAKRAIRRLATVSDAARTIILDKQLAIKVTCN

Query Match 0.1%; Score 20; DB 1; Length 184427;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 128283 CTCCTCGGGCCATGACGCC 128302
Db 65128 CTCCTCGGGCCATGACGCC 65147

RESULT 12
AH002374S1/c 165 bp RNA linear VRL 11-APR-2003

LOCUS AH002374S1 165 bp RNA linear VRL 11-APR-2003
DEFINITION Middleburg virus nonstructural polyprotein gene, partial cds.
ACCESSION K00699
VERSION K00699.1 GI:311523

KEYWORDS
SEGMENT
SOURCE Middleburg virus
ORGANISM Middleburg virus

REFERENCE
AUTHORS Ou, J.H., Trent, D.W. and Strauss, J.H.
TITLE The 3'-non-coding regions of alphavirus RNAs contain repeating
sequences

JOURNAL J. Mol. Biol. 156 (4), 719-730 (1982)
MEDLINE 83010261
PUBMED 6288962

REFERENCE
AUTHORS Ou, J.H., Strauss, E.G. and Strauss, J.H.
TITLE The 5'-terminal sequences of the genomic RNAs of several
alphaviruses

JOURNAL J. Mol. Biol. 168 (1), 1-15 (1983)
MEDLINE 83268700
PUBMED 6308269

FEATURES
source
1..165
/organism="Middleburg virus"
/mol_type="genomic RNA"
/db_xref="taxon:11023"

CDS
53..>165
/codon_start=1
/product="nonstructural polyprotein"
/protein_id="AAA46337.1"
/db_xref="GI:555233"
/translation="MARPVKIDVEAESKVKSLQVRFQFETEAQVTPN"

BASE COUNT 45 a 42 c 40 g 35 t 3 others
ORIGIN

Query Match 0.1%; Score 19; DB 1; Length 165;
Best Local Similarity 100.0%; Pred. No. 8.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 131128 TGACCTGCTCTGCTCGAT 131146
Db 155 TGACCTGCTCTGCTCGAT 137

RESULT 13
AF251159 824 bp DNA linear VRL 12-DEC-2000

LOCUS AF251159 824 bp DNA linear VRL 12-DEC-2000
DEFINITION Human herpesvirus 1 mutant gamma1 34.5 gene, complete sequence.
ACCESSION AF251159
VERSION AF251159.1 GI:11640715

KEYWORDS
SOURCE Human herpesvirus 1
ORGANISM Human herpesvirus 1

REFERENCE
AUTHORS Ling, J.-Y., Chen, T.-M. and Stroop, W.G.
TITLE Direct Submission
JOURNAL Submitted (03-APR-2000) Ophthalmology, Mail Slot: 523, University
of Arkansas for Medical Sciences, 4301 W. Markham, Little Rock, AR
72205, USA

REFERENCE
AUTHORS Ling, J.-Y., Chen, T.-M. and Stroop, W.G.
TITLE Direct Submission
JOURNAL Submitted (03-APR-2000) Ophthalmology, Mail Slot: 523, University
of Arkansas for Medical Sciences, 4301 W. Markham, Little Rock, AR
72205, USA

REFERENCE
AUTHORS Ling, J.-Y., Chen, T.-M. and Stroop, W.G.
TITLE Direct Submission
JOURNAL Submitted (03-APR-2000) Ophthalmology, Mail Slot: 523, University
of Arkansas for Medical Sciences, 4301 W. Markham, Little Rock, AR
72205, USA

FEATURES
source
1..824
/organism="Human herpesvirus 1"
/mol_type="genomic DNA"
/strain="4GC"
/db_xref="taxon:10298"
/clone="5-13"
28..786
/gene="mutant gamma1 34.5"

BASE COUNT 72 a 392 c 282 g 78 t
ORIGIN

Query Match 0.1%; Score 19; DB 1; Length 824;
Best Local Similarity 100.0%; Pred. No. 8.9;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 132498 CCGCGCGCCCGCGCCGCC 132516
Db 60 CCGCGCGCCCGCGCCGCC 78

RESULT 14
AF251158 947 bp DNA linear VRL 12-DEC-2000

LOCUS AF251158 947 bp DNA linear VRL 12-DEC-2000
DEFINITION Human herpesvirus 1 gamma1 34.5 gene, complete cds.
ACCESSION AF251158
VERSION AF251158.1 GI:11640713

KEYWORDS
SOURCE Human herpesvirus 1
ORGANISM Human herpesvirus 1

REFERENCE
AUTHORS Ling, J.-Y., Chen, T.-M. and Stroop, W.G.
TITLE Direct Submission
JOURNAL Submitted (03-APR-2000) Ophthalmology, Mail Slot: 523, University
of Arkansas for Medical Sciences, 4301 W. Markham, Little Rock, AR

REFERENCE
AUTHORS Ling, J.-Y., Chen, T.-M. and Stroop, W.G.
TITLE Direct Submission
JOURNAL Submitted (03-APR-2000) Ophthalmology, Mail Slot: 523, University
of Arkansas for Medical Sciences, 4301 W. Markham, Little Rock, AR

REFERENCE
AUTHORS Ling, J.-Y., Chen, T.-M. and Stroop, W.G.
TITLE Direct Submission
JOURNAL Submitted (03-APR-2000) Ophthalmology, Mail Slot: 523, University
of Arkansas for Medical Sciences, 4301 W. Markham, Little Rock, AR

REFERENCE
AUTHORS Ling, J.-Y., Chen, T.-M. and Stroop, W.G.
TITLE Direct Submission
JOURNAL Submitted (03-APR-2000) Ophthalmology, Mail Slot: 523, University
of Arkansas for Medical Sciences, 4301 W. Markham, Little Rock, AR

REFERENCE
AUTHORS Ling, J.-Y., Chen, T.-M. and Stroop, W.G.
TITLE Direct Submission
JOURNAL Submitted (03-APR-2000) Ophthalmology, Mail Slot: 523, University
of Arkansas for Medical Sciences, 4301 W. Markham, Little Rock, AR

72205, USA

FEATURES Location/Qualifiers

source 1..947

/organism="Human herpesvirus 1"

/mol_type="genomic DNA"

/strain="+GC"

/db_xref="taxon:10298"

151..909

/codon_start=1

/product="gamma1 34.5"

/protein_id="AAG39340.1"

/db_xref="GI:11640714"

/translation="MARRRRRRDPRRRRPPGPGVPTAQSQVSTSTNSEPAVRSAP
AAAPPSPGAGPSPSCSLLRQWLHVPSASDDDDDDPSPPEPAPEARPTAAP
RPRSPGAGGCGGAGNSHPSPRFLRLRVTAERLARLRRLRRAGGAPEP
PATPTPATPTPATPARVRSFPHVRVRLVWASARLARLRGSGNARERADARF
RRVAAVAVIGPCGPEARARALARGAGPANSV"

CDS

BASE COUNT 93 a 444 c 312 g 98 t

ORIGIN

Query Match 0.1%; Score 19; DB 1; Length 947;
Best Local Similarity 100.0%; Pred. No. 8.9;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 132498 CCGCGCCCCCGCGCGCCC 132516
|||||

DB 183 CCGCGCCCCCGCGCGCCC 201
|||||

RESULT 15

LOCUS HS1LS81 1213 bp DNA linear VRL 02-AUG-1993

DEFINITION HSV-1 (strain USA-8) L-S inversion region.

ACCESSION K01836

VERSION K01836.1 GI:330170

KEYWORDS repeat region; terminal inverted repeat.

SEGMENT 1 of 2

SOURCE Human herpesvirus 1
Human herpesvirus 1
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Simplexvirus.

REFERENCE 1 (bases 1 to 1213)
Davison, A.J. and Wilkie, N.M.
Nucleotide sequences of the joint between the L and S segments of
herpes simplex virus types 1 and 2
J. Gen. Virol. 55 (Pt 2), 315-331 (1981)

JOURNAL 82032334

MEDLINE 6270266

PUBMED

COMMENT Original source text: Herpes simplex virus type 1 strain USA-8 DNA.
This sequence contains a single b'a'c' sequence. See comment for
other HSV-1 L-S inversion region entries.

FEATURES Location/Qualifiers

source 1..1213

/organism="Human herpesvirus 1"

/mol_type="genomic DNA"

/db_xref="taxon:10298"

<1..330

/note="b' repeat"

311..327

/note="DRI repeat"

331..744

/note="a' repeat"

408..495

/note="reiteration Ia (8 copies)"

495..639

/note="reiteration Ib (6 copies)"

726..742

/note="DRI repeat"

745..>1213

/note="c' repeat"

974..>1213

/note="reiteration II (15 copies)"

BASE COUNT 138 a 569 c 352 g 154 t

ORIGIN 1 bp upstream of HinfI site.

Query Match 0.1%; Score 19; DB 1; Length 1213;
Best Local Similarity 100.0%; Pred. No. 9;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 132498 CCGCGCCCCCGCGCGCCC 132516
|||||

DB 186 CCGCGCCCCCGCGCGCCC 168
|||||

RESULT 16

HEPVS/C 1303 bp DNA linear VRL 03-NOV-1982

LOCUS HEPVS Fragment from the Herpes b'a'c' region (L-S component junction).

DEFINITION V00460 J02223

ACCESSION V00460 J02223

VERSION V00460.1 GI:59814

KEYWORDS repetitive sequence; terminal repeat.

SOURCE Human herpesvirus 1
Human herpesvirus 1
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Simplexvirus.

REFERENCE 1 (bases 1 to 1303)
Mocarski, E.S. and Roizman, B.
Site-specific inversion sequence of the herpes simplex virus
genome: domain and structural features
Proc. Natl. Acad. Sci. U.S.A. 78 (11), 7047-7051 (1981)

JOURNAL 82082583

MEDLINE 6273905

PUBMED

FEATURES Location/Qualifiers

source 1..1303

/organism="Human herpesvirus 1"

/mol_type="genomic DNA"

/db_xref="taxon:10298"

BASE COUNT 146 a 711 c 290 g 156 t

ORIGIN

Query Match 0.1%; Score 19; DB 1; Length 1303;
Best Local Similarity 100.0%; Pred. No. 9;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 132498 CCGCGCCCCCGCGCGCCC 132516
|||||

DB 61 CCGCGCCCCCGCGCGCCC 43
|||||

RESULT 17

LOCUS HS1LSFA/C 1303 bp DNA linear VRL 02-AUG-1993

DEFINITION HSV-1 (strain F+) L-S inversion region.

ACCESSION J02223

VERSION J02223.1 GI:330173

KEYWORDS repeat region; terminal inverted repeat.

SOURCE Human herpesvirus 1
Human herpesvirus 1
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Simplexvirus.

REFERENCE 1 (bases 1 to 1303)
Mocarski, E.S. and Roizman, B.
Site-specific inversion sequence of the herpes simplex virus
genome: domain and structural features
Proc. Natl. Acad. Sci. U.S.A. 78 (11), 7047-7051 (1981)

JOURNAL 82082583

MEDLINE 6273905

PUBMED

REFERENCE 2 (bases 185 to 685)
Mocarski, E.S. and Roizman, B.
Structure and role of the herpes simplex virus DNA termini in
inversion, circularization and generation of virion DNA
Cell 31 (1), 89-97 (1982)

JOURNAL 83129341

MEDLINE 6297756

PUBMED

COMMENT Original source text: HSV-1 (strain F+) DNA, clones PB115 and
PB104.

The herpes simplex viral genome consists of a long and a short unique segment (UL and US) each of which is flanked by regions of repetitive sequence. The repeated sequence flanking the UL segment lies with opposite orientation at each end and is labeled ab at one end and b'a' at the other. The repeated sequence flanking the US segment also lies in opposite orientations and is labeled a'c' at one end and ca at the other end. Thus the complete genome can be represented by: ab-UL-b'a'a'c'-US-ca. The region represented by b'a'a'c' is called the L-S region. The two segments UL and US can recombine in many ways. A population of virions is found to have equimolar concentrations of four different species of DNA molecules differing only in the orientations of the UL and US segments with respect to one another. Because of this the L-S region has also been called the inversion region. The four species of DNA can be represented by:

```
ab-UL-b'a'a'c'-US-ca
ab-UL-b'a'a'c'-SU-ca
ab-LU-b'a'a'c'-US-ca
ab-LU-b'a'a'c'-SU-ca
```

Due to the frequency with which the UL and US segments recombine, the L-S or -b'a'a'c'- region is very polymorphic, with varying numbers of copies of a' being present; and varying numbers of shorter repetitive sequences (called 'reiteration' sequences) within a' being present.

Compared with EMBL id = hspsv, dated 08-JUL-1982.

FEATURES

source 1..1303

```
/organism="Human herpesvirus 1"
/mol_type="genomic DNA"
/db_xref="taxon:10298"
```

repeat_region

<1..184

/note="b' repeat"

repeat_region

185..685

/note="a' repeat"

repeat_region

185..204

/note="DR1 repeat"

repeat_region

205..268

/note="Ub region [2]"

repeat_region

269..497

/note="reiteration Ia (DR2 in [2]) (19 copies) [2]"

repeat_region

497..608

/note="reiteration Ib (DR4 in [2]) (3 copies) [2]"

repeat_region

608..665

/note="UC region [2]"

repeat_region

665..685

/note="DR1 repeat"

repeat_region

686..>1303

/note="c' repeat"

repeat_region

914..1217

/note="reiteration II (19 copies) [2]"

BASE COUNT 145 a 711 c 290 g 157 t

ORIGIN 1 bp upstream of BstEII site.

Query Match

Best Local Similarity 100.0%; Pred. No. 9;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 132498 CCGCGCGCCGCCGCC 132516

Db 61 CCGCGCGCCGCCGCC 43

RESULT 18

HS1ICP345B

LOCUS

DEFINITION

Herpes simplex virus type 1 infected-cell protein (ICP34.5) gene,

complete cds.

ACCESSION

M33700

VERSION

M33700.1 GI:330116

KEYWORDS

Infected-cell protein 34.5; neurovirulence factor.

SOURCE

Human herpesvirus 1

ORGANISM

Viruses; dsDNA viruses, no RNA stage; Herpesviridae;

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

Original source text: Herpes simplex virus type 1 (strain MGH-10)

DNA.

Draft entry and computer-readable sequence for [1] kindly submitted

by J.Chou, 13-APR-1990.

Location/Qualifiers

1..1346

/organism="Human herpesvirus 1"

/mol_type="genomic DNA"

/db_xref="taxon:10298"

134..871

/note="infected-cell protein 34.5"

/codon_start=1

/protein_id="AA45791.1"

/translation="MARRRRHRGPRRPPGPTGAVPTAOSQVSTPNSPVRSA

AGGPPSCSLRLQWLVHDESDDDDDDDPDPPEPAEAPRPAAPRPSPP

GAGCGGANSHPSPRFLRLALRLATLRLTAELRLRLRAGGEGAPRPTATP

ATPATPTATPAPRVRRSPHVRVWMSAARLARLRGSRARERADRRRRVAA

EAIVGPGTGEARARALARGAGPANSV"

BASE COUNT 161 a 576 c 437 g 172 t

ORIGIN

Query Match

Best Local Similarity 100.0%; Pred. No. 9;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 132498 CCGCGCGCCGCCGCC 132516

Db 166 CCGCGCGCCGCCGCC 184

RESULT 19

HS1ICP345C

LOCUS

DEFINITION

Herpes simplex virus type 1 infected-cell protein (ICP34.5aa) gene,

complete cds.

ACCESSION

M33701

VERSION

M33701.1 GI:330118

KEYWORDS

Infected-cell protein 34.5; neurovirulence factor.

SOURCE

Human herpesvirus 1

ORGANISM

Viruses; dsDNA viruses, no RNA stage; Herpesviridae;

Alphaherpesvirinae; Simplexvirus.

1 (bases 1 to 1367)

Chou,J. and Roizman,B.

The herpes simplex virus 1 gene for ICP34.5, which maps in inverted

repeats, is conserved in several limited-passage isolates but not

in strain 17syn+

J. Virol. 64 (3), 1014-1020 (1990)

JOURNAL

MEDLINE

PUBMED

COMMENT

Original source text: Herpes simplex virus type 1 (strain CVG-2)

DNA.

Draft entry and computer-readable sequence for [1] kindly submitted

by J.Chou, 13-APR-1990.

Location/Qualifiers

1..1367

/organism="Human herpesvirus 1"

/mol_type="genomic DNA"

/db_xref="taxon:10298"

134..892

/note="infected-cell protein 34.5"

/codon_start=1

/protein_id="AA45792.1"

/db_xref="GI:330119"
/translation="MARRRRRRGPRRRPPGPGTGAAPTASQVSTPNSSEPAVSAP
AAAPPPAGGPPSCSLLRQMLQVPSASDDDDDDMPSPPEPAPEARPTAAAP
RRSPPPGAGGGADPSHPSPRPRLRLRLAEHLRLRLRAGGEGAPEP
PATPATPATPATPATPARVRESPHVRHLVYVMSAARLARAGSWARERADRAR
RRRAVEAVIGVCGCPKARARALARGAGPANSV"
BASE COUNT 160 a 591 c 445 g 171 t
ORIGIN

Query Match 0.1%; Score 19; DB 1; Length 1367;
Best Local Similarity 100.0%; Pred. No. 9;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 132498 CCGCGCGCCCGCGCGCC 132516
|||||
Db 166 CCGCGCGCCCGCGCGCC 184

RESULT 20
LOCUS HS1ICP345A 1399 bp DNA linear VRL 02-AUG-1993
DEFINITION Herpes simplex virus type 1 infected-cell protein (ICP34.5) gene,
complete cds.
ACCESSION M33699.1 GI:330114
KEYWORDS Infected-cell protein 34.5; neurovirulence factor.
SOURCE Human herpesvirus 1
ORGANISM Human herpesvirus 1
VIRUSES: dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Simplexvirus.
1 (bases 1 to 1399)
Chou, J. and Roizman, B.
The herpes simplex virus 1 gene for ICP34.5, which maps in inverted
repeats, is conserved in several limited-passage isolates but not
in strain 17syn+
J. Virol. 64 (3), 1014-1020 (1990)
JOURNAL 90156494
MEDLINE 2154589
PUBMED

COMMENT Original source text: Herpes simplex virus type 1 (strain F) DNA.
Draft entry and computer-readable sequence for [1] kindly submitted
by J. Chou, 13-Apr-1990.

FEATURES
source
1..1399
/organism="Human herpesvirus 1"
/mol_type="genomic DNA"
/db_xref="taxon:10298"
133..924
/note="infected-cell protein 34.5"
/codon_start=1
/protein_id="AAA45790.1"
/db_xref="GI:330115"
/translation="MARRRRHRGPRRRPPGPGTGAAPTASQVSTPNSSEPAVSAP
AAAPPPAGGPPSCSLLRQMLQVPSASDDDDDDMPSPPEPAPEARPTAAAP
RRSPPPGAGGGADPSHPSPRPRLRLRLAEHLRLRLRAGGEGAPEP
PATPATPATPATPATPARVRESPHVRHLVYVMSAARLARAGSWARERADRAR
RRRAVEAVIGVCGCPKARARALARGAGPANSV"
BASE COUNT 164 a 614 c 449 g 172 t
ORIGIN

Query Match 0.1%; Score 19; DB 1; Length 1399;
Best Local Similarity 100.0%; Pred. No. 9;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 132498 CCGCGCGCCCGCGCGCC 132516
|||||
Db 162 CCGCGCGCCCGCGCGCC 180

RESULT 21
LOCUS HS1LS17C 1766 bp DNA linear VRL 02-AUG-1993
DEFINITION HSV-1 (strain 17) L-S inversion region, clone k1.
ACCESSION K01835

VERSION K01835.1 GI:330169
KEYWORDS repeat region; terminal inverted repeat.
SOURCE Human herpesvirus 1
ORGANISM Human herpesvirus 1
VIRUSES: dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Simplexvirus.
1 (bases 1 to 1766)
Davison, A.J. and Wilkie, N.M.
Nucleotide sequences of the joint between the L and S segments of
herpes simplex virus types 1 and 2
J. Gen. Virol. 55 (Pt 2), 315-331 (1981)
JOURNAL 82032334
MEDLINE 6270266
PUBMED

COMMENT Original source text: Herpes simplex virus type 1 strain 17 DNA,
clone k1.
See comment in other HSV-1 L-S inversion region entries. This
sequence contains a single b'a'c' sequence.

FEATURES
source
1..1766
/organism="Human herpesvirus 1"
/mol_type="genomic DNA"
/db_xref="taxon:10298"
<1..328
/note="b' repeat"
311..331
/note="DRI repeat"
329..728
/note="a' repeat"
408..631
/note="reiteration I (18.5 copies)"
710..730
/note="DRI repeat"
729..>1766
/note="c' repeat"
928..959
/note="reiteration Ira (2 copies)"
960..1066
/note="reiteration IIb (6.7 copies)"
1167..1489
/note="reiteration III (19 copies)"
/note="complement(1527..>1766)
/product="Ymw Immediate Early 175 mRNA"
BASE COUNT 167 a 935 c 436 g 228 t
ORIGIN 1 bp upstream of HinfI site.

Query Match 0.1%; Score 19; DB 1; Length 1766;
Best Local Similarity 100.0%; Pred. No. 9.1;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 132498 CCGCGCGCCCGCGCGCC 132516
|||||
Db 186 CCGCGCGCCCGCGCGCC 168

RESULT 22
LOCUS HS1ICPL 1794 bp DNA linear VRL 02-AUG-1993
DEFINITION Herpes simplex virus type 1 (a region x, infected cell protein
gene, complete cds.
ACCESSION M12240
VERSION M12240.1 GI:330122
KEYWORDS Infected cell protein.
SOURCE Human herpesvirus 1
ORGANISM Human herpesvirus 1
VIRUSES: dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Simplexvirus.
1 (bases 1 to 1794)
Chou, J. and Roizman, B.
The terminal a sequence of the herpes simplex virus genome contains
the promoter of a gene located in the repeat sequences of the L
component
J. Virol. 57 (2), 629-637 (1986)
JOURNAL 86115412
MEDLINE

PUBMED 3003394
COMMENT Original source text: Herpes simplex virus type 1 (HSV1, strain F)
DNA, passed in Vero cells, clones PRB13196, 3197, 3198].
Draft entry and computer-readable sequence for [1] kindly provided
by F.J.Jenkins, 03-JUN-1988.
FEATURES
source
1. 1794
/organism="Human herpesvirus 1"
/mol_type="genomic DNA"
/db_xref="taxon:10298"
65..>1228
/note="ICP mRNA (alt.)"
80..>1228
/note="ICP mRNA (alt.)"
145..1221
/note="Infected cell protein"
/codon_start=1
/protein_id="AA45794.1"
/db_xref="GI:330123"
/translation="MLACOTLPRLHALCLHPPRRHAGPPRRPPTGAVPTAOPV
TSTPNSPAPVRSAPAAPPPPPGPPSCSLRLQMLHVESASDDDDDDDDPSP
PEPAPGAPPAAPRRSPRPGAGCGCAAPSPSPRPRLRLRLVTEHLAR
LRDARAGGAGAPATPATPATPATPATPATPATPATPARRSKPTVRHL
VWASARLRAAARGPASGPTGLSGAGWRPRSSGAWGPGCRALPAGPARRTS
NVTPEAWSSAEELRTKPLSRDDGRNAYIRMEPARPRGGPSEGGTGSAGRQRG
PANQPPSLRGPPMAGPAHFVW"
1794..>1794
/product="alpha-0 mRNA"
BASE COUNT 222 a 728 c 603 g 241 t
ORIGIN
SmaI site.
Query Match 0.1%; Score 19; DB 1; Length 1794;
Best Local Similarity 100.0%; Pred. No. 9.1;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 132498 CCGCGCGCCCGCGCGCC 132516
|||||
Db 219 CCGCGCGCCCGCGCGCC 237
RESULT 23
AF015716 2038 bp RNA linear VRL 13-JAN-1999
LOCUS Alfaifa mosaic virus VRU movement protein (P3) and coat protein
DEFINITION genes, complete cds.
ACCESSION AF015716
VERSION AF015716.1 GI:2654871
KEYWORDS Alfaifa mosaic virus
SOURCE Alfaifa mosaic virus
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Bromoviridae;
Alfamovirus.
REFERENCE 1 (bases 1 to 2038)
AUTHORS Thole,V., Miglino,R. and Bol,J.F.
TITLE Amino acids of alfaifa mosaic virus coat protein that direct
formation of unusually long virus particles
J. Gen. Virol. 79 (Pt 12), 3139-3143 (1998)
JOURNAL MEDLINE 99094642
PUBMED 9880033
2 (bases 1 to 2038)
REFERENCE Thole,V. and Bol,J.F.
AUTHORS Direct Submission
TITLE Submitted (23-JUL-1997) Institute of Plant Molecular Sciences,
Gorlaeus Laboratories, Leiden University, Einsteinweg 55, Leiden
JOURNAL 2333 CC, The Netherlands
FEATURES
source
1. 2038
/organism="Alfaifa mosaic virus"
/mol_type="genomic RNA"
/strain="VRU"
/db_xref="taxon:12321"
242..1144
/gene="p3"
/gene="p3"

CDS
242..1144
/gene="p3"
/codon_start=1
/product="movement protein"
/protein_id="AAD04692.1"
/db_xref="GI:2654872"
/translation="MENTKTNASGSGISSSSFSVSYAEMLADEYSKMSNSITLP
NOLKCTQVLVNSGAAPVVLYSVKSKSLINMLPKIGRMVYVHSAIYLYVNPIL
KSSSGSTTLKLFNEATGELVDVTDHATACLEPAGYPSIIAKDAKGDHKLTVH
AVASTNANSVGVLYPIWDELSRKQILEGAPLRIETETPPVDILNAGKLTQV
LDRTRIGVSGSKGPNVYLEPRKAVKAKATVETPEGFGVNTIVKGIAPTVIDAGS
PKGLGVKGFYTESFIKDELIPDH"
1194..1859
/product="coat protein"
/codon_start=1
/protein_id="AAD04693.1"
/db_xref="GI:2654873"
/translation="MSSSOKKAGKAGKPKYRSQNTAALRKAOLPKPPALKVPKAPT
NIIIPQTCWQOSLIGTPLSLSSNSNGARLYEFLDFAPARILEEDLIRVWFSTP
SHAGSFCLTDDVTEDGRAYAHGNPMQEPHGAFLHAKERGFELVTFAPTHACMON
FKSYVAVALCLDFDALPEGRNPSYRNEVWERKAFPRAGPLRSLLITVGLFPDADDL
DRQ"
BASE COUNT 550 a 441 c 456 g 591 t
ORIGIN
Query Match 0.1%; Score 19; DB 1; Length 2038;
Best Local Similarity 100.0%; Pred. No. 9.1;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 121169 GTGCATCTGTCGCCAAT 121187
|||||
Db 358 GTGCATCTGTCGCCAAT 376
RESULT 24
AF015717 2038 bp RNA linear VRL 13-JAN-1999
LOCUS Alfaifa mosaic virus 15/64 movement protein (P3) and coat protein
DEFINITION genes, complete cds.
ACCESSION AF015717
VERSION AF015717.1 GI:2654874
KEYWORDS Alfaifa mosaic virus
SOURCE Alfaifa mosaic virus
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Bromoviridae;
Alfamovirus.
REFERENCE 1 (bases 1 to 2038)
AUTHORS Thole,V., Miglino,R. and Bol,J.F.
TITLE Amino acids of alfaifa mosaic virus coat protein that direct
formation of unusually long virus particles
J. Gen. Virol. 79 (Pt 12), 3139-3143 (1998)
JOURNAL MEDLINE 99094642
PUBMED 9880033
2 (bases 1 to 2038)
REFERENCE Thole,V. and Bol,J.F.
AUTHORS Direct Submission
TITLE Submitted (23-JUL-1997) Institute of Plant Molecular Sciences,
Gorlaeus Laboratories, Leiden University, Einsteinweg 55, Leiden
JOURNAL 2333 CC, The Netherlands
FEATURES
source
1. 2038
/organism="Alfaifa mosaic virus"
/mol_type="genomic RNA"
/strain="15/64"
/db_xref="taxon:12321"
242..1144
/gene="p3"
/gene="p3"
/codon_start=1
/product="movement protein"
/protein_id="AAD04694.1"
/db_xref="GI:2654875"

translation="MENTKNASGSGSSSSFSYSVAEMHLLADEVRNMSMILG
NOKICTOLVLSNGCAPVVLIVSKKRSKSLRMLPKTGQRYVHSHATVLLMNPIL
KSSSGSTILKLFENATYGLVVDHDTQACIFAGRPRLSILADAKGHDKLIVH
AASTNANSAGVLYPIWEDLSRQILERGADEFKPIAETEPYDLNNGKLTDFV
LDRTFLVGSRRPDLLEPRAKYTKAKTEFIEPGLINPTIVNGITPTVRIDAGS
PKGCVPGKGFYSEFIRKDELLPDH"
1194, 1859
CDS
/codon_start=1
/product="coat protein"
/protein_id="AAD04695.1"
/db_xref="GI:2654876"
translation="MSSQKKGAGKAGKPTKRSQNYALRKAOLPKPALVPAKPT
NTILPQCGVMQSLGTPLSLSSNGIGARPLYSRLKDPVARIILEDILFNVISITP
SHAGSFCTIDYTTEDGRAYAHGNPMQEPFGAFHANEKGEELVETAPTHAGMOMN
FKSHAAVALCLDFDALPEGSKNPSYRRENVVERAKFPAPRLSLITVVKLEDDADL
DRQ"
BASE COUNT 544 a 445 c 458 g 591 t
ORIGIN
Query Match 0.1%; Score 19; DB 1; Length 2038;
Best Local Similarity 100.0%; Pred. No. 9.1;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 121169 GTGCATCCTGGGTCCCAAT 121187
|||||
DB 358 GTGCATCCTGGGTCCCAAT 376
RESULT 25
LOCUS BHV4GH 2121 bp DNA linear VRL 12-SEP-1997
DEFINITION Bovine herpesvirus type 4 glycoprotein H gene.
ACCESSION Z79633
VERSION Z79633.1 GI:1515108
KEYWORDS glycoprotein H.
SOURCE Bovine herpesvirus 4
ORGANISM Bovine herpesvirus 4
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae.
REFERENCE 1 (bases 1 to 2121)
AUTHORS Lomonte, P., Fillee, P., Lyaku, J. R., Bublolt, M., Pastoret, P. P. and
Thiry, E.
TITLE Analysis of the biochemical properties of, and complex formation
between, glycoproteins H and L of the gamma2 herpesvirus bovine
herpesvirus 4
JOURNAL J. Gen. Virol. 78 (Pt 8), 2015-2023 (1997)
MEDLINE 97410287
PUBMED 9267002
REFERENCE 2 (bases 1 to 2121)
AUTHORS Lomonte, P.
TITLE Direct Submission
JOURNAL Submitted (29-AUG-1996) Patrick Lomonte, Virology, University of
Liege, Faculty of Veterinary Medicine, Bd De Colonster, Liege,
4000, BELGIUM
FEATURES
source Location/Qualifiers
1. 2121
/organism="Bovine herpesvirus 4"
/mol_type="genomic DNA"
/strain="V. TEST"
/db_xref="taxon:10385"
/tissue_type="kidney"
1..>2121
/codon_start=1
/product="glycoprotein H"
/protein_id="CAB01909.1"
/db_xref="GI:1515109"
/db_xref="SPTREMBL:096635"
translation="MKLPIFLFLSLCHSYCAVRGDSLEENKNTLTHPDGK
VIVNTPRLDVLSPQIVQOMDEANVEENLDYNTKTTGLKPLQIKRLNHNHHC
QGSQTVRDNISQIHAIQDAYLGNFIEIOSRLIFSDNPREKNVTFGSDHFFPKDY
ATITWGNENRISGVTSPFSYVTMANKGQIKDOTTILFSGFSLPAKGVANPNVE
VAKYNLMVVLASKNCGSANLTNFELEINIVKONPAEFIDIOSDFMAIDSEGG
CNTDSMDERKILLFFRVVSHFKITRTLQKKYIYVMSCISITDLADLILRMISKCPA

SGVNLGFSISTIAIDQNTPEPKSEGNRYADTIPNTILSRGEYNTEDVVRVY
KRTLEDMTMEFSYFTTSGTORTILFKTWRLNFTHDNHNVAKSLITTSYLLSSMC
TNVEGLADMTFNRHIDIHETFPCEKSLRDFDSYDKLQSNAPKLESTTKVNTGT
TGFVLVHDFHFKNRKYQVPEIKCHIQAKIQONIIAIIPLFTVTVLSSDKLENTLYE
ITFEVLKSGMFLSVLRPDCSTREPDEHGGVLSLPIVYNSNLTGCPFCFDSAVI
IGLESMTYINNTVIOKNEFLDVSPEFDDNHLVHVLMLMNGTVVEIGARRKKVYSI
ILFTIKRNGFTLMITFELKMLSYVI"
BASE COUNT 697 a 322 c 388 g 714 t
ORIGIN
Query Match 0.1%; Score 19; DB 1; Length 2121;
Best Local Similarity 100.0%; Pred. No. 9.1;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 129813 TGGAAATAAGAGCGCGTA 129831
|||||
DB 2006 TGGAAATAAGAGCGCGTA 2024
RESULT 26
LOCUS AF359760/c 3008 bp DNA linear VRL 05-JUN-2002
DEFINITION Buffalo herpesvirus 1 glycoprotein B gene, complete cds.
ACCESSION AF359760
VERSION AF359760.1 GI:19481399
KEYWORDS
SOURCE Buffalo herpesvirus 1
ORGANISM Buffalo herpesvirus 1
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Varicellovirus.
REFERENCE 1 (bases 1 to 3008)
AUTHORS Ros, C. and Belak, S.
TITLE Characterization of the glycoprotein B gene from ruminant
alphaherpesviruses
JOURNAL Virus Genes 24 (2), 99-105 (2002)
MEDLINE 22012763
PUBMED 12018712
REFERENCE 2 (bases 1 to 3008)
AUTHORS Ros, C.
TITLE Direct Submission
JOURNAL Submitted (14-MAR-2001) Chemistry and Biochemistry, University of
Bern and ZIB Bioplasma AG, Bern, Freiestrasse 3, Bern 3012,
Switzerland
FEATURES
source Location/Qualifiers
1. 3008
/organism="Buffalo herpesvirus 1"
/mol_type="genomic DNA"
/strain="B6"
/db_xref="taxon:171005"
270..3008
/codon_start=1
/product="glycoprotein B"
/protein_id="AAL88794.1"
/db_xref="GI:19481400"
translation="MAARGAEPAAAGGDRGRRGRRHRLPRGRVLAALRGPAAGGG
ARALAAALILMAAALILAAAPARPTTGDDPDNGTVRAALRLQAAGESRRVYCP
PPSGATVRLAPARPCPEYELGRNTBEGIVLENAPYFKAVITYKNIVTTTRA
GSTAAITNOYTDVDPVGLGELTDLVDKWKWCLSKAEILRSGRVAAFDNEDWEAP
LKPARLSAPGVGRWHTTDEVYTAGSAGLITGTSVNCIYEVARSVPYDSFSLST
GDIITMSPFGLRDGAHREHTSYSPERPOOLEGYKKRDMAGRLKEPVSPLTQTH
VTVAMDVPARKKNVCSLTKWRADMDLRDSRGNFRPTARLSATFVSDGHTPALONY
PLSPCVTEEAANVRYRERFNATHVLSGLLEYTLARGGVYAFRRPLSNAKLKYL
QELARSGTLEGLFAAGSGAAAPKVPARRARSPTPPAPASGGGDDANKRY
TTVSAEFAALQFTYDHIODHNTMFSLATSWCLONKERAALAAKLPASAASA
ALDRRAARMGLDAAVYCHELGEGRVTEISNRAPGVCSRPVSPFAGNSSEYV
EGSGEDNEELLGRELVEPCALNKRYPREFGADVYENAVYVRVPLAELEVTSTV
DNLTVLEDEPFLPVEYTRAEADTGLIYSEIQRNOLHELRLSPYIDRVYKTDGN
AIMGLANFQDGLCAVGQAVGTVLGAAGALSTVSGIASGVANPFGALATGLVLG
LVAFLAVRYTISRLSNPMKALYITTRALKDDKGAAGPGEDEEEDAKLEOARE
MIKMSYLSVAVEROEHKARKSNKCGPLIANRLTOLALRRAPRAYOOLPMSDVGA"

Query Match 0.1%; Score 19; DB 1; Length 3008;
Best Local Similarity 100.0%; Pred. No. 9.2;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 121273 GCGGCGGCGGCGGCGGCG 121291
DB 1756 GCGGCGGCGGCGGCGGCGGCG 1738

RESULT 27
AF078726/c 3113 bp DNA linear VRL 05-JUN-2002
LOCUS Bovine herpesvirus 5 strain N565 glycoprotein B gene, complete cds.
DEFINITION AF078726 AF359759
ACCESSION AF078726.2 GI:19483797
VERSION
KEYWORDS
SOURCE Bovine herpesvirus 5
ORGANISM Bovine herpesvirus 5
VIRUSES; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae.
1 (bases 1 to 3113)
Ros.C. and Belak.S.
REFERENCE Studies of genetic relationships between bovine, caprine, cervine,
AUTHORS and rangelierine alphaherpesviruses and improved molecular methods
TITLE for virus detection and identification
JOURNAL J. Clin. Microbiol. 37 (5), 1247-1253 (1999)
MEDLINE 99221732
PUBMED 10203465
REFERENCE 2 (bases 1 to 3113)
AUTHORS Ros.C. and Belak.S.
TITLE Characterization of the glycoprotein B gene from ruminant
JOURNAL alphaherpesviruses
MEDLINE 22012763
PUBMED 12018712
REFERENCE 3 (bases 1 to 3113)
AUTHORS Ros.Bacnuna.C.
TITLE Direct Submision
JOURNAL Submitted (16-JUL-1998) Dept. Virology, National Veterinary
Institute, Box 585, Uppsala 751 23, Sweden
4 (bases 1 to 3113)
Ros.Bacnuna.C.
REFERENCE Direct Submision
AUTHORS Submitted (24-SEP-2001) Chemistry and Biochemistry, University of
TITLE Bern and ZJB Bioplasma AG, Freiestrasse 3, Bern 3012, Switzerland
JOURNAL Sequence update by submitter
REMARK On Mar 15, 2002 this sequence version replaced gi:5668973.
COMMENT Location/Qualifiers
FEATURES
source
1. 3113
/organism="Bovine herpesvirus 5"
/mol_type="genomic DNA"
/strain="N565"
/db_xref="taxon:35244"
270..3113
/product="glycoprotein B"
/protein_id="AAD46112.2"
/db_xref="GI:19483798"
/translation="MATRGAGAPAGACAGYGRGRCGRRLAPRGVLAALRSPAPAGAGCG
ARALAAALIMAMALLLAAPAGARPTTPVPGACGASPARPASPASASIRPADG
PDGDDPDNSTDVARALRLAQAAGENSREYVCPSPGATVRLAPARPCPEYELGKNY
TEGICAIYENIAPYTFKAYIYKNIYVTTAGSTYAAITNOYTRVPGLEITDL
VDKMKRLSKAEYLRSGRVYAFDRDEDPWEAPLAKPARLSAEPVALQFYDHIQDHYN
SAGLYRTGTSVNCIVEVEKRSVYPYDFALSTGDIIMSPEGLRGAHREHTSYSP
ERROOIEGYKRDMAKGRRLKPEVSRNPLRTOHYVYAMVMPKRVKVCSTTKRDE
MLBDSRGNFRPTARSLATPVS DGHTPALONVPLSDCTEEGAVERYSIKRRENAT
HVLSGLETTYLAGRGVVAFRPMLSNALAKLYQELARNSGTLGGLFAAGSGAAAAA
APKPYRRARRASPTTPAPASGDCGDANKRVTYVSAEPAALQFYDHIQDHYN
TMTPLATSMCLQNKERALMAEAKLINSAAASALDRRAARMLGDMAAVYCHEL
GEGRVFTENSMRAGGVGVSRRPVSAFGSESPVPGCOLGENELLGRLVETRAEL
HKRYFRGADYVYENYAVYRRVLAELVYSFVULINTLVLEDRFLPLEYVTRAEL
ADTGLDIYSIORNOLHRLRFDIDRVYKTDGNMAIMKGLAFEGGLGAVGAVSTY
VIGAGAAALSTVSGIASFVANPFGALATGLVLAVLAFLAARYTSRLKSNPMKALY

Query Match 0.1%; Score 19; DB 1; Length 3113;
Best Local Similarity 100.0%; Pred. No. 9.2;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 121273 GCGGCGGCGGCGGCGGCG 121291
DB 1858 GCGGCGGCGGCGGCGGCGGCG 1840

RESULT 28
CPGVTC14.7 5175 bp DNA linear VRL 07-JUL-2002
LOCUS Cydia pomonella granulosis virus TC14.7 DNA.
DEFINITION X79773
ACCESSION X79773.1 GI:727219
VERSION
KEYWORDS TC1-like transposable element; transposable element; transposable
element TC14.7.
SOURCE Cydia pomonella granulovirus
ORGANISM Cydia pomonella granulovirus
VIRUSES; dsDNA viruses, no RNA stage; Baculoviridae; Granulovirus.
REFERENCE 1
AUTHORS Jehle,J.A., Fritsch,E., Nickel,A., Huber,J. and Backhaus,H.
TITLE TC14.7: a novel lepidopteran transposon found in Cydia pomonella
JOURNAL granulosis virus
MEDLINE 95193235
PUBMED 7886941
REFERENCE 2 (bases 1 to 5175)
AUTHORS Jehle,J.A.
TITLE Direct Submision
JOURNAL Submitted (15-JUN-1994) J.A. Jehle, Biologisches Bundesanstalt fuer
Land- und Forstwirtschaft, Inst. fuer Biochemie &
Pflanzenvirologie, Messeweg 11-12, 38104 Braunschweig, FRG
FEATURES
source
1. 5175
/organism="Cydia pomonella granulovirus"
/mol_type="genomic DNA"
/strain="CIGV-M"
/isolate="mutant CIGV-WCp5"
/db_xref="taxon:28289"
/map="7.0-10.1 genome %"
1..171
/note="CpGV specific sequence"
misc_feature
/note="CpGV specific sequence"
171..172
/note="duplicated integration site TA"
repeat_region
173..4898
/transposon="TC14.7"
173..201
/rpt_type=INVERTED
/rpt_type=INVERTED
1460..2491
/rpt_type=TERMINAL
/note="putative transposase pseudogene"
pseudo
/codon_start=1
/db_xref="REFSEQ:CAA56167"
1910..2008
/note="putative"
4870..4898
/rpt_type=INVERTED
/rpt_type=INVERTED
4899..4900
/note="duplicated integration site"
misc_feature
/note="CpGV specific sequence"
4900..5175
/note="CpGV specific sequence"
BASE COUNT 1699 a 874 c 915 g 1687 t
ORIGIN
Query Match 0.1%; Score 19; DB 1; Length 5175;

Best Local Similarity 100.0%; Pred. No. 9.3;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 130092 GAAATGATTAACCTATA 130110
|||||
Db 3712 GAAATGATTAACCTATA 3730
RESULT 29
HPV10 7919 bp DNA linear VRL 24-FEB-1999
LOCUS Human papillomavirus type 10 genomic DNA.
DEFINITION X74465
ACCESSION X74465.1 GI:396901
VERSION E1 gene; E2 gene; E4 gene; E6 gene; E7 gene; early protein; L1
KEYWORDS gene; L2 gene; late protein.
SOURCE Human papillomavirus type 10
ORGANISM Human papillomavirus type 10
Virus(es): dsDNA viruses, no RNA stage; Papillomaviridae;
Papillomavirus.
REFERENCE 1 (bases 1 to 7919)
AUTHORS Delius, H. and Hofmann, B.
TITLE Primer-directed sequencing of human papillomavirus types
JOURNAL Curr. Top. Microbiol. Immunol. 186, 13-31 (1994)
MEDLINE 94265501
PubMed 8205838
REFERENCE 2 (bases 1 to 7919)
AUTHORS Delius, H.
TITLE Direct Submision
JOURNAL Submitted (06-AUG-1993) H. Delius, Deutsches
Krebsforschungszentrum, Abteilung ATV, Im Neuenheimer Feld 506, W
6900 Heidelberg, FRG
FEATURES
source
1. 7919
/organism="Human papillomavirus type 10"
/mol_type="genomic DNA"
/db_xref="taxon:10603"
/clone="insert in SalI site of pBR322"
102..548
/gene="E6"
102..548
/gene="E6"
/note="alternative"
/codon_start=1
/product="envelope protein"
/protein_id="CA52492.1"
/db_xref="GI:396902"
/db_xref="SWISS-PROT:P36802"
/translation="MSMGAQEPRIILLCRNGCILEDLRLCCTICTKQTLAETLAF
ALRELYLVNRAGVYGGACARLLIQLGYVRRLKYDYIYEGVEEETKOSIIYIOLIRIC
YCHKPLVREKDRHNERRLHKISGIWMGSCYCWSRCTVRIPO"
524..784
/gene="E7"
524..784
/gene="E7"
/codon_start=1
/product="envelope protein"
/protein_id="CA52490.1"
/db_xref="GI:396903"
/db_xref="SWISS-PROT:P36818"
/translation="MHGPHYVDIELSLAPEDIPVGNOLDEEDYTDAYEPAQOAVR
VYETCRKCSIPRLRYVECSHADITALQLGLITKLVCPRKY"
791..2836
/gene="E1"
791..2836
/gene="E1"
/codon_start=1
/product="envelope protein"
/protein_id="CA52491.1"
/db_xref="GI:396904"
/db_xref="SWISS-PROT:P36720"
/translation="MDNNTGTEGACSESRAGWFIWEAIVDRRTGDPISDDDEE
DEAGEDPVDPIIDTRSLGDGQVAYAEFLFOQGTAAADDAVAVQYKRRKAPSPYSPVCE

gene
CDS
OASIEHELSPRLDAIKIGROSARKKRLFEIPDSGCGOTQVDTESGPKYQOGSETOD
GRQDDGESVQSTLDPTGNONGRONNDEGSGRNNDEGSGOEBERAGDGEDSLQST
TGKGGAGVEVELIRASNNKATLIGKFKDFGYNELIRHRSDETSCADWVAVCFVFE
CTVAGEIKITLIQPLCDYAHIOVLPCQMGMDYLMVRYRKARNRETVAKGLSTLNVYE
SOMLIEPPKRLSGPALYWKYTSKSSGSDYVGEPEMVIROTWHGAMEDQFSLSM
VOMAYDHDITDESTLAYEVALIADTDSNAAFSLSSOAKYTKACMGKRYKRGDA
RMSSEMIWPRGDKVQGDGDKPPIVOELRQDVDFEIPICAFKFTLOGVPSKSLVY
GPADTGKSYFCHSLRFLGGAVIYLAASSSHFHLQPLSEAKTIGLLDQATSCVNTIDT
YLNALDGNQICVDRKHALLQLKCPPLLITTNINPLTDERKFLRSRLDLETKNPF
PVTTQGEPMYTLNQNMKCFEFLRLMARLSTLPDEBEHGNPSBPRVCVQGNARTI"
2778..3908
/gene="E2"
2778..3908
/gene="E2"
/codon_start=1
/product="envelope protein"
/protein_id="CA52492.1"
/db_xref="GI:396905"
/db_xref="SWISS-PROT:P36781"
/translation="MFTLANRDLKACQKMLELYEKSDKLEDOITTHMHLRENNALLY
KAREGLTHIGHQVPPPLSVYKAKARANAIEVHALQOLQESAVAHBFWTLRDSREMX
DTAPKGGCKKRGITVEVRYDDESKACQYQVRELQYQNSDDRWKVPKQSYEGLY
YTHENMNIYYVNEFDACVYGETKMEVHGAKYIHHDAFDPVSTREISTPGVCTS
NTPEASTQAOAGASEGPEOKRORLEAVDGOHQOQROGSKDSTOKAARAGGOVSDFT
RLCDTRSAHVPYRHPSPDCAPVITHLRDPSNLKCFRRLHGGKRLKLSRSSSTWRKSC
ESENQAAFWTLWYSDTQTEFLNVAVPPEIQVILIDMSIF"
4430..5842
/gene="L2"
4430..5842
/gene="L2"
/codon_start=1
/product="late protein"
/protein_id="CA52493.1"
/db_xref="GI:396907"
/db_xref="SWISS-PROT:P36747"
/translation="MVAORARRRRKASATOLYRNCASGTCPPDVPVFKVGTSLADRI
LQMSIGSVYIGGIGTIGSGTGGTGTGVPSTRGCTVYDVSPAPVPPVPEVQSPSP
STVNLDESLINSSTIIPFSGISGFEVTSATITPAVLDITPASENNVIYSSNFPN
PAFTEPSLVEPQSGEVSGHLLISTPAGTHGHEIPMDIFASGTETEPISSTPVG
VSRLAGPRLYSRANTQVAVSDPAFLSPSSLLFDNPFEPDEETIIFBPPSPSRVP
DPDFLDIVRLRHPALTSRGTGVRSLRGKFSMRTSGKIGARVHYQDLSPAPAE
DIEMEPILAPASDPTIYDIFADVDGDVAFTEGYSRTQSGRWNTTSLSTSTKG
NMTIPVSPVDVTLHNGPDIVLPISAGMPVPLSPADTTHYVYIDGDFILMPVTFE
SRHRRKRKVSFFPADGTLAL"
5739..7334
/gene="L1"
5739..7334
/gene="L1"
/note="alternative"
/codon_start=1
/product="late protein"
/protein_id="CA52494.1"
/db_xref="GI:396908"
/db_xref="SWISS-PROT:P36732"
/translation="MAGISTFGLIPSPDIIVANVSHIFLOAMLRSSNLVYLPT
PVSKVLTSDIYVTRNTIYTAGTSRLTLTVCHPPIPIPKSSNNKVDPKVSAFOYRFR
VRLPDPNKFGLPARIYNPDALRYMACTGEVGRGKPLGVLGSLHLYLKLDETESS
NIAHGPIGDSRDNISVDNKOTQICITGGTPMGEGHKGCTPCRNPAQDCPLLELI
TSPLODDMVDTCGAMDFTALDNKSDVPIDICQSTCKPDIYLGMAABVYSGSMFEY
LRROQLFARHFPNRAVSDAIPDPTFLKNSGGGAGVSAVSPTPGSMVTSBAOLF
NKPYMLRACGHNNGCNANOLIVYVYDPTSRNMCLCVPSLSPATYATATPEKEL
RHGEEDLOFTIQLCKVTLPDLMAYLHTNNSSLDEWMLDLPSTSTLEDYTRFLS
SSAITCQKDPTEKQDPAKLNFMWDLDKDRSLDLSQPLPGRKFLLOLGVRSSAV
SVRRPATSATGSTAARKRTKK"
5823..>7331
/gene="L1"
/codon_start=1
/product="late protein"
/protein_id="CA52495.1"
/db_xref="GI:396909"
/db_xref="SPTREMBL:081958"
/translation="MALMRSSDLVYLLPPTPVASKVLTSDIYVTRNTIYTAGTSRLLT
VGHPIPIPKSSNNKVDVYKSAFOYRVPVRLPDRNKRGLPARIYNPDALRYMACT

TGVENRGQPLGVLGSHPLYNKLEDTENSNIAGPIGDSRDNISVDNKOTLCIIG
 CTPPMKEHKGKTPCRRNPAGDCDPLELTSTP IQDGDWDTGCGAMDPAIDLTNSD
 VPIDICOSTKCPDYDLGMAAEPYGDSEFLLRREOLFARHFENRASAAGDAIDTETL
 KSNGGADVSAVSPTPSGSWTSEALFNKRYMLBRAOGHNGICMANOLFVTVVD
 TRSTNMCLCQPSSEASPTATYDTATKREYLIRNHEEYDLOEIPOLCKYTLTPDLMATLH
 TMMSSLEDMNEGLTLPSTSLDTYRFLSSSAITQCKDTPPEKODPPAKLNFMDVD
 LKRFSLDISQPLGCRKFLQLGCVRSANVSKRPATSTATGTAARRKTKK"

BASE COUNT 2169 a 1651 c 1981 g 2118 t

ORIGIN

Query Match 0.18; Score 19; DB 1; Length 7919;
 Best Local Similarity 100.0%; Pred. No. 9.4;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 131993 TATATTTTAAATTTGCT 132011
 ||||||||||||||||
 Db 7490 TATATTTTAAATTTGCT 7508

RESULT 30
 BHV130KB/c 30000 bp DNA linear VRL 14-AUG-1996
 LOCUS
 DEFINITION Bovine herpesvirus type 1 (Cooper) DNA (30 kb).
 ACCESSION 248053.1 GI:971311
 VERSION 248053.1 GI:971311
 KEYWORDS
 capsid protein; deoxyribonuclease; helicase/primase complex;
 integral membrane protein; major capsid protein; myristylated
 virion protein; origin-binding protein; serine/threonine protein
 kinase; viral packaging; virion glycoprotein H (gH); virion
 glycoprotein M (gM); virion protein.
 SOURCE
 ORGANISM Bovine herpesvirus 1
 Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 Alphan herpesvirinae; Varicelloviruses.
 REFERENCE
 AUTHORS 1 (bases 1 to 30000)
 TITLE Vlack,C., Benez,V., Lu,Z., Kutish,G.F., Paces,V., Rock,D.,
 Letchworth,G.J. and Schwyzer,M.
 Nucleotide sequence analysis of a 30-kb region of the bovine
 herpesvirus 1 genome which exhibits a colinear gene arrangement
 with the UL21 to UL4 genes of herpes simplex virus
 virology 210 (1), 100-108 (1995)

JOURNAL MEDLINE 95313343
 PUBMED 7793062
 REFERENCE 2 (bases 1 to 30000)
 AUTHORS Schwyzer,M.
 TITLE Direct Submission
 JOURNAL Submitted (19-JAN-1995) Martin Schwyzer, Institute of Virology,
 Faculty of Veterinary Medicine, University of Zurich,
 Winterthurerstr. 266a, Zurich, CH-8057, Switzerland
 FEATURES
 source
 1. 30000
 /organism="Bovine herpesvirus 1"
 /mol_type="genomic DNA"
 /strain="Cooper"
 /db_xref="taxon:10320"
 /clone="psd106, pBH21, psd72"
 <1. 84
 /note="UL22"
 /codon_start=1
 /product="virion glycoprotein H (gH)"
 /protein_id="CAA8811.1"
 /db_xref="GI:971312"
 /db_xref="SPTREMBL:065562"
 /translation="GTTTIAAKMLCSSLVPLANGYSVPVF"
 132. 137
 /note="UL22"
 /codon_start=1
 /product="putative protein"
 /protein_id="CAA8812.1"
 /db_xref="GI:971313"
 /db_xref="SPTREMBL:065563"
 polyA_signal
 CDS
 complement(234. 1958)
 /note="UL21"
 /codon_start=1
 /product="putative protein"
 /protein_id="CAA8812.1"
 /db_xref="GI:971313"
 /db_xref="SPTREMBL:065563"

/translation="MELAVSHVVAHNHGVSVSAADVAIVYAGTVSVARGGEAV
 KFELELRGMDRSRRAVANYRALAAVPLAPAGDDEDDPGGCAFVCLRLRPR
 GAGELRAGWDRSGEDVPGDPTVLAECFVSAGVLTGYDAERRYLHEDVPTI
 TNALSGFVYAPNRECFALMAGCRPPRGPAPYACAFSLPRCGGLRRAGSEADRS
 PATTVEYVTTARAFAFPPOARREAAVSSVYVRLPRTYNNAAHMGPPLSAATPPCRG
 CVSPCCADAVVLLSDHWAGIDETLNEARGDLVAATAVLPKPRRCGVGSVADYGS
 FCOFRAFCOFLRLRWGMAACSCYGALEHAESYANYPHRAAPDEGCVADAANDTLRE
 LCVLGFRAEALRLADLGEPPAPAEKGGAGDGGDYDCDCDDAAAAAARALDLEMTAV
 LSLASRTRRIYETGSADELRABEGVRAMLHLVAGGAAGAGARADLGTAAPIV
 TIMEAEQITAFDRAPARAHGVCTLRALVDRRLCAAGITTPSDSEYEDGNSDGSEGC
 EACAGTEP"
 2070. 2765
 /note="UL20"
 /codon_start=1
 /product="putative integral membrane protein"
 /protein_id="CAA8813.1"
 /db_xref="GI:971314"
 /db_xref="SPTREMBL:065564"
 /translation="MLGPESALLRAREPEPLGADAEEGAAGASPGDSDDEDELL
 RCVALSAYGDDVDFLTRSPRLAPRADRAFAVYVFGASAPAGLPACCLFLYYR
 TFGDAPFAVGAATLAYARLAAAGFLYAGRADLPGRGPRALLAALVARRAAV
 FAVALPAAFGAPALFLRLSAVAADGARAAGLLAGLAATYADLYCIVTGFAPR
 AMNRVCLGSHVAV"
 2780. 2785
 /note="UL20"
 not canonical ("TATAAA")
 2838. 6995
 /note="UL19"
 /codon_start=1
 /product="major capsid protein"
 /protein_id="CAA8814.1"
 /db_xref="GI:971315"
 /db_xref="SPTREMBL:065565"
 /translation="MDROSEPPRAPAPVATGGVSGOVLSNTEVACHRALFFRQOVRSD
 DNGLYAAAFDALGTCYCNITTVLPFLELGISVACVCTKPELVYHBTQIREFYQDM
 IARDGHPVDQPVHNWVKRINRRSUSAFTSAEALGLAEESDSTQVSSRAALY
 IQDLARVQVJDSFERGTADQLRLYLEKAPMSLSVPLSRREDRLVGSRAALY
 SELKRPYRDADFFLNKSEGAPELAKITTDYVGCAASVAAPRLTHCTDRGPVDS
 VLVTTGRIKRLGVALADSEADYVYTGERTVSGTLNVTALTMKALRGDQVVA
 HILGDEGTAPGLAVADYDPAVAPVATVAGDRVLFLALEKRYVQATVPYPL
 VGMNDLTFVAPLGLYKRPADRYSRHSSGAPPPGHPPRPFPRSVYFKDKDALTFY
 SFGAMGTGLCHPSFLDVPVLAALRGQRREAEKWLGGATVADPGQELADQVRIHL
 DAWHALPFRPRRVMECAMPEQWAVAFNPNMPLERLADDFGLPAPVHALPGPNP
 QVPMQAMPRIINGNIPVPLCYVDGDFGRFELSVDYRHRLSATVAAGVAFGRPNY
 PMAFYIEAVIHGSERTFCALRLVMQCTSYRNSGCAEAFVNSFPVAVYINAYLIG
 ELPEDCYAVYKDLLEHLHALRLVDETVTHAPRGEOHEALNHALLDVLPLCLMG
 DCDVAMALQRTTRRAARAVNGAAPVHARRELAENFRVNGDLYNNRVRGGGPPA
 YVPVPHGDEVLAKITYAVVPAFARGACSSMGVHTDRYPLQVOSVYVVDLPDEEP
 PAPERHRRHLPNTNLVANSFNLVLAHARAADADALLVQEAVTNAERTSVVVVDA
 GPDAGATAATATRMKRTLDAAHLHGGLVLAAMAYQORDETLDDGAFEPAVHAFACPDHL
 HAMRGLQONALLAARHVPVPVHVGANYVATVROPVNHAAGSADENTLTVALMGY
 FKLSPLALTHQLRGLHPRGLTVVRODRATEMLFAEKASERYFVGOLQVNRHEAV
 GGYGFTLTPQHARVDLCGYTAAVYAAAAMARTPLDLCNTPONLMTGDPVNGDND
 GFVRYVAGSRIRPQGPAPLFGPIAPAPAGTARGOAVCEFLATPVSAIDLATFRSC
 NPGRSAGAAVYADGESDADLMEHDHGGQGPAPHRATVPNMAOSRHSYDRLYNGY
 NMSGASVYSPCKFFTPPAVSAKDRMSGLIEVGGVGSVSTSDLELQKPPGCE
 LVEDPCALFOEAVYPLCASDALLRLRLAAGGAAGVEGRLEEGHFAQYLIRASVY
 RGLPLVPG"
 complement(3969. 6050)
 /note="UL19.5"
 putative antisense ORF overlapping UL19"
 7084. 8034
 /note="UL18"
 /codon_start=1
 /product="capsid protein"
 /protein_id="CAA8815.1"
 /db_xref="GI:971316"
 /db_xref="SPTREMBL:065566"
 /translation="MAOPFAFEVEIVPGLDSHGLAALQCEKGVFFTLRRRVPL
 ADVAIAFSVNGVAVPDLGMAAYRCGFPPVIVRVAPRGMAAPLIGGPPRGFLION
 TGPFDCNGDANYCLPPLGLPARALALASGABELFPMTYPLQOARLVARVARYAE
 ALCDRAAARARADAVMTHNGRRTQVTPDVLCBEGADAPARTVLNNVENVNBSGLL
 LSLIPNLITQGLDGVANALVOLGSASREAGOLLRLRPAAPRQDGGRRFCLYGALAAW

polyA_signal
ISSATRLGDAGARPLAKVCTFDGFSVVRGSEKAPITVPL"
8089. .8094
/note="UL19, UL18"
complement(8135. .8140)
polyA_signal
/note="UL15"
complement(8143. .8148)
polyA_signal
/note="UL15"
complement(8178. .9362,12734. .13756))
CDS
/note="UL15"
/codon_start=1
/protein_id="CA88116.1"
/db_xref="GI:971317"
/db_xref="SPTREMBL:Q65567"
/translation="MEGAVGEQSARHYQRLIRERORRAERGAEPDGGARGEDDA
RVPFLDFVAAPKRQTVVGVGTLLHGCELPALPAASRLITSMARAGLMTGT
GEAHYSRELACVLALIRPAHPAPAEAAHCNAYSVMASGAFQAVAAVAR
FSRLVGTFSHLGGDDADPPRAKARVEPSSGRLTELFOKMLIPATVPAATL
LGEHAERGAFLRVAFNPPDSDAVAHFORATVYVPRRHGTWPLVLAALAT
FKGIKIGTTHAIRKATPEVEFEIYARLBQWNGGERVDKCEVISFSPDGRSTIV
ASSHTNGIRGQDNRLFVDEANFIRPAVOTIVGLMQASCKIIIVSSTNGKASTS
FLYNKGSASDGLNVTYICNEHTPRVAHAGGAGACSCYVINKPVEITMDAARAT
TEFLNSEMOETIIGGEVARRAEPAPVETRAEGEOLFLRPTAAARGWPPRLVYID
PATNSNARASGGLAVGRHRSWLVGLHEHFLPALTGSSAAETARCAVCFQAVMA
VHRRRLDGLFVAVGNSGSDSAVALAIGVREELDSIAGSAGVAMPAAETREYVCPGSS
AVAYPEFLQOKTKAAPDHTRIFNSGRVYASODLASTVTLQIDTPVYTLPEQNLNT
ESTAGPGGARFSGRKRAADDLMALMAVAVGSLPPTDGAFCPLARPPAD"
complement(9363. .12733)
intron
/note="intron (UL15)"
9433. .11538
CDS
/note="UL17"
/codon_start=1
/product="putative protein"
/protein_id="CA88117.1"
/db_xref="GI:971318"
/db_xref="SPTREMBL:Q65568"
/translation="MEAHLANETKHCLARGSAAGTVVHLIISDCLRAAGADPGRLE
TASGAPGAAGAPRGSGARADFSAAQTRPHGSGACSAWPEVPAAYPAALASVIL
PTQAPARPRITAAAGCGDGRGLFVSIPVLPBEGEGCFPPPTTRAILRLMAGSELV
DLTRYEBLEPAGTRYEADVRLAALCMQFVHYTRRHAGLPAVAALAAEHMEACITG
GRAPPLPPGGQIRPERLIAEGGFDPAVAVLEDSDEVALIRRAAVVARRHLR
ARAPIGGRVAAAGILQGARATAACAATAVLPPDAATALLPATEPAAAGGIGAVA
BALAGDTLVATAATROARTTEWFDAGICALGDTPCDAMRRRLSLVARHETEG
GEVVAVYEOSAGMGWRAPRPARPESVAGLARGAREGVAAHRAALISAARIELAR
HPFLAAPLEGEGAPPEVFDAGAEVLLAERKACARALIVAMRACEARDLPQRFH
DVREAQCELEDAVRVPAFLRALASALGASAEFLUSALCAAAVALUSITSGRG
VLPYHACFSLLAGERALLFDYFSFGGEVITKRSPLAATTAQESGRSPSIRLDA
GAKSGRAPACGSPGESYAYACVGSFRLRCYVFPGSGFALADVAAHLDMPARLCE
AAGRLGRLPAPPGAPAP"
11572. .12591
CDS
/note="UL16"
/codon_start=1
/product="putative protein"
/protein_id="CA88118.1"
/db_xref="GI:971319"
/db_xref="SPTREMBL:Q65569"
/translation="MAEDPAAAGALLARALTEELGCLHVTDSRVKTYVAVATLGR
LARLVSPEDASPAVAVRTLYITPRKSELPRRHHVLYLFGAVARCAVAGVTRAL
VPGSTRVAARVADVAAPADLPDPSAEVVPAPAEHVDPFAFAFARPRDARAL
QIADGVWMSYADRLYLYQMDALALALCPAGMRSRLSGVGLRSLHSGCGCACTAKY
HIDALNAPAEBCADVCPCAPCLMKRKARDVDVAGDSLEFVLETTGVAARVLIGS
RRPRITGALPELLAGVGRGENVPVNGAQMLVMDDVTRLASSCRMARSCAAR
GSPWG"
12678. .12683
polyA_signal
/note="UL17, UL16"
13819. .14487
CDS
/note="UL14"
/codon_start=1
/product="putative protein"
/protein_id="CA88119.1"
/db_xref="GI:971320"
/db_xref="SPTREMBL:Q65570"
/translation="MATPALAGDPAAGSRTAARRRRLLEAHRREAIFFKSRVVDIV
AGADRDPAITHAFTAKAARRDLCGGQIRAAARVAVRQAHARDIETRVAAQAAVAAVL

Query Match
Best Local Similarity 100.0%; Score 19; DB 1; Length 30000;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 122895 GCTGGCAGCGCTTGCACG 122913
|||||
DB 18572 GCTGGCAGCGCTTGCACG 18554
RESULT 31
SV1344259/c 35450 bp DNA linear VRL 18-MAR-2002
LOCUS Sulfolobus virus SIRV-2 genomic DNA.
DEFINITION AJ344259
ACCESSION
VERSION
KEYWORDS
AJ344259.1 GI:17221347
orf 109; ORF102; ORF103a; orf103b; ORF103c; ORF105a; ORF105b;
ORF1070; ORF108; orf110; ORF111; ORF112; ORF114; ORF116; ORF119a;
ORF119b; ORF119c; ORF121; ORF131a; ORF131b; ORF134; orf154; ORF156;
ORF158a; ORF158b; ORF176; ORF207; ORF249; ORF269; orf309; ORF310;
ORF335; ORF356; ORF399; ORF436; ORF488; ORF55; ORF564; ORF56b;
ORF59b; ORF62a; ORF64; ORF69; ORF73; orf76; ORF83a; ORF83b; ORF84a;
ORF84c; ORF90; ORF91; ORF94; ORF95; ORF98.
SOURCE
ORGANISM
Sulfolobus virus SIRV-2
Sulfolobus virus SIRV-2
1
Virusess; dsDNA viruses, no RNA stage; Rudiviridae; Rudivirus.
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
1. .35450
/organism="Sulfolobus virus SIRV-2"
/viroion
/mol_type="genomic DNA"
/strain="HVE10/4"
/specific_host="Sulfolobus islandicus"
/db_xref="taxon:157899"
/country="Iceland"
1138. .1389
/note="ORF83a"
/codon_start=1
/product="hypothetical protein"
/protein_id="CAC8276.1"
/db_xref="GI:17221348"
/translation="MKVERVCKKITEKTLNTSLICVIGKKMKQVVQVQGTREYES
EDDLISVTHELARGFTVEKIASLIGSVKRVRYRLSC"
1584. .1943
/note="ORF19a"
/codon_start=1
/product="hypothetical protein"
/protein_id="CAC8277.1"
/db_xref="GI:17221349"
/translation="MHICKSGEKRMSKOIGKNISYSISSLVEDFLETOKOVLTP
KRIFKDKQMDQDLINELEFDLVKPDNITVYDSAITQMFPEFKLSVIRIYFKKALE
NHKIVFLEKVEMKYH"
2121. .2432
/note="ORF103a"
/codon_start=1
/transl_table=1

/product="hypothetical protein"
 /protein_id="CAC87278.1"
 /db_xref="GI:17221350"
 /translation="MKKMKPEFLKKNMNPVENSEIWEVDLIFSEIELEIPEDEYKDLT
 KNADPLQEIINDTGVNIYTDYTEWMEFNNOYLELEIDYRQNDKITLLELHRRKKYK
 K"
 CDS
 2635..2907
 /note="ORF90"
 /codon_start=1
 /transl_table=11
 /product="hypothetical protein"
 /protein_id="CAC87279.1"
 /db_xref="GI:17221351"
 /translation="MDEDLVEESDNISVLKCKCKGKGVIGIVEKKEISYAKVLKCK
 HFSMGYIDKKEVONNSLFGIITIIHPIFYITGKNKKYLLYKVKMLR"
 2982..3311
 /note="ORF109"
 /codon_start=1
 /transl_table=11
 /product="hypothetical protein"
 /protein_id="CAC87280.1"
 /db_xref="GI:17221352"
 /translation="MNVNQEKIVSLVENFPDKSNKPIETIKLNGKVMNEEDYDL
 IGLAMTLARGKLEIYERISLYFSEFCVKNNEIYIRMFETREKQOLKIEMT
 RLIFKCO"
 3477..3827
 /note="ORF116"
 /codon_start=1
 /transl_table=11
 /product="hypothetical protein"
 /protein_id="CAC87281.1"
 /db_xref="GI:17221353"
 /translation="MRMGQYIPDEIILKAEKVKNASDRKNILKMIIRKMEIKII
 EKKKFNITIPYIOKRINIFNGEFGFEDSYKKNDEKIEVITKVLKRYENGELK
 LGLKFEKSIINKIS"
 3959..4354
 /note="ORF131a"
 /codon_start=1
 /transl_table=11
 /product="hypothetical protein"
 /protein_id="CAC87282.1"
 /db_xref="GI:17221354"
 /translation="MSQKVEFPLNVELESEKVEPOVKLYKFFNVENVYHNSKISS
 EASGNLYLEIKDELNVYDGVICAPSLSHSISDRNENQVEINANGAYEFKIK
 FVCKISVLARONRMYLIFKVESLPEISRY"
 4542..4853
 /note="ORF103b"
 /codon_start=1
 /transl_table=11
 /product="hypothetical protein"
 /protein_id="CAC87283.1"
 /db_xref="GI:17221355"
 /translation="MSFSYISISDKMISENVKLLKEMNSFIKSEKEKIEENPPL
 ILNKSRTIEAFGRKNSILYTRFDLWNLLEFDKYLIVYENDDKKFIHKKIKLK
 N"
 complement(5053..5388)
 /note="ORF111"
 /codon_start=1
 /transl_table=11
 /product="hypothetical protein"
 /protein_id="CAC87284.1"
 /db_xref="GI:17221356"
 /translation="MRRKIGROIOTIRFPFAKLOKYOILTPPEICERKHIINKNO
 GKLYIFEDSELTVMGYGROYINNLKKGIFYEKVADPKINRKYVICINKDYLPOI
 QNLINNNK
 5562..5879
 /note="ORF105a"
 /codon_start=1
 /transl_table=11
 /product="hypothetical protein"
 /protein_id="CAC87285.1"
 /db_xref="GI:17221357"
 /translation="MEFEDLDVLYVFFENPEMKSPEEFKELEPTEENGPKYLVGPV

DSRNKKSSSEIEEPIYQNDNLIKLPFYVYTKGNTKIYIRKIYGMREKRLNEDEE
 NNI"
 5897..6085
 /note="ORF62a"
 /codon_start=1
 /transl_table=11
 /product="hypothetical protein"
 /protein_id="CAC87286.1"
 /db_xref="GI:17221358"
 /translation="MKILVNDGONLIIERRKRVKSFEGEAPYITGVDKNGRISYS
 IEPDLKLGKIGIRIKYV"
 6144..6452
 /note="ORF102"
 /codon_start=1
 /transl_table=11
 /product="hypothetical protein"
 /protein_id="CAC87287.1"
 /db_xref="GI:17221359"
 /translation="MIFNSPIYOKYIILNNAKAVATIRKKFYKIGOKYIILKRDREF
 GKIIAKAPVTEYCLSKYVKFSGFENVESMLNEABRLHNDKIDSEKYEIIVIMTNLYF
 "
 complement(6441..7373)
 /note="ORF310"
 /codon_start=1
 /transl_table=11
 /product="hypothetical protein"
 /protein_id="CAC87288.1"
 /db_xref="GI:17221360"
 /translation="MKLVPEFTSSKELLFOTDPEVLYLNOLHNKITYKKNETWVDSGF
 QISLYNLKISVEDLYQKYTYNAYAFSLDPSIFEPLNRNFEYELLYKIEYIER
 IIPVILHLYPLREVDALDFYKQYDYLAFGIVASSKILIVAFPMYYIIRYVKRL
 HVLGMSAPYFIOSYDAESMDTSYTRISGFEIEMFDGTRRYGNKKRLLTKEEER
 QLYEFLDKTNPFPKYSNLIQIINAMILKYNNMINENKTYIAKKLRMGDSLY
 NEIQONKINMEIKTKKTPOTKKSNRELEIELE"
 complement(7382..8561)
 /note="ORF399"
 /codon_start=1
 /transl_table=11
 /product="hypothetical protein"
 /protein_id="CAC87289.1"
 /db_xref="GI:17221361"
 /translation="MEFERKSSGIKIFENIIDISINLLWGLISGLSYPLVSSLLK
 NVNLLVAILGVAPEIPIQLMFOYRLTKYPLNGGDVAYIRAFSSKRYTVGISLMLT
 VLSQPLIGDLVLNFINQOEOLFVIESFPVLLIANKKIYAKVIDYLAQIIT
 IATIRKSPFQFOFTISMTLSALLFDASPTAFNAISYIGELIKKSSWVG
 FVSGYIAIILSIIDSYGNLITFLMIPMFSPYINKIOSRLIOMSPKXVPEK
 SKIPNVLLIFITANTIANVLENLGNISFGDGLLFTFNNFTIYAFAYIKLMNDRI
 LEFTVLSLAQIFLFFLYGQNIIFKVISGNIETTILRIIIPIIIGATVYLLRS
 KINVMPK"
 complement(8818..8988)
 /note="ORF56b"
 /codon_start=1
 /transl_table=11
 /product="hypothetical protein"
 /protein_id="CAC87290.1"
 /db_xref="GI:17221362"
 /translation="MQTQEGSKQKQKAVFGIYMDKDLKTRLYVCAKANNLQLOATE
 EAKREYLOKRCG"
 complement(9013..9372)
 /note="ORF119c"
 /codon_start=1
 /transl_table=11
 /product="hypothetical protein"
 /protein_id="CAC87291.1"
 /db_xref="GI:17221363"
 /translation="MDLKVNLHFHSYIYTYVTTNNYKYGDTKIFKKFROYIYNH
 DKNSHVSIKETTENSGLHYHILVFTNKKLDYSRVHKHMPHPSDIRIELVPKNMSDI
 KNYKYMILTKRKDIKMS"

Query Match 0.14; Score 19; DB 1; Length 35450;
 Best Local Similarity 100.00; Pred. No. 9.6;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 123892 TTCTGTTTTTTTCTTTT 123910
DB 33492 TTCTGTTTTTTTCTTTT 33474

RESULT 32
AB096160/c 106873 bp DNA linear VRL 05-JUN-2003
LOCUS Cercopithecine herpesvirus 1 DNA, UL region, complete sequence.
DEFINITION AB096160
ACCESSION AB096160
VERSION AB096160.1 GI:28804635
KEYWORDS
SOURCE Cercopithecine herpesvirus 1 (monkey B virus)
ORGANISM Cercopithecine herpesvirus 1
Virus; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Simplexvirus.

REFERENCE
AUTHORS 1
TITLE Ohsawa, K., Black, D.H., Sato, H., Rogers, K. and Eberle, R.
JOURNAL Sequence and genetic arrangement of the u(L) region of the monkey B
MEDLINE virus (Cercopithecine herpesvirus 1) genome and comparison with the
PUBMED Arch. Virol. 148 (5), 989-997 (2003)
12721804
2 (bases 1 to 106873)
REFERENCE Ohsawa, K., Black, D.H., Sato, H., Rogers, K. and Eberle, R.
AUTHORS Direct Submission
TITLE Submitted (17-NOV-2002) Kazutaka Ohsawa, Nagasaki University School
JOURNAL of Medicine, Laboratory Animal Center for Biomedical Research;
1-12-4 Sakamoto, Nagasaki, Nagasaki 852-8523, Japan
1 (E-mail: k.ohsawa@net.nagasaki-u.ac.jp, Tel: 81-95-849-7133,
Fax: 81-95-849-7148)

FEATURES
source Location/Qualifiers
1. 106873
/organism="Cercopithecine herpesvirus 1"
/mol_type="genomic DNA"
/db_xref="taxon:10325"
74..805
/gene="UL1"
74..805
/gene="UL1"
/codon_start=1
/product="glycoprotein L"
/protein_id="BAC58040.1"
/db_xref="GI:28804636"
/translation="MALGAVSAARCLMLFHLFVLSVAAPSVVSPASPSPPV
EYVIRSVARVTDILKFAELIPAGVITWRYEAPSIDYARDIGLFIYHSGDLTV
VWDKRAORAYWNPFLFAGFLDELGHAFEPANALFETTRFALYKVRILASRSDAA
SSTPVPGCVDAEYSRTKCPDGRPTGIMNEPRIRPFAPNDEASPOQSLAPATP
TPPKRTERPAKPRGNATRTAPRA"
681..1634
/gene="UL2"
681..1634
/gene="UL2"
/codon_start=1
/product="uracil-DNA glycosylase"
/protein_id="BAC58041.1"
/db_xref="GI:28804637"
/translation="MKRARSRSPPQRPPLPPPDGFTSPRGNPEETRPQPPAAHESP
REATATPARARRRCPCPAVTFDSOPSPRSGLDADADRPPALDWTGFRRLVWG
EAMRPVLEPELSNPLTAOLMAEYERRCRYEVLPPREDVFSWTRRCTPDEVVITIGD
DPRYHOGAAGHGLAFSVRGTPTTPPSIRNLILAARNCCPDALAAHCKELKMARGVLL
LMTTTLVRRGEPASHAKMGWDRFVASAVRRLAASRGVLFMLGAHAQNAIRDPDVH
RVLTYSHPSLSKVPFSSCRHFCLANQYLRESLAPVDMST"
1770..2453
/gene="UL3"
1770..2453
/gene="UL3"
/codon_start=1
/protein_id="BAC58042.1"
/db_xref="GI:28804638"
/translation="MSSLSAAVPSPTLAVLSMGNAFAPQDSRRAMAADPAATEPEA
LALLPAPRATTDEPPDRALADHVAFTMTFVSSVDELGRQLTDTTRKDLRLSLV

gene
CDS
complement(2570..3181)
/gene="UL4"
complement(2570..3181)
/gene="UL4"
/codon_start=1
/protein_id="BAC58043.1"
/db_xref="GI:28804639"
/translation="MAASPATLAVSLHGATSSACVLPDAEQVCAFDGCTRAISRG
CLRKDTLSGAVVROTQPYGLLVMDCRDFPCAYRVRGSRGROTLERMDTCLCAVFP
DSWVSTRGESVRSPTAGIVTYVWGEDSIYIVTYGSPGGEAEPLDPDSSPLDA
PCPTSPPAVSPASAEAGAADLVEWKEIQLSPTLGEGHEP"
complement(3233..5881)
/gene="UL5"
complement(3233..5881)
/gene="UL5"
/codon_start=1
/product="component of DNA helicase-primase complex"
/protein_id="BAC58044.1"
/db_xref="GI:28804640"
/translation="MARVGGDASVSPPPOPREPSVOFDEAFNLFTSMHGIPTIER
VRELAHRELEAARVPRIQWFRDVALEPAGILRPEFPAYVLLTNGSGSTCQOT
LNBVDVCVTGATRIAONMYKLSAFLSPRINTIHPERGGRHNOYQCHXYTL
ASNPASVEDLQDRDLTYNEVITADITRRVAAAGGDEDRNEFRALATILESTMGJEG
ALTRLAFTHGLAPFTFRSNIVIDEAGLHGLLTAVYCCMMNTNALHTPOYAGL
RVLVCGVSPQTQASLESTFEHOKLRCSROSENNVLYICRNTLEVRALIRSNATF
INNRCEVHEFGNLMKALEGLPLEHNOFVDRAVVPSPFTNPANLGMRLSSSH
KVSVAAMRLHMLKVARREGFEVFSPLPTFVSKAFEPYELHOPALVTEKMTAA
NGRITNYSQSDODAGARARLVHSKQOLVARNDTYVLSNQLAVTTRLRLLVGSF
GTRSFVAYLRDSDVYKTTGEMILVERATYFSLRILFGLIHTYINPLIRGLDAARRAR
AYERMGALIRELLSGATGAGPATPDQNASGGSASAPAEARAFDEKTLGARATD
ABEPEDDLVNVFAGLNEDELDFYCHTYVEQETTAAVAHAQGLKRAFLGARYHLRE
LFGAEAFGAGFTGYNDVYTFRCGEVWIGSMRGLMSVALQTSYTLTGFTVARYVFA
EEVRRHAAGGLAELEESPLPYVVLRODHGMSVYNTNISEFVESREELAMATNA
DYGISMLAMTTTRSGSLDKVAICFTPGNRLNSAVYAMSRITSSSELRNMLNLR
EHRERDVTISEHLSLRDPVLIY"
5757..7931
/gene="UL6"
5757..7931
/gene="UL6"
/codon_start=1
/product="minor capsid protein"
/protein_id="BAC58045.1"
/db_xref="GI:28804641"
/translation="MIGMIPCDMVDYFKKASRNWTEGSRGSGDDTLASPTRAMAE
RHPBARPPARFPDAPRPDDGQVQVHPPTPTMLREALLGELGTGEGQGVNVRS
SEAVYRLOLAAYFGALLNAARHDLADRRHRYAARRLEPRLVRYGAGPDGAAY
AERYVDTRMALIRASLLDPARGLACFNQGGGPGPSRYIDMLMCGILVPMRPR
EEEVTRLEAFISDHALPRDLATVAGAVERAPAPGLELARFDSARIADYDVCLEFYH
PRGEWRVDPAGAOGECEVLMPLMTDRLFLFSPMORLSRETIYACRALREHAAVC
RLRNAASVYLWGRKNDGDRGAAGARASRLAGDEBDKASASRLVRLIINMGGM
RHIGDINDTVRAYLDEAGGHLIDSAVNDLFCFGATGATGAPGAGADPAAPQOOLQ
AFOTSVNNINMGLEGIYNNLFGTTERLETNMDATOLDRDIELRARIAGLADBOQ
RAADPRAREAPAGDDDLRTYDITIDVSKADDDPVYVNSGHOVVPYADDELFS
RLMEHELKCFKTSIRHTNNGRETALETFSGALALFAVATPVSVALPAMGALITPN
GVLEGEELMEALFEKTRVQTYLTDLAALFAVAVARAARAPPAPEADDDRVREPR
GGRSPVADGARGGNGRGPEDAMGGRDGHGLDRRGDGGRRP"
7882..8772
/gene="UL7"
7882..8772
/gene="UL7"
/codon_start=1
/protein_id="BAC58046.1"
/db_xref="GI:28804642"
/translation="NATSPRAPEETRAALRRAVAGDRDLGVAAEISHQALLRMACE
VQATRHVYRTATGYRVNVTDPDRHLHVLDDGCEPDALIASDAFARCRDSSAHGPF
APAAYVLARDHVHSLCVPPLVPLPHRLSVPHLEDFELACLIMTYENCPRAHMCAR
FVKISAMLAALGRRTSPEDRVCLILRSQMMINTLMFVHVHPEPDQVLPDHWCMAR
VLLANPEPILITALEFRAGSRYVRLPVGCRASILECVAYNPQCVLAAGMASDEFRAGLV
SMWSSDAPKTQTSALFYRLV"
complement(9447..11232)

CDS
/gene="UL8"
complement(8947..11232)
/gene="UL8"
/product="component of DNA helicase-primase complex"
/protein_id="BAC58047.1"
/db_xref="GI:28804643"
/translation="MGDAGLWVAEESICATITTYTAWLPRTTRDLVLLTFCRDARG
DGAARAEVSIATSTELQAFYGAETSAVAAVAARPAAPLETLNDVLMRLAY
ACALVALEREVRALFAPARAMPDRGLVRIETLPGSGPAPALNDVQATLT
DPLALAHYAARPDARLAMARLAITDITQCSAASLTIRITGARRRETTITLTP
PVRRGAVADVFEVEARVLRPRGHAQVAVRVLVPRGYEYFVAGAGCFAPALIAER
QWYLVHAGPGLPPIFAFLGEPERGAVDHFSVLGPPGAAVTLKSGGAAPAPAA
LAAHLEAGAMPAGARALGPAPARMAVAASAAERLPPALRPAAGELDLPPAYIG
PVCALARFREPQPLRALALVELGRDPRDPRDLRGARRMDLGGEGAAQDA
PMPREYALATDEPREVPARVARTLDIGTSAVGVGERKAGAVDMVACGGGGRWAG
LVNDRPDAGAGAAAAARARALAAASSEALAGLGLDAPRVLVEGTTTHAVLM
SOTGAFWNSDTEDEDLREGFLRGPAVYAAVAARRALAAVAAVAGSEGAEEALRI
AHADCDRLVMEAFERRLDAYGVAVETPSDRDDPLPTAAF RGALIDARVERVAVR
CGPDGGSVSPIDILYPRPLVLPIDCAHHLREVLAEWAVEFGALTGLMGCGCFAY
PEERSLFMEDNGAGVNNK"
complement(11284..13908)
/gene="UL9"
complement(11284..13908)
/product="ori-binding protein"
/protein_id="BAC58048.1"
/db_xref="GI:28804644"
/translation="MSSPTROSADTTNADPTWTHQVHHAARETGSFSSVAGPILLAP
IAEEDLAQYSSSILARMLYGGDLAEVPRVPMVIERADGPVSPFAGAPTSYCV
TVVAPMGSGKTALLRMLKEAHSPTSVLVYSCRSFTQTLAARFAASGLEEYTV
PSTNTIMDDRPFHRLIYOVESLHRYGPNLLNNYDVLVDEVMTSGOLYSMPMOGL
RYDALMLRLRACPRITAMDATANQIDPLCGLGEKNGVYGVXMAAPGSEERCL
FIQRCEPEVLQALEEGGGAAPPAKGTCTFGELEARLACNNVCLSSSYSEI
AARFCRRFTDVALVLLHSITPQDVTTWGEYRVYITVTVTGSLSPVHFDSFAVX
PANYGDMVYVOSLGRVRTLREGLLVMDGARSEPEVPMNLNHHVGAARMPA
OESOVYGLCRRFGKCDASARGETAARSSRYARFYKHYERCTLACLDLSLIL
HTLLTLCVBARWGHGEVSPDFCRFLRGALDVLRAORLLRELRADGTINSLQAO
AADTEVGFVEKTYLRPDVSPAEIVAMRGLNGPGRTRFVHLIIEACTLRVTAMHS
SAVFRRLYHRYGVTPYGPAGDIEVALQPLTPYVELFRICGGIAGRLRMBSA
SGSEBNSAPVDLALMPHYERYIQDLLEVGHCNVTGDSLSEAVRATVDLSEGP
ARGAIGEAHIALMLFRIWGLGELGVQTVKSTHTFPGVYKMLTKDAIVGLLDHID
RSACRTRHQLYLALMAHKRDFAEARFLRAPAWGRCLARACAGAPPTDVLVEALSE
LPAAEMPTOGALDFTTI"
13775..15193
/gene="UL10"
13775..15193
/gene="UL10"
/product="glycoprotein M"
/protein_id="BAC58049.1"
/db_xref="GI:28804645"
/translation="MGRPASRGPATETGDEPVSRAAMTWCVQVAFVVSALCLVLL
IVAHFERGEPCEFYASAASVGPANDIAEVGVAAPRLDAOSLVGTVATLMLAV
AAVWVATGATARRRRODAEELDAARMAVMTATHTLIGNACVWLQITVLLAHSYSA
LHVTYVHLFACITLPAHFCTRGVSTGYLROVHGLMDVAPTHRIITLVGAVRVMA
MLFGALICTAPAAVSATTAALNEPLISAPGVLCIAAFAALVLLVLAIVEGLISVY
RVULGPHVCAIAGAIVGTAEITYTNGVYVAETQPGAGTQVRYTLALVAFALYMA
GVRCVAYLVHREHRTFRFHHMDTKHRAKSARIVRGSRAIRGSDPGARGAALVE
PIYSEVKYAGESDVRDDSEYTEGHEIYDEVASDPEVTYARIQHRPREDVEDVT

Query Match 0.1%; Score 19; DB 1; Length 106873;
Best local similarity 100.0%; Pred. No. 10;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 33
AF318573

LOCUS AF318573 106873 bp DNA linear VRL 18-MAY-2001
DEFINITION Bovine herpesvirus 4 long unique region, complete sequence.
ACCESSION AF318573 AF271211
KEYWORDS AF318573.1 GI:12802528
SOURCE
ORGANISM
Bovine herpesvirus 4
Bovine herpesvirus 4
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae.
REFERENCE
AUTHORS 1 (bases 1 to 106873)
Zimmermann,W., Broll,H., Ehlers,B., Buhk,H.J., Rosenthal,A. and
Goltz,M.
TITLE Genome sequence of bovine herpesvirus 4, a bovine Rhadinovirus, and
JOURNAL identification of an origin of DNA replication
J. Virol. 75 (3), 1186-1194 (2001)
MEDLINE 20583805
PUBMED 11152491
REFERENCE 2 (bases 1 to 106873)
Zimmermann,W., Broll,H., Ehlers,B., Buhk,H.-J., Rosenthal,A. and
Goltz,M.
TITLE Direct Submmission
JOURNAL Submitted (03-NOV-2000) Project P24, Robert Koch-Institut, Nordufer
20, Berlin D-10555, Germany
FEATURES
source
misc-feature
CDS
/note="long unique region; LUR"
1..106873
complement(445..633)
/note="ORF B01"
/codon_start=1
/evidence="not_experimental"
/product="hypothetical protein pB01"
/protein_id="AAK07921.1"
/db_xref="GI:12802529"
/translation="MEGDVSMVAFGRKRTRODLNNSAGNVCACVLRKHNHVSAGC
CAVRNNSFHLSPGMWP"
614..4480
/note="segment protein; ORF3 B0FA1"
/codon_start=1
/product="v-FGAP-synthase"
/protein_id="AAK07922.1"
/db_xref="GI:12802530"
/translation="MDTSPSILCFVSRRAPLSNCEOVITQOTSGOLPLTSVLOY
EYFRWLVNGEBOAVRFLVPRDLKSSHCGLPPHSSSLTKDLSRLSTVGVSPA
PETALSRDLVAITQSMGSLAPMSNLQILKIVSLTICINLNPSSKIMSTLRRL
CPDLSLFRPKGEIVGAFETHGAPQGLGKAFVGGFLNASSGASGFMET
PQHPQOTIVQONFCKTAYIVPVYWIPEISTYSSGHMTDGLAATYGGOLQVAPDN
LKEFLNSPQMGNEVYSQGLIASTVSTTSPRSSYELPRTDMDAMVIMNRC
SLPCOGYFEPPIVESHLPIDSVPEGPILAEFGACFSRNITTDLPETRRHINVIOLGT
FTSHSDSGREVRLGALKILMSFLRPSYVKISLVKVCETMHNALISCGOTYGIK
ITVSALRPPPLNTGLPFTASNRQONMTIKQHLNIVAPLVLAIENTPNTDITVAK
AGCAIHGCOYVAGRTOKRHLIVHDKQONVREI SLKRYSPYLPSTNLOQS
ENMODSSMDMTLPSSLTYLLEHLKHPAGCKOFIVKHLDRLSGGRVAAQOQGIARDI
PISDYSLIVSLDLSLAAPDRGSENPATSESLDPLVNNEPYPGICSAIGCPILS
TYPRPIGAVAIYVESLINTVSAPEKRIIDVTCNPNTDSTDSHGILIEAGREF
CSOLGICGFTSCCTTSNRGOKLNNSLVRYLVYVTAPEKDVTOGLTPDKPDSSI
VWLPJSTETHEFTVTSQLEFRDPSHSHIINIDPLVYAKLITVAKHLNHSITISCHD
GGGLITACFEMAVAGASIALVPODEDDVLETSPEGLMVEVPVAKSTNLOQS
TSDITIVDGRTLPVSANFTVYSYKRIIFRESLDMVENMHHFSKEDMRYPCFY
OGTPEDPKDOLHLEFQSPMCHGPYKXQVWVYLLPGNTDSDLLVLAEEAGFRN
IVSTFTDKYKIVTDTTNVNGICLTGATINEDATLIDKAI SMYTKHNSVYGLKRLI
NSDVEFSLAIGHACIILPENKFMGYNKNSNTMYCKENSGAMESRNIENFIPENPH
AAVLQSMKSLPGLPMIOTGHLGFAPHPSETYEMLSHGMVATQFGADISAGALYTP
ONPTAGYTTISGLCSADGRHLALLHDPLGSNNLMQWPHIPKMPPLKVSPPKRMFLDLH
IWANKYREMDQPPPPHDPPLRNKIKVM"
4608..4811
/note="ORF B02; B0FA2"
/codon_start=1
/evidence="not_experimental"
/product="hypothetical protein pB02"

/protein_id="AAK07923.1"
/db_xref="GI:12802531"
/translation="MASPTQYCHRWRYHGPBRSAKISYGYKRDYTHQLTSKNSAYS
GMSPOCSCADLNKLFVQSQPIIS"
5286..5513
/note="ORF B03"
/codon_start=1
/evidence=not_experimental
/product="hypothetical protein pb03"
/protein_id="AAK07924.1"
/db_xref="GI:12802532"
/translation="MGEPVMLFHPQPCPTSLKHGLYIKYIKSYLRATFLVRN
HIGPKRDTFRPGGPPSLIVQRLAKR"
5943..9347
/note="ORF 6"
/codon_start=1
/product="single-stranded DNA-binding protein MDBP"
/protein_id="AAK07925.1"
/db_xref="GI:12802533"
/translation="MAAKTAAQGOYEDNIGSKADIPGCGIYVYKKEETPPKNSLLG
NGPFGTSMVPLLGLLVEPFPINAKAHRKIDTTPVSVKTSYHAEVIMESNIDC
FTPIFHGTLPOLOQETRDLEGPSPSPITNNISLQDLCGTNCDIEVILSVIT
EGFERLYHGHMILPLGHVEEVOISPOHAKRIPLIDEDLSKIAPRMKRFSHSDVS
QYFNSLYTAIAOARVADATVIOAMESOPRODHKKMKVHKKDPSSSSRPDGL
SLMDVSASELAVSYGLSEIDAPDMSALDYTSMPITFDCITTEEDPDLAHLAMNK
OSIHVNOLPSTNSMLYTRIQONPRTAKDILVYNSYIQLHGLSTSEATQDEYGO
PFGVOSNLSSSTYTHHLAASWCPNTLAVCYLQFCQHQKSTQSNYSIN
VGTAASSDMCLCOGKRPVNCINLFLRLRDRPPIITSHRDRYIITGSGMNDID
ILGNFASREKEDGAQVEYOKATYVQLQTLKLEGMKIDTTPKESQVADIPSP
IKFKVIDAHVDTEVLEKINCMKNINRETIKSIHVIQYCCNFCQPCPELVLG
YKSLITLIDVCLPCNMCYRQDMSNGMGPTEMLKMYOTLMTNFGCCCPDRLVIG
AEKMHSDPCEPDYDAINGIIFSPKTOVRSRMLVYPTIKIKIRIIFENSSG
SEAIOSGFLSGSKKDNITVIGPYMKFLNTHKIMFPOTKSSLFMMHTSTKQIPL
ITGPVKQDLVALANIEYNSKLHSEIDVLDIIPNLITYAKIKLNLMLLRACQGOLEY
STYLACVPTVRYGGEYPRVHLNEEFLEGTQYKLVQNTAQIQAATLKEDYAOAG
KLRIITVPMVINKYTGINGNNGIIFHCNGICGYFMGRGVDRNLIFENAPFKQSNAYK
RKHKVMPITVDNLIKRTYTPSTPEVENTRDIRIMLLEDKQNONIFRDVYLIVG
LGCACADLTADDLQGLGEYIYMSDELISROSISDAGVPMCEDSVSFLEGEVYSEB
QLERTGLEBQTTSAFTSBDFFQASGLSTIAAGKRRKILNCMLSDFDL"
9352..11430
/note="ORF 7"
/codon_start=1
/product="transport protein"
/protein_id="AAK07926.1"
/db_xref="GI:12802534"
/translation="MARELAAYSQVDELSEKTSLSLFCDPRAIDLAFORNRKRLK
LIDALYHLVEONRTFECSELSLEHLINITYITMOKLECNLENIYEKDFAMLHS
DLCEHRTVNLCEFGDCVPIPSLIIINDIEFERSLNSVEFCISRNNADELEETINP
LGTLRNISPIDPLILPSISCMNCMLNETSILPMOGENVETIANSINCTHQAIVABE
PVQGLFENELMHLNIPYDGTDNKQVLETSRIRNASIEAIDONITEKYSQHLEIS
NLITWNGSHSDSPKLSCSOMATLILQHETRMASHROKVASHLATTPRIHFEDSYRA
YPIESLFCGGLFYSIMDNIALKQDCSTAFKASHNYTIERKNELVRLNMLAPSH
TKBEDIDKPNISIQARTHTIGETTSQDIFSDAARAKNMYLOKTTGKLTQDCLST
OGKIMCNTLILRTGWYTYKEAAILKNHPIRKRFILPOMHNHYTAIINELYESKFI
KNSLYOKLSEHIDSTIIOFYSLITGLVGPFPSPPIILLANCLDAKVAHNRK
MLISEVIMPSMEKPMIDAEFNAPYNTGTGKINSVQOCARVITELVNASLSYRWME
KDLNIVSPSTLSPNLFSPKTFKSGIITYEKTAPLFIHDTNGWLFKDIYALLYHH
LQLTSHKNVL"
11420..14044
/gene="gb"
11420..14044
/gene="gb"
/note="ORF 8"
/codon_start=1
/product="glycoprotein B"
/protein_id="AAK07927.1"
/db_xref="GI:12802535"
/translation="MYKTLIFPALLIVGSPNQTITSTTSPISSTSTSTSTSTK
PSNTSTNSSLASPOMTSTSKBSTDQGSTPIPIVTDOTASKNFKYKRVCSASS
SGELFRPDLQCEPTDKRKHVEGILLVLKNLIVPIFKVRYKRIATSVYVGMGO
AAVNRDIDRAIPYNEISMDRTYHCFSAATVINEILMTYIDRDESNVPLQAPV
GLTENIRYPSOPLIYAEPMGFPIYRVTNVEVDVMDARSVEYTHPTALGDIT
EISPFCHNNSQCTTGNTSDATKVMVLEENHGYDYERRGHPIKDKRIIFLKEDEYITIS

WKADREARATDEYIWKTPPAITQITNESHFVYANEVYATSLTNSOEBELKONTLEI
LNCNASTINETLEETVYKFNKSHRIDGEVYKYKNGGLFLTQAMKPLNLTSEHNTYTI
ERNKKTGNKSRQKSVDPKTPOGAKMSTAAQVAYHLLRFSNMHILIEELTKYCRQ
KDNILMYELTKINPVSAIYKGPVAKVAGDAFMYSECINVOASVNIHKSMRND
DPKYQSRPLSTFKFVNSTAFPRGOLGRNLIILNTHVERTCRPTAHYFPVKMTHY
FKDKYKVTMDTNNISTIDTFLTNLPIIDINDIKYVELYSETERKASADILEMTRK
EYNTQKRLASREDLNTIDLNDRKLKLESEMADIGDGVVNTFSGITVFGS
IVGGSVFSEFNPIGGVRIILLIVVFPVFLVSRRTNNMNPAPIKMLIPNIDKASEQ
NIQPLGGEIRKIRILGMHLOOOSHEGKSEEBASHKPGILLGGLDILLRRGYTRLP
TFDPSGNDTSETHQKYV"
14184..17201
/gene="DPOI"
14184..17201
/gene="DPOI"
/note="ORF 9"
/codon_start=1
/product="DNA polymerase"
/protein_id="AAK07928.1"
/db_xref="GI:12802536"
/translation="MEFPNPIYSKKKDKRISCVDDPKKTNPYCLVPCKCTPPTP
GVISITTTDPEVLEHODKEPIFTSGHQRYSWALRTPAPIPKDLFPHVVDIE
TIVYDRCDDPIQFQDILPNGVULKIQDQASGVQVQOMYFVYLPDGVN
LSYVIOQTLNGVKNKQCFSTIOERKKILKEYPDILPYVYKTLISAPTEINQVGLN
TSGCEVFEESVNASSTRFIIIDNKSTGWSQSNPHRISORSDTLEPFCGGLD
PHEEQOMPPTINSPIECCGBOGFCATDEDLVIOISITWVGSSESPKNTILS
LGTDPLANDVYEFPSBLDMFAETFLRKFNIIDFYGVINIANFDPTIIDRATQVY
NIPRHFETKTVISGTFEVDNPMNAGAFMRSEFKIKISGLVIMDYOVCKRILSDY
KLNVNARKCMQTOKEEDVYKEIPSLFSGENGARARISGCVLSDVLIDLAKYPMIH
EISIAKAKKIPARVLEDDQOIFVSCSLLEAKRHEFILPQAPGPGYGATVIN
PIGPEVNTPLIVVFPASLYPSIIQAHNLCSYTMIODONLHLHKLDPDYEFTHSTGP
IHFPKHOKTSLSTEDLTAMVAKRTIKRELKELANDDQPMKTIIDKQOLAKVQNSVY
GFTGVASGILPCTIPIAETVITQGTMLIEKSAPEVMTTPRESLISYVYPPCDPDAF
RVITGDHDSLETECGRYPMOSVLPNPAUKLETTTKALFKDPIKLEAEKFOCLMLTK
KRYIGILISDLVKMGVDLIRKTCASVQTTSEKILDLVLPDPVKQAAOYLCHQAA
KVYSDGIPVGCQKIDVLNNSYALALATGKVSLELFTSELSRFGEEKYTTLPHLVY
YRKJMSNBEELPOHDIRLPHYEIKGDQRCSDLAEDPTYVSQKIPISVETYDKLI
HGVAIIQCLGNNSMNTVELVNFVNIPYSFT"
17297..18577
/note="ORF 10; BORFBI; conserved in other
gamma-herpesviruses"
/codon_start=1
/product="unknown"
/protein_id="AAK07929.1"
/db_xref="GI:12802537"
/translation="MTSTLVEFSIEGQVNICNIIILMTNLKDI PVQGGYMLVKVY
FILPLSNQILNNYISFGIYVOSIFELDEYAOCTAMVOCREPGITPELEIPIHVTEN
MPLFLVKTQMTIINSLSLAIIFMKPTCPTGCSYSTAPETIPPOSHLHLLPS
TDQHLTLISGAILCNKHTYATMYRPGSQMGEFHEHTMASGRDLODACVKGWVSD
IKNIMMEVYVNGIXYSVNTNHRKRDHIMTILKFPVYMKPNDIIVSVLPSTPLS
CGKVTYVITDSEKILKPGETLNLKATKTYTIRGNSTAAVMEITNTNPNYLTIEPTTM
LPMPTLOVTTIKNPNMIIITIKDLAIAACVYYSYTLDRDPASPASVYFNPQDLTITW
EDSMNAPTEIGNIYISRCHNLKSENPSPMDPT"
complement(118848..19345)
/note="ORF B04; short ORF of immediate early transcript 1

Query Match 0.14; Score 19; DB 1; Length 108873;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CDS

QY 129813 TGGAAATAGAGCGCGTA 129831
|||||
Db 31557 TGGAAATAGAGCGCGTA 31575

RESULT 34
BHYIGEN/c 135301 bp DNA linear VRL 07-Apr-2000
LOCUS BHVIGEN
DEFINITION Bovine herpesvirus type 1.1 complete genome.
ACCESSION AU004801
VERSION AU004801.1 GI:2653291
KEYWORDS complete genome.
SOURCE Bovine herpesvirus type 1.1
ORGANISM Bovine herpesvirus type 1.1

viruses; dsDNA viruses, no RNA stage; Herpesviridae; Alphaherpesvirinae; Varicelloviruses.

REFERENCE
AUTHORS
TITLE
1 (bases 99702 to 103033)
Mirth U.V., Fraefel,C., Vogt,B., Vlicek,C., Paces,V. and Schwyzer,M.
Immediate-early RNA 2.9 and early RNA 2.6 of bovine herpesvirus 1 are 3' coterminal and encode a putative zinc finger transactivator protein

JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
2 (bases 103034 to 111027, 127191 to 135300)
Schwyzer,M., Vlicek,C., Menekse,O., Fraefel,C. and Paces,V.
Promoter, spliced leader, and coding sequence for BICP4, the largest of the immediate-early proteins of bovine herpesvirus 1
Virology 197 (1), 349-357 (1993)

JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
3 (bases 111028 to 114234, 123984 to 127190)
Schwyzer,M., Mirth,U.V., Vogt,B. and Fraefel,C.
BICP22 of bovine herpesvirus 1 is encoded by a spliced 1.7 kb RNA which exhibits immediate early and late transcription kinetics
J. Gen. Virol. 75 (Pt 7), 1703-1711 (1994)

JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
4 (bases 66900 to 96900)
Vlicek,C., Benes,V., Lu,Z., Kutish,G.F., Paces,V., Rock,D., Letchworth,G.J. and Schwyzer,M.
Nucleotide sequence analysis of a 30-kb region of the bovine herpesvirus 1 genome which exhibits a collinear gene arrangement with the UL21 to UL4 genes of herpes simplex virus
Virology 210 (1), 100-108 (1995)

JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
5 (bases 1 to 31444)
Schwyzer,M., Stryger,D., Vogt,B., Lowery,D.E., Simard,C., Labolisiere,S., Mista,V., Vlicek,C. and Paces,V.
Gene contents in a 31-kb segment at the left genome end of bovine herpesvirus-1
Vet. Microbiol. 53 (1-2), 67-77 (1996)

JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
6 (bases 1 to 135301)
Schwyzer,M., Paces,V., Letchworth,G.J., Mista,V., Buhk,H.J., Lowery,D.E., Simard,C., Bello,L.J., Thiry,E. and Vlicek,C.
Complete DNA sequence of bovine herpesvirus 1
Unpublished

JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
7 (bases 30801 to 67800)
Schwyzer,M., Vlicek,C., Lowery,D.E., Bello,L.J., Meyer,G. and Mista,V.
Gene contents in a 37-kb segment centered in the UL part of the bovine herpesvirus 1 genome: the last gap
Unpublished

JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
8 (bases 96901 to 99695)
Letchworth,G.J. and Kutish,G.F.
DNA sequence of the BHV-1 UL1 to UL3.5 genes
Unpublished

JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
9 (bases 114235 to 122983)
Goltz,M., Buhk,H.J., Broll,H., Lewin,M., Mankertz,A., Boerner,B., Borchers,K. and Weigelt,M.
Nucleotide sequence of the HindIII O and K fragments located in the US region of the bovine herpesvirus 1 genome
Unpublished

JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
10 (bases 121402 to 123983)
Schwyzer,M.
Glycoprotein E and US9 genes of BHV1
Unpublished

JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
11 (bases 1 to 135301)
Schwyzer,M.
Direct Submission
Submitted (08-SEP-1997) Institute of virology, Faculty of

FEATURES

source
Veterinary Medicine, University of Zurich, Winterthurerstrasse 266A, Zurich CH-8057, Switzerland
Location/Qualifiers
order(1)..4014,102918..111027,127191..135300)
/organism="Bovine herpesvirus type 1.2 (strain K22)"
/villon
/mol_type="genomic DNA"
/strain="K22"

source
/db_xref="taxon:31519"
order(4015)..9664,15010..22094,26636..102917,114235..123983,135301)
/organism="Bovine herpesvirus type 1.1 (strain Cooper)"
/villon
/mol_type="genomic DNA"
/strain="Cooper"

source
/db_xref="taxon:10323"
9665..111962
/organism="Bovine herpesvirus type 1.1 (strain P8-2)"
/villon
/mol_type="genomic DNA"
/strain="P8-2"

source
/db_xref="taxon:10324"
order(111963..15009,22095..26635)
/organism="Bovine herpesvirus type 1.1 (strain 34)"
/villon
/mol_type="genomic DNA"
/strain="34"

source
/db_xref="taxon:31517"
order(111028..114234,123984..127190)
/organism="Bovine herpesvirus type 1.1 (strain Jura)"
/villon
/mol_type="genomic DNA"
/strain="Jura"

intron
/db_xref="taxon:31518"
<1..472
/note="3' part of intron spliced out from transcript over covalently joined genome ends, leading to immediate-early RNA 1.5 and circ protein"

repeat_region
235..430
/rpt_type="DIRECT"

mRNA
/rpt_unit="235..248
466..1280
/product="UL1.1 (cIrc)"
/note="transcribed from alternative late promoter"

CDS
486..1229
/evidence="experimental"

gene
/note="immediate-early and late myristylated protein (villon)"
/codon_start=1
/product="cIrc protein"

polyA_signal
/protein_id="CA06078.1"
/db_xref="GI:2653292"

gene
/db_xref="SPRMBL:001342"
/translation="KCARASAPAGPPPAHAVALDLGGCTIDPCGDAEVFVSCPT
RPVYHMRKRTAHTTPVHFVGRVAIILPCRKPMYLMRGAVYGEPTGLRLADS
LHFDTTAGLOQDHLCDVTYLDQMDPVTTPTTLELADPAFPPTPARARS
TLRRASMRPAPFCFHOLLAEGSIDLCSPQAAAPGCSLLPACDSGDAAFCPCDAGE
TARDCTADAAAPSPALSRYSVRSVF"

polyA_signal
1259..1264
/gene="cIrc"

gene
1259..1264
/gene="cIrc"

polyA_signal
/complement(1649..7237)
/gene="UL52"

polyA_signal
/note="synonyms: UL53, UL54"
complement(1649..1654)
/gene="UL52"

CDS
/complement(1658..2860)
/gene="UL52"

nucleus
/note="early BICP27 affecting mRNA processing (cell nucleus)"
/codon_start=1
/product="UL54 protein"

/gene="1L"
complement(755.1756)
/gene="1L"
/function="Unknown"
/citation={2}
/codon_start=1
/product="1L protein"
/protein_id="CAC21239.1"
/db_xref="GI:12056160"
/db_xref="SPTREMBL:O9DHV2"
/translation="MEYITDGVLRKSFRRDFDKGKIKELKFMLSNEDSOLIRHROFI
PCEILVLEKSEKRTQVGAARVLASSLTIDYINVCHELTIVCEKGVGNDNRISIT
EDRRRREYTLVHLSSPKNGKTDVCGDKTYISTADPLLEKRSQLSNVQEGEK
IIVLVKVFLLRKADYIFTLAREFSKDYKFEKSGDRNLCYALVEVNSPFAVESGYI
TVSGRCILNVRKOLVKYKAVEKTDVCMCTEISDFGYNLNVEGDMAMKELKAVK
EDLWPSSEDDYELRELVDYVSSNLKTKYDVYVLSGDDDEFQYVSLANIRCFST"
complement(1869.2885)
/gene="2L"
complement(1869.2885)
/gene="2L"
/function="putative soluble MHC-I-like protein"
/note="related to swinepox virus C1L and chicken MHC-I"
/citation={2}
/codon_start=1
/product="2L protein"
/protein_id="CAC21240.1"
/db_xref="GI:12056161"
/db_xref="SPTREMBL:O9DHV0"
/translation="MDKLLFSTIVANCNCITLKYNTVTYTLKDGLYDGYFYHYNQ
LVTKISINHTRGVNVFRADMFNISRPHFGNDIVFNFWYSLMKETLEINKNST
KTTSLSLITGCTGTGLGSGYVETANGPLARHTGDKRPTKMTGRKQVMTLVK
NTLMKDVKAYLGFEYWGCSLALIDYOKMAKGRIPKDTPTVYTGNELDGKMTLEC
TVNSFYPDVITKMISEHFGKGYKYNVPEMGKSNVEGEGPCFPNNIKKDKDA
NTWSLTDLVRTSKMSQPCVCFHDTLEAQQYTSCSGCNGELYDHLXRTTEGEGE
DEED"
complement(2838.2885)
/gene="2L"
/citation={2}
complement(2932.3600)
/gene="3L"
complement(2932.3600)
/gene="3L"
/function="Unknown"
/note="related to swinepox virus C5L and vaccinia virus
strain Copenhagen K7R"
/citation={2}
/codon_start=1
/product="3L protein"
/protein_id="CAC21241.1"
/db_xref="GI:12056162"
/db_xref="SPTREMBL:O9DHV9"
/translation="MEIKIMEKYIKLKSNEFAQCSIFPVNADFAFYDORPNLNL
LKILREFVGCNRLIYDILSIVSTKCKIKDENNLILTSYLNKKKPIFKMKNYF
KNSIDDIYVFNKNNNIVSCGKVFELKMYDEIAKQYDEKLHKDINNRKLNK
YKINLYEMEGDPIINCKVSIQVSIIFDVPLYNDDFQVQSIRYMLKEELI
STLN"
complement(3630.4346)
/gene="4L"
complement(3630.4346)
/gene="4L"
/function="Unknown"
/note="related to swinepox virus C5L and vaccinia virus
strain Copenhagen NZL"
/citation={2}
/codon_start=1
/product="4L protein"
/protein_id="CAC21242.1"
/db_xref="GI:12056163"
/db_xref="SPTREMBL:O9DHV8"
/translation="MDYKSLITKYVCIYKSNKNKPYEERKKNFYSPEDPIDPEDEI
VGIFFLEPLOCFTYTQILSKSINKQEVLEIMSELKDDVYENFTYITPHHLVD
SMVSVNFNIMKKEFSEFONNNNNHVKIRFETISYDELAIMHGOLYIKNAILE
INSPROYSFSIYKRRKRIIDTISVNIIDIKIKIGFISTLSVHDTVYDSNPISYIFE

DISFYHRQFNKNTLSLP"
complement(4386.4856)
/gene="5L"
complement(4386.4856)
/gene="5L"
/function="Unknown"
/note="related to swinepox virus C7L"
/citation={2}
/codon_start=1
/product="5L protein"
/protein_id="CAC21243.1"
/db_xref="GI:12056164"
/db_xref="SPTREMBL:O9DHV7"
/translation="MSDICQNDVOCERNPFCGNEFYRVVHIKQMLWINSKKE
CNICKTYNKKTYVFSRKNMPCNDKKTLPKFFTLFALVTFELTITLSNMANLV
TGINDLCSITFLIVYVWVLTSSCFVSFVVAIVYDFLEAKKNSFTTIREY"
complement(4920.5369)
/gene="6L"
complement(4920.5369)
/gene="6L"
/function="Unknown"
/note="related to vaccinia virus strain Copenhagen B1R"
/citation={2}
/codon_start=1
/product="6L protein"
/protein_id="CAC21244.1"
/db_xref="GI:12056165"
/db_xref="SPTREMBL:O9DHV6"
/translation="MERCPSICLVDCUNRDDIRQIITVYIYMSWYSRSRSPAGYF
QVLMFRADSEIVFGENRHIYVKNFTGLIEDTVQAVKCTIGNALRESVNDLCA
SLAEYWGCEPLPNDLSQAALMTILSDDDYSFIDLCILVRLKKR"
complement(5433.6488)
/gene="7L"
complement(5433.6488)
/gene="7L"
/function="putative CC chemokine receptor"
/note="related to Macaca mulatta chemokine receptor and
human CC chemokine receptor type 8"
/citation={2}
/codon_start=1

Query Match 0.18; Score 19; DB 1; Length 144575;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 130399 AAATTAATAATAATA 130417
Db 7826 AAATTAATAATAATA 7844

RESULT 36
LOCUS HELCG
DEFINITION Human herpesvirus 1 complete genome.
ACCESSION X14112 D00317 D00317 D10879 S40593
VERSION X14112.1 GI:1944536
KEYWORDS capsid associated tegument protein; capsid protein; complete genome; deoxyribonuclease; deoxyuridine triphosphatase; DNA polymerase; envelope protein; herpes simplex virus; host shut-off factor; immediate early protein; integral membrane protein; IRS; LAT; latency associated transcript; major capsid protein; membrane associated phosphoprotein; minor capsid protein; myristylated tegument protein; neuroinvolence factor; neuroinvolence factor (ICP34.5); protease; protein kinase; ribonucleotide reductase large subunit; ribonucleotide reductase small subunit; RL1 gene; RL2 gene; RSL gene; subunit of replicative DNA polymerase; tegument protein; tegument/envelope protein; thymidine kinase; TRL; TRS; UL; UL1 gene; UL10 gene; UL11 gene; UL12 gene; UL13 gene; UL14 gene; UL15 gene; UL16 gene; UL17 gene; UL18 gene; UL19 gene; UL2 gene; UL20 gene; UL21 gene; UL22 gene; UL23 gene; UL24 gene; UL25 gene; UL26 gene; UL26.5 gene; UL27 gene; UL28 gene; UL29 gene; UL3 gene; UL30 gene; UL31 gene; UL32 gene; UL33 gene; UL34 gene; UL35 gene; UL36 gene; UL37 gene; UL38 gene; UL39 gene; UL4 gene; UL40 gene;

U141 gene; U142 gene; U143 gene; U144 gene; U145 gene; U146 gene; U147 gene; U148 gene; U149 gene; U149A gene; U15 gene; U150 gene; U151 gene; U152 gene; U153 gene; U154 gene; U155 gene; U156 gene; U16 gene; U17 gene; U18 gene; U19 gene; urc11-DNA glycosylase; US1 gene; US10 gene; US11 gene; US12 gene; US2 gene; US3 gene; US4 gene; US5 gene; US6 gene; US7 gene; US8 gene; US8A gene; US9 gene; very large tegument protein; viron glycoprotein B; viron glycoprotein C; viron glycoprotein D; viron glycoprotein E; viron glycoprotein G; viron glycoprotein H; viron glycoprotein I; viron glycoprotein J; viron glycoprotein K; viron glycoprotein L; viron glycoprotein M; viron protein; viron protein U147.

SOURCE
ORGANISM
Human herpesvirus 1
Viruses; dsDNA viruses, no RNA stage; Herpesviridae; Alphaherpesvirinae; Simplexvirus.
1 (bases 132605 to 145833)
McGeoch,D.J., Dolan,A., Donald,S. and Rixon,F.J.
Sequence determination and genetic content of the short unique region in the genome of herpes simplex virus type 1
J. Mol. Biol. 181 (1), 1-13 (1985)
2984429

REFERENCE
AUTHORS
McGeoch,D.J., Dolan,A., Donald,S. and Brauer,D.H.
Complete DNA sequence of the short repeat region in the genome of herpes simplex virus type 1
Nucleic Acids Res. 14 (4), 1727-1745 (1986)
86148504
3005980

JOURNAL
MEDLINE
3 (bases 9001 to 117360)
McGeoch,D.J., Dalrymple,M.A., Davison,A.J., Dolan,A., Frame,M.C., McAb,D., Perry,L.J., Scott,J.E. and Taylor,P.
The complete DNA sequence of the long unique region in the genome of herpes simplex virus type 1
J. Gen. Virol. 69 (Pt 7), 1531-1574 (1988)
2839594

JOURNAL
MEDLINE
4 (bases 113322 to 126373)
Perry,L.J. and McGeoch,D.J.
The DNA sequences of the long repeat region and adjoining parts of the long unique region in the genome of herpes simplex virus type 1
J. Gen. Virol. 69 (Pt 11), 2831-2846 (1988)
89036163

JOURNAL
MEDLINE
5
2846760
Dolan,A., McKie,E., Maclean,A.R. and McGeoch,D.J.
Status of the ICP34.5 gene in herpes simplex virus type 1 strain 17
J. Gen. Virol. 73 (Pt 4), 971-973 (1992)
92341080

JOURNAL
MEDLINE
6
1321882
McGeoch,D.J.
Direct Submission
Submitted (17-JAN-1989) McGeoch D.J., MRC Virology Institute, Institute of Virology, Church Street, Glasgow G11 5JR, GB
Revised by [7]
7 (bases 1 to 152201)
Dolan,A.
Direct Submission
Submitted (16-APR-1997) Dolan A., MRC Virology Institute, Institute of Virology, Church Street, Glasgow G11 5JR, GB
On or before Apr 24, 2003 this sequence version replaced gi:221721, gi:221712, gi:251863, gi:59499.
See also x06461 and x02138.
Residues 1 - 8661 and 148674 - 152260 of TR-L and TR-S, resp. have not been sequenced but are derived from IR-L and IR-S sequences.

FEATURES
SOURCE
1. 152261
/organism="Human herpesvirus 1"
/mol_type="genomic DNA"
/strain="17"
/db_xref="taxon:10298"

LTR
1. .9212
/note="TRL (Terminal Repeat, Long)"
1. .401
/note="a sequence (terminal redundancy)"
98. .313
/rpt_type="TANDEM"
/rpt_unit=98. .109
99. .326
/note="reiteration set 7"
513. .1539
/gene="RL1"
513. .1259
/gene="RL1"
/codon_start=1
/product="neovirulence factor (ICP34.5)"
/protein_id="CAA32348.1"
/db_xref="GI:1944537"
/db_xref="SPTREMBL:O12396"
/translation="MARRRRRGRRRRRPPPGTGAVPVPAOSQVSTNSPSEAVSAPA
AAPPPPPAGPPSPCSLLKRWLVHVESASDDDDDDPDSPPPEPAEAPTAAPR
PRPPPGVGGGADPSHPSPRPLRLRLRVAAEHRLRLRARGGAGEAPP
ATPATPATPATPATPARVRFSPHVRVRLVWASARLARLRGWSARERADARRRRRV
AEAEAVIGPCICGPEPARALARAGCAPANSV"
997. .1040
/gene="RL1"
/note="reiteration set 6"
997. .1032
/rpt_type="TANDEM"
/rpt_unit=98. .996
1534. .1539
/gene="RL1"
2115. .5681
/gene="RL2"
join(2115. .2317, 3083. .3749, 3886. .>5638)
/note="IE110"
/gene="RL2"
join(2261. .2317, 3083. .3749, 3886. .5489)
/note="IE110"
/function="modulator of cell state and gene expression"
/gene="RL2"
/codon_start=1
/protein_id="CAA32336.1"
/db_xref="GI:59500"
/db_xref="GOA:P08393"
/db_xref="SWISS-PROT:P08393"
/translation="MEPRPGASTRRRPPRGPRQREPAVPVWFFPCDDRLPDSSEAEETE
VGGRGDADHDDDSASEADSTDELFEGLGPGGVGAAGSGSPREEDPGSCGA
PRPDGDEGDCVACSTDELAFLRCQTFPCMRFCIPCKRTMOLRNTPLCNKL
VYLIVGTSPSGSFSTIPLVNDPOTRMAEEAEVRAGTAVDELTGNTORPAPYLTGLGH
TVRALEPHPEPTDEDDDDLDLDADVDVPPARPPRPPRGAAPVPTGASHAABO
PAARITAPPSAPITGPHSSSNTNTTSSGGGSGSROARAARFGASGSGGVGVGVY
EAEGRPGRGTGLVNRPAFLANNRDLVISDSPASPHRPPAPMPGSAPRPPAS
AAASGPARPRAVAPCVARPPPGPRAPAGAPARPADARVPQSHSLAQAANO
EOLICRARATVARGSGGVGEGPRGAPSGAALPESAAVEOEAAYPRRRRS
GOENRPOSTRPLAPAGAKRATHPPSDSGGGGPGTPTLTSAAASSSSAS
SSAPTPAGAAASSAAGASSASASSAGAVCALGROBETSIGPPAASGPRRCAR
TRAETSGAVPAGCITRLPLISGVSSVVALSPYKNKTITGCTPILDMETGNICAYV
LVDTGNATRLRAAVPGWSRRTLPLETAGNHVPPETPTAPASEMNSLWMTPVGNML
FDQGLVGLDFFRSRLSRHHPWSGOGASTRDECKO"
2261. .2317
/gene="RL2"
/note="IE110"
/number=1
2318. .3082
/gene="RL2"
/note="IE110"
/number=1
2465. .2625
/gene="RL2"
/note="reiteration set 5"
3083. .3749
/gene="RL2"
/note="IE110"

LTR
1. .9212
/note="TRL (Terminal Repeat, Long)"
1. .401
/note="a sequence (terminal redundancy)"
98. .313
/rpt_type="TANDEM"
/rpt_unit=98. .109
99. .326
/note="reiteration set 7"
513. .1539
/gene="RL1"
513. .1259
/gene="RL1"
/codon_start=1
/product="neovirulence factor (ICP34.5)"
/protein_id="CAA32348.1"
/db_xref="GI:1944537"
/db_xref="SPTREMBL:O12396"
/translation="MARRRRRGRRRRRPPPGTGAVPVPAOSQVSTNSPSEAVSAPA
AAPPPPPAGPPSPCSLLKRWLVHVESASDDDDDDPDSPPPEPAEAPTAAPR
PRPPPGVGGGADPSHPSPRPLRLRLRVAAEHRLRLRARGGAGEAPP
ATPATPATPATPATPARVRFSPHVRVRLVWASARLARLRGWSARERADARRRRRV
AEAEAVIGPCICGPEPARALARAGCAPANSV"
997. .1040
/gene="RL1"
/note="reiteration set 6"
997. .1032
/rpt_type="TANDEM"
/rpt_unit=98. .996
1534. .1539
/gene="RL1"
2115. .5681
/gene="RL2"
join(2115. .2317, 3083. .3749, 3886. .>5638)
/note="IE110"
/gene="RL2"
join(2261. .2317, 3083. .3749, 3886. .5489)
/note="IE110"
/function="modulator of cell state and gene expression"
/gene="RL2"
/codon_start=1
/protein_id="CAA32336.1"
/db_xref="GI:59500"
/db_xref="GOA:P08393"
/db_xref="SWISS-PROT:P08393"
/translation="MEPRPGASTRRRPPRGPRQREPAVPVWFFPCDDRLPDSSEAEETE
VGGRGDADHDDDSASEADSTDELFEGLGPGGVGAAGSGSPREEDPGSCGA
PRPDGDEGDCVACSTDELAFLRCQTFPCMRFCIPCKRTMOLRNTPLCNKL
VYLIVGTSPSGSFSTIPLVNDPOTRMAEEAEVRAGTAVDELTGNTORPAPYLTGLGH
TVRALEPHPEPTDEDDDDLDLDADVDVPPARPPRPPRGAAPVPTGASHAABO
PAARITAPPSAPITGPHSSSNTNTTSSGGGSGSROARAARFGASGSGGVGVGVY
EAEGRPGRGTGLVNRPAFLANNRDLVISDSPASPHRPPAPMPGSAPRPPAS
AAASGPARPRAVAPCVARPPPGPRAPAGAPARPADARVPQSHSLAQAANO
EOLICRARATVARGSGGVGEGPRGAPSGAALPESAAVEOEAAYPRRRRS
GOENRPOSTRPLAPAGAKRATHPPSDSGGGGPGTPTLTSAAASSSSAS
SSAPTPAGAAASSAAGASSASASSAGAVCALGROBETSIGPPAASGPRRCAR
TRAETSGAVPAGCITRLPLISGVSSVVALSPYKNKTITGCTPILDMETGNICAYV
LVDTGNATRLRAAVPGWSRRTLPLETAGNHVPPETPTAPASEMNSLWMTPVGNML
FDQGLVGLDFFRSRLSRHHPWSGOGASTRDECKO"

exon
1. .9212
/note="TRL (Terminal Repeat, Long)"
1. .401
/note="a sequence (terminal redundancy)"
98. .313
/rpt_type="TANDEM"
/rpt_unit=98. .109
99. .326
/note="reiteration set 7"
513. .1539
/gene="RL1"
513. .1259
/gene="RL1"
/codon_start=1
/product="neovirulence factor (ICP34.5)"
/protein_id="CAA32348.1"
/db_xref="GI:1944537"
/db_xref="SPTREMBL:O12396"
/translation="MARRRRRGRRRRRPPPGTGAVPVPAOSQVSTNSPSEAVSAPA
AAPPPPPAGPPSPCSLLKRWLVHVESASDDDDDDPDSPPPEPAEAPTAAPR
PRPPPGVGGGADPSHPSPRPLRLRLRVAAEHRLRLRARGGAGEAPP
ATPATPATPATPATPARVRFSPHVRVRLVWASARLARLRGWSARERADARRRRRV
AEAEAVIGPCICGPEPARALARAGCAPANSV"
997. .1040
/gene="RL1"
/note="reiteration set 6"
997. .1032
/rpt_type="TANDEM"
/rpt_unit=98. .996
1534. .1539
/gene="RL1"
2115. .5681
/gene="RL2"
join(2115. .2317, 3083. .3749, 3886. .>5638)
/note="IE110"
/gene="RL2"
join(2261. .2317, 3083. .3749, 3886. .5489)
/note="IE110"
/function="modulator of cell state and gene expression"
/gene="RL2"
/codon_start=1
/protein_id="CAA32336.1"
/db_xref="GI:59500"
/db_xref="GOA:P08393"
/db_xref="SWISS-PROT:P08393"
/translation="MEPRPGASTRRRPPRGPRQREPAVPVWFFPCDDRLPDSSEAEETE
VGGRGDADHDDDSASEADSTDELFEGLGPGGVGAAGSGSPREEDPGSCGA
PRPDGDEGDCVACSTDELAFLRCQTFPCMRFCIPCKRTMOLRNTPLCNKL
VYLIVGTSPSGSFSTIPLVNDPOTRMAEEAEVRAGTAVDELTGNTORPAPYLTGLGH
TVRALEPHPEPTDEDDDDLDLDADVDVPPARPPRPPRGAAPVPTGASHAABO
PAARITAPPSAPITGPHSSSNTNTTSSGGGSGSROARAARFGASGSGGVGVGVY
EAEGRPGRGTGLVNRPAFLANNRDLVISDSPASPHRPPAPMPGSAPRPPAS
AAASGPARPRAVAPCVARPPPGPRAPAGAPARPADARVPQSHSLAQAANO
EOLICRARATVARGSGGVGEGPRGAPSGAALPESAAVEOEAAYPRRRRS
GOENRPOSTRPLAPAGAKRATHPPSDSGGGGPGTPTLTSAAASSSSAS
SSAPTPAGAAASSAAGASSASASSAGAVCALGROBETSIGPPAASGPRRCAR
TRAETSGAVPAGCITRLPLISGVSSVVALSPYKNKTITGCTPILDMETGNICAYV
LVDTGNATRLRAAVPGWSRRTLPLETAGNHVPPETPTAPASEMNSLWMTPVGNML
FDQGLVGLDFFRSRLSRHHPWSGOGASTRDECKO"


```

/note="IE110"
/number=3
intron complement(4953..6907)
/note="stable LAR (latency associated transcript)"
polyA_signal
5636..5641
/gene="RL2"
/note="IE110"
5676..5681
/gene="RL2"
/note="IE110"
5733..5877
/note="reiteration set 4"
8554..8583
/note="reiteration set 3"
8806..8826
/note="reiteration set 2"
9032..9212
/note="reiteration set 1"
9213..117160
/note="UL (Long Unique region)"
9337..10011
/gene="UL1"
9337..10011
/gene="UL1"
/codon_start=1
/product="vtrion glycoprotein L"

Query Match      0.1%; Score 19; DB 1; Length 152261;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY    132498 CCGCCGCCCCGGCCGCC 132516
       |||||||
Db     125829 CGCCCGCCCCGGCCGCC 125811

RESULT 38
AF533768/c AF533768 bp DNA linear VRL 19-MAY-2003
LOCUS      Cercopithecine herpesvirus 1 strain E2490, complete genome.
DEFINITION
ACCESSION  AF533768
VERSION     AF533768.1 GI:30844242
KEYWORDS
SOURCE      Cercopithecine herpesvirus 1 (monkey B virus)
ORGANISM    Cercopithecine herpesvirus 1
VIRUSES:    dsDNA viruses, no RNA stage; Herpesviridae;
             Alphaherpesvirinae; Simplexvirus.
REFERENCE   1 (bases 1 to 156789)
AUTHORS     Perejygina,L., Zhu,L., Zurkuhlen,H., Mills,R., Borodovsky,M. and Hilliard,J.K.
TITLE       Complete sequence and comparative analysis of the genome of herpes B virus (cercopithecine herpesvirus 1) from a rhesus monkey
JOURNAL     J. Virol. 77 (11), 6167-6177 (2003)
MEDLINE     22628476
PUBMED      12743273
2 (bases 1 to 156789)
Perejygina,L., Zhu,L., Zurkuhlen,H. and Hilliard,J.
AUTHORS     Direct Submission
TITLE       Submitted (31-JUL-2002) Department of Biology, Georgia State University, 24 Peachtree Center Ave, Atlanta, GA 30303, USA
JOURNAL
FEATURES
source
1..156789
/organism="Cercopithecine herpesvirus 1"
/mol_type="genomic DNA"
/strain="E2490"
/species.host="Macaca mulatta"
/db_xref="taxon:10325"
1..223
/note="a sequence"
224..9021
/note="terminal copy of large repeat region"
2194..4636
/gene="RL2"
```

CDS
join(2194..2241,2461..3003,3125..4636)
/gene="RL2"
/note="modulator of cell state and gene expression"
/codon_start=1
/product="immediate early protein ICP0"
/protein_id="AAP41493.1"
/db_xref="GI:30844317"
/translation="MEPSRGLGAPARPAAPADALIEDDLVLSRYFPEDTSDDD
DNDDAAVDDDDPSADAAADGTGLSAPAPRETCAVCTERIDEAOLCMFPELFHF
CIPDLAKTWLMRNSCPLCNAAVSYLIVGANGSYSTIPVYNDPRTRRDMEPRACT
AVDFIWDRCGERPSSVTIGGRTVALSPARKGRGVGRVSRPPRPPPPAPA
PDSPPASLSLRPSADPTFHPAPAGAPAPAPGDAHAHASTRGAGARGAAAR
APAPGNAPATVIDSDSPSRPSGGAAPPVAVARPPAPAPAGAGARQAV
HOTQQAQAQAQTQARAQAVLAQALQAQARQAQOPRPGAQVPPGAQVPPGAQV
PPGAQVPPGAQVPPGAQVPPGAQVPPGAQVPPGAQVPPGAQVPPGAQVPPGAQV
ARRRASASGAAPATRGKRBSLPPPGGAPAPAPAPAPAPAPAPAPAPAPAP
PPPPQAAPPPPPAPPPPPVETRRDSSSGPRRAGEGPKCYKTRHVDGAPAPAGT
RYLPISGVSSVVAAPYLNKTVTGDCLPVDMETGDIGAVVILGRACNARALAEAS
PGMSRRTRLPEAARGVSPPEYPGDPAPAHGLMTPVGMPLPDGALLGGRSHDSRH
PWTGPAADPPPTRGSGP"
2194..2241
/gene="RL2"
/number=1
2461..3003
/gene="RL2"
/number=2
3125..4636
/gene="RL2"
/number=3
3003..3125
/note="unique long region"
9072..9746
/gene="UL1"
9072..9746
/gene="UL1"
/note="proposed start codon is GTC"
/codon_start=1
/translation="except-(pos:9072..9074,aa:Met)
/product="vifon glycoprotein L"
/protein_id="AAP41419.1"
/db_xref="GI:30844243"
/translation="MFLRSVSAPSVSPASSPSPPEVYIRSVARFVGLIKRA
GLELPAGGVTRWEAPRSIDYARIDGIFLRHCGDITVWDMGAKQARAVNPELFSA
GLEDLGHAFPPANALETTRTFALYKEVRLASRSDAASSTVPVPCVAVYERTSD
CPDRTPTGIMNEPRIRRRFSAPNDEASPOQSLAPARTPTPPKTHPPARKRGNATR
TAPRRA"
9814..10575
/gene="UL2"
9814..10575
/gene="UL2"
/note="proposed start codon is GTC"
/codon_start=1
/translation="except-(pos:9814..9816,aa:Met)
/product="uracil-DNA glycosylase"
/protein_id="AAP41420.1"
/db_xref="GI:30844244"
/translation="MTPDOSPPRSRSLGIDAHADRPALDMTGFRRRPLVGEAMRY
LEPLSNPLTAOLMAEYERBCRGVEVLPREDVSMTRPCTPDEVYIIIGDYNRP
GQAGLAFSVRPGTPTPPSLNITLAARNCCPDALAHGCELEKAWAGVLLWTTLT
VRREKPSHAHMGWDRFVASAVRRLASRGLVFMGHAHQAONAIRPDPRVHRVLTTS
HPSPKSVPPSSCHRFCLANQYLERSLAPVDMST"
10711..11394
/gene="UL3"
10711..11394
/gene="UL3"
/codon_start=1
/product="UL3"
/protein_id="AAP41421.1"
/db_xref="GI:30844245"
/translation="MSLSLEAAVPSLTAVLSMGMAFAPODSPRANAADRAHTPEPA
LALPPAPRATDPPPPRALDADHVAFTDMKSSVDELGRDLOTITKIDELSLV
NFAIACRTSSSFGAAGARPDQREGRRPPSHKSLQMFVLCQRANANRVRQOLA
VIASRKPRKYYTRSSDGRISPAVVFVHEFVSADAVYIHRDNYIGPGPPHRTPPRCP

gene
complement(11509..12120)
/gene="UL4"
complement(11509..12120)
/gene="UL4"
/codon_start=1
/product="UL4"
/protein_id="AAP41422.1"
/db_xref="GI:30844246"
/translation="MAASPTNIAISLNGTATSSACVLPDAQVYVACDGCRAIASRG
CLRODITSRGAVVVRQTPVGLVWVDRTDPCATRGSRGQRHLEKMDNLTCAVFP
DSWSSSTRGESSVRSPTAGITVWVGEDSITITVTVGSPPGGEALDPPSSPDLA
PGVSPAPVAPSAEAGAADLVEVKEETIQLSPTLFCGHEP"
complement(12172..14820)
/gene="UL5"
complement(12172..14820)
/gene="UL5"
/codon_start=1
/product="component of helicase-primase complex"
/protein_id="AAP41423.1"
/db_xref="GI:30844247"
/translation="MARVGGDASVSSPPPEQPREPVQPRDEAFNTFSMGIQPIER
VRELAEHLEAPRVPLQMFQDAVATPAGLPREFPFAVYLLITGAGSGKSCVOT
LNEVLDVVGATRIAAQNMVYKLSGFLSPINTIFHEGFRGNHQAQVGHVPL
ASNPAVEDLQRLDTIYWEVIADITRRAVAAAGGADGRNEFPALATLESTMGLOG
ALTRIAFTGALPAPFRSNVIVIDEAGLGHLLTVAVYCMNTNALVYHPQYAGL
RPVLCVGSPTOTASLESTFEHOKRCSIQSESVLTYLCNRTLRVYARLPBSMAIF
INNRKYHEHGNLMKALEGLPTEEHMOFVDPEVFPESITTPANLPQWTRLFSSH
KEVSAIMARLHAHLKVARREGFEVSVLPVLFVSARAFDETLTHOPALIVEWIA
NAGRITNYSQSDODAGRARLEVHSSKQVLVARADYVYVLSQIAVTRLRKLWFGS
GTFERSFVAVLRDSSFVKTGCEMLVEFAYQFSLRIFGLHIFYNLFRLPGIDARAR
AYERGALVTRRELISGATGAGPATPGQAASGGEASAAPGAEARADPFTIGARAD
AEPEDDLDVVFAGLNEOELEDFCYHTVDQPEPTTAHVHQAQFGLRKRAPIGRVILRE
LEGAFEGAPGCVYVDVNTTRGCEVYMGSRGLMSALDQSTDTLITGTYARVATA
BEVRRHAGGLALESPLPVYLKDOHFMSVNTNISEVESERLANATNA
DYGISSMLAMTITRSQGLSLDKVAICETPGNLINSAVYAMSRTSSSEFLMNLPLR
ERHERDVISHEILISALRDPDLIVY"
14819..16870
/gene="UL6"
14819..16870
/gene="UL6"
/note="role in DNA cleavage/packaging"
/codon_start=1
/product="capsid protein"
/protein_id="AAP41424.1"
/db_xref="GI:30844248"
/translation="MAERHPPARAPRPPDAPRPPDGCNVQVHPPTMLFREALL
GELGYTGQGVYVNVRSSEAVYTRQLOAAVFGALLNAAHRLDEADMRHVAARLEPE
RLVRYRGAGADGDVAAVAERYVDTWRALASLIDFARGLADCFAGCGPGVGFSSRY
IDMLMGLVPMVRPREGEVYTORLEAFISDHALPRDLATVAGAVERRAAPLRELABA
FDSARIDVYDVYCLFYHPRGGEWVRPACAGORECVLAMPRLMTGSRLLFDSMORL
SREIVACRALREHARVCRLRNAASVYKVLGRKNGDGAAGAAVSRALGEDASRA
GSAASRLVRLILINKGMRHIGDINDVYRATIDEGGHLIDSAADVPLPGRGATGRP
AAGGADPAAPRQOOLRQAFQTSVNNNGMLEDYINNLFTEILREPLNDLQAQLD
RDIELRRARLGAUDROQRAADPGRAPAEAGODLTDYDIDVSRAMDYVAVAS
FOHOYVPSYKODLERLSRLMEHLLREFKISRHNNGGREAIYSSGALDIAFVAPF
ASVAPRAMCALITPGVCIAGEETLMAIRKKTPVQVYVYLTDLALFVADVHARSRP
PAPRPADPRRVRRPPGRSSRPVDAORPGCRGEDAMGCRGDGHLDPRRGCGGR
P"
16821..17711
/gene="UL7"
16821..17711
/gene="UL7"
/note="role in DNA cleavage/packaging"
/codon_start=1
/product="capsid protein"
/protein_id="AAP41425.1"
/db_xref="GI:30844249"
/translation="MANSPTAEETAAALBRAVAGDRDLVGVAAISHOALLMACE
VROATRTVFTATGCVRVAVVTPDHRHLFVLDDGCPDADLALASATPARKDQSHHRE
AFAVVLAKEHDVHSLVPLVPLRHSVEMPEHLEDELACLLALENCRAHATASAF
FVVISAMVLAALGRTSPFDRVRLCLLSSCGMNTJLMFNHVEFPDQVLPVHCNAR
YLIANNPPLITLALFRAGPSRVFRLPVQBRASILECVAVYNQGVLAAGMASEDFRAGLV

gene
complement(17886..20171)
/gene="UL8"
complement(17886..20171)
/gene="UL8"
/codon_start=1
/product="component of helicase-primase complex"
/protein_id="AAP41426.1"
/db_xref="GI:30844250"
/translation="MODAGLWVAESGICATITLTATLPPRTDRRLVLLYPCRDARG
DGAARPAEVSIASTELQAFYGPATISAGAAVAARAASPAAPLETINDPYLMALY
ACAIVLAEREYGRALFAPARVAMPRTGLVARIESLPGRSPAPRAALDVNAQIAT
DPLAIAHYAARPDRLAMARLAIDTPOCASASLTIVRIDTGARERETITLTP
PVRRGVAADVEVEEAVLRPRGHAQAVTAVLVPRGYEFVAGESAPALIMFR
QWLYVHAGPGLPIFAFLGPEFEGGAVDHFSVLGFGWATLKSGSAAAPPA
LAAHAELAGMAPAGAFALGPAPARAAVSAALERLPPALRRPAAAGLIDPPAVIG
PYCLARFRPGLOPRLALVYELGIDGRADPRDPLRGARRMRDLAGGCGAEOA
PWPREYLAATDEVRREYPAVARTIDGIVSANGVLEKAGAVDMAVCCDGGGRWGV
LVNDFDAAGAGAAAAAERARALAAASSEALAGWGLDAPPLVLEGTYTHAVLW

Query Match 0.1%; Score 19; DB 1; Length 156789;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 122053 GGGGGCGGGTGGCGGCGC 122071
|||||
DB 63159 GGGGGCGGGTGGCGGCGC 63141
|||||

RESULT 39
AF250284/c 232392 bp DNA linear VRL 30-AUG-2000
LOCUS AF250284 Amsacta moorei entomopoxvirus, complete genome.
DEFINITION AF250284
ACCESSION AF250284
VERSION AF250284.1 GI:9944523
KEYWORDS
SOURCE
ORGANISM
Amsacta moorei entomopoxvirus
Amsacta moorei entomopoxvirus
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Entomopoxvirinae;
Entomopoxvirus B.
1 (bases 1 to 232392)
Bawden,A.L., Glassberg,K.J., Diggs,J., Shaw,R., Farmerie,W. and
Moyer,R.W.
Complete genomic sequence of the Amsacta moorei entomopoxvirus:
analysis and comparison with other poxviruses
Virology 274 (1), 120-139 (2000)
20396580
PUBMED 10936094
2 (bases 1 to 232392)
Bawden,A.L., Glassberg,K.J., Diggs,J., Shaw,R., Farmerie,W. and
Moyer,R.W.
Direct Submission
Submitted (28-MAR-2000) Molecular Genetics and Microbiology,
University of Florida, P.O. Box 100266, Gainesville, FL 32610, USA
FEATURES
source
1..232392
Location/Qualifiers
/organism="Amsacta moorei entomopoxvirus"
/mol_type="genomic DNA"
/db_xref="taxon:28321"
500..1882
/gene="AMVITR01"
500..1882
/gene="AMVITR01"
/note="LRR gene family member"
/codon_start=1
/product="AMVITR01"
/protein_id="AAG02973.1"
/db_xref="GI:9944790"
/translation="MELPVMELIIFNYLNDTKLQFLDSKCIISKLIYKLNYSCLK
EIKNFINKELIYNNYIKSLEMGIENFKLKYCNTRIDSKIGENIKLEIKELCYC
NTNINSLYIKNLINLTGECENYIYKIGENININKEPCSTYILDSLEIKENLI
NLOKNCSTHTIYSLGELNINLEKDCSTYSISLKEIKNLINLKECEYNIYS
LKEIOLNINLKKDCSYTKINSKLQNLINLKLDPHNTNITSLEKIGENINTEIKLN

gene
complement(1926..2108)
/gene="AMVITR02"
complement(1926..2108)
/gene="AMVITR02"
/codon_start=1
/product="AMVITR02"
/protein_id="AAG02986.1"
/db_xref="GI:9944803"
/translation="MLINYSBYSKSEYSSSFELLISVFNYSKILRIFSKISLVFCIL
LRIEISICTEIGIYY"
2273..2545
/gene="AMVITR03"
2273..2545
/gene="AMVITR03"
/codon_start=1
/product="AMVITR03"
/protein_id="AAG02975.1"
/db_xref="GI:9944792"
/translation="NANEDMLNFIYIKUDNYSILYDKDLINGIANDKINSNNYNTL
LKSMDCKLIEMSYNLSKDSLLEIKLLNENFTLKYIQAKN"
complement(2542..2934)
/gene="AMVITR04"
complement(2542..2934)
/gene="AMVITR04"
/codon_start=1
/product="AMVITR04"
/protein_id="AAG02987.1"
/db_xref="GI:9944804"
/translation="MFWLLIPSFICCEPKOSKYPFCDIYYDCINNNLKNCSNNNE
VRYNNTCITOSEYKNITGNYCHRCNNKNTLIPGIHYNPLMCNKLNSMCCFEDBNYIY
CPEONNKYIMWIDYNTDOCKSLEKIKY"
complement(2971..3786)
/gene="AMVITR05"
complement(2971..3786)
/gene="AMVITR05"
/codon_start=1
/product="AMVITR05"
/protein_id="AAG02988.1"
/db_xref="GI:9944805"
/translation="MDVERNLINRLSTFONDYKRYIYSILLLIITILICYIIF
AKKESNNYNDSTKINNIRKIYNNNNVMDDEFKAIIRYKRYKLNKSEEGKIEIRA
RSRTSLVNNNTDIIIDRCGVKNMKMMIIDEHCNDYDNIVVYVRLNCGNDRSR
EIONSEKMYENINIMYENSEKYNVIDIYCNVNNNNNGMYKKNNKIIINIKTKILSRL
KRYEMHLSHIFIYKHDPLNSYTFPIEYINDKNEIDBERIYMKNNIRNCT"
3871..4416
/gene="AMVITR06"
3871..4416
/gene="AMVITR06"
/codon_start=1
/product="AMVITR06"
/protein_id="AAG02978.1"
/db_xref="GI:9944795"
/translation="MDFIKLQIDAIRSITDNLNIPIGRRKINKNVCFNCKMPEPNN
OICNYCKLCSGCKNLNNLSIKKFSKRYGVRNKKFNILCDICKNFECIECH
KLENNYNDIVYELNIDSIDKVGVCFLCINILCDSCNRLTITNINYSKNNVYL
RIFYNDEFNNNYKICIREYI"
complement(4597..4872)
/gene="AMVITR07"
complement(4597..4872)
/gene="AMVITR07"
/codon_start=1
/product="AMVITR07"
/protein_id="AAG02989.1"
/db_xref="GI:9944806"
/translation="MDSIKSTSTKSTDLSEIYVNTDOSIKSTSTKSTSTSTDSID
LINPDSIKSTSTSTDSINLDESTIKSTININSKOYLQMKWTFILK"
complement(5383..6939)
/gene="AMVITR08"
complement(5383..6939)

```

/gene="AMVTR08"
/codon_start=1
/product="AMVTR08"
/protein_id="AAG02990.1"
/db_xref="GI:9944807"
/translation="MNIRKICKILFGLFEVTTIIYHNITNNDEYDIERNITEIYK
ILKKYKRNIDINNEYLRKNDLSEITEFTSEIKSTDTJDPFKSTDSIKSTDLSEIYS
NTDTSIKSTDSIKSTDLSEILSNNTDSIKSTDSIKSTDLSEILSNNTDSIKST
DSIKSTDSIKSTDSIKSTDSIKSTDSIKSTDSIKSTDSIKSTDSIKSTDSIKSTDL
SEIYSNTDTSIKSTDSIKSTDSIKSTDSIKSTDSIKSTDSIKSTDSIKSTDSIKST
STDSIKSTDLSEILSNNTDSMSDSIKSTDSIKSTDSIKSTDSIKSTDSIKSTDSIK
DLSEIYSNTDTSIKSTDSIKSTDLSEILSNNTDSIKSTDSIKSTDSIKSTDSIKST
DSIKSTDSIKSTDSIKSTDSIKSTDSIKSTDSIKSTDSIKSTDSIKSTDSIKSTDS
TIKSTDSIKSTDSIKSTDSIKSTDSIKSTDSIKSTDSIKSTDSIKSTDSIKSTDSIK
KYLDPDSIKST"
7018..7224
/gene="AMVTR09"
7018..7224
/gene="AMVTR09"
/codon_start=1
/product="AMVTR09"
/protein_id="AAG02981.1"
/db_xref="GI:9944798"
/translation="MLRIELKNYSHNNVAFCKLCNLMANVRGLKTHYTRVHTKLL
LVNYPPEIILITNKOEYWRPMI"
7248..7748
/gene="AMVTR10"
7248..7748
/gene="AMVTR10"
/codon_start=1
/product="AMVTR10"
/protein_id="AAG02982.1"
/db_xref="GI:9944799"
/translation="MNKIOYIGFNNLLNLNLIQILSTINKKTYAKITTTIENNRPHVPL
YFYKTRFRFTIYISYCTVPENNERIRIRINNTPKLFAEPDGRLLITDKNE
LFFINVIYIMNDSKIVDAIFLNNIYLFYFIFMFIFLYIYIYINRKDLV
KKNNIH"
7783..8163
/gene="AMVTR11"
7783..8163
/gene="AMVTR11"
/codon_start=1
/product="AMVTR11"
/protein_id="AAG02983.1"
/db_xref="GI:9944800"
/translation="MSVNNINYNDKICIDCYNKKYKNEKKKKTOLPDLILFICYL
VLSIRPLTYITICTEENKIOYIILICYIILMIGITSYAVKIDIKENATISFLI
DVCKKRRHRSSLPFTESLMPDV"
complement(8177..8737)
/gene="AMVTR12"
complement(8177..8737)
/gene="AMVTR12"
/codon_start=1
/product="AMVTR12"
/protein_id="AAG02991.1"
/db_xref="GI:9944808"
/translation="MDKYIILNGFITIFSOICNEYDCLNKIKIONHIVNNNITID
GYDIHDKIITYTNKKYKLGNNINMRYEINIRINIRIFYDSKNKMSCYKKCK
YDYICKINDNEYFMDVLPMDYINSNIIECDNDIRPNKVGKLSKLIIPSTILL
ITILLITLLRFITYIKRIFHTYESVR"
complement(8798..8992)
/gene="AMVTR13"
complement(8798..8992)
/gene="AMVTR13"
/codon_start=1
/product="AMVTR13"
/protein_id="AAG02992.1"
/db_xref="GI:9944809"
/translation="MYGDEKGTOMYENIHRYDNEYILFYTKDEFKHKISDKIDNEN
DVFKNITLNIINIYIKNTDFY"
9826..10068
/gene="AMV001"
9826..10068

```

```

/gene="AMV001"
/codon_start=1
/product="AMV001"
/protein_id="AAG02707.1"
/db_xref="GI:9944524"
/translation="MDESILKTNFWEIIFIIISVSGSISISIANFNGMLWIIISNI
SSIAFYFKQYPLCLQOCVFLTTIIGIYYNMKLL"
10272..10703
/gene="AMV002"
10272..10703
/gene="AMV002"
/translation="putative dUTPase"

```

Query Match 0.1%; Score 19; DB 1; Length 232392;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 220583 AAAATAAAAAATAATGT 130529
AAAATAAAAAATAATGT 220565

RESULT 40
HSEI1/c
LOCUS
DEFINITION Equine herpesvirus type 1 immediate-early protein (IE) gene, 5'
ACCESSION M30497
VERSION M30497.1 GI:330906
KEYWORDS Immediate-early protein.
SEGMENT 1 of 2
SOURCE Equine herpesvirus 1
ORGANISM Equine herpesvirus 1
VIRUSES; dsDNA viruses; no RNA stage; Herpesviridae;
Alphaherpesvirinae; Varicellovirus.
REFERENCE 1 (bases 1 to 780)
AUTHORS Hartly R.N., Colle C.F., Grundy F.J. and O'Callaghan D.J.
TITLE Mapping the terminal and intron of the spliced immediate-early
transcript of equine herpesvirus 1
JOURNAL J. Virol. 63 (12), 5101-5110 (1989)
MEDLINE 90064773
PUBMED 2555546
COMMENT Original
FEATURES
source location/Qualifiers
1..780
/organism="Equine herpesvirus 1"
/mol_type="genomic DNA"
/strain="Kentucky A"
/db_xref="taxon:10326"
/lab_host="L-M cell"
27..31
/gene="IE"
94..99
/gene="IE"
123..235
/partial
/gene="IE"
/number=1
236..607
/gene="IE"
324..383
/gene="IE"
/note="ORF1: putative"
/codon_start=1
/product="unknown protein"
/protein_id="AAG6351.1"
/db_xref="GI:808674"
/translation="MEPLQORCEGVAPRPASr"
344..499
/gene="IE"
/note="ORF2: putative"
/codon_start=1
/product="unknown protein"

CDS
-Inton
CDS

Query Match	Best Local Similarity	0.1%; Score 18;	DB 1;	Length 780;
Matches 18;	Conservative 0;	Mismatches	0;	Indels 0;
Gaps	0;			
QY 13673	CCCGGGCCTCTCCCCCGC	13690		
Db 538	CCCGGGCCTCTCCCCCGC	521		
RESULT 41	AF251159/c	824 bp	DNA	linear VRL 12-DEC-2000
LOCUS	AF251159	824 bp	DNA	linear VRL 12-DEC-2000
DEFINITION	Human herpesvirus 1 mutant gamma1 34.5 gene, complete sequence.			
ACCESSION	AF251159			
VERSION	AF251159.1	GI:11640715		
KEYWORDS	Human herpesvirus 1			
SOURCE	Human herpesvirus 1			
ORGANISM	Human herpesvirus 1			
REFERENCE	Viruses; dsDNA viruses, no RNA stage; Herpesviridae;			
AUTHORS	Alphaherpesvirinae; Simplexvirus.			
TITLE	1 (bases 1 to 824)			
JOURNAL	Ling, J.-Y., Chen, T.-M. and Stroop, W.G.			
REFERENCE	2 (bases 1 to 824)			
AUTHORS	Ling, J.-Y., Chen, T.-M. and Stroop, W.G.			
TITLE	Direct Submission			
JOURNAL	Submitted (03-APR-2000) Ophthalmology, Mail Slot: 523, University			
FEATURES	of Arkansas for Medical Sciences, 4301 W. Markham, Little Rock, AR			
source	72205, USA			
location/Qualifiers				
1..824				
/organism="Human herpesvirus 1"				
/mol_type="genomic DNA"				
/strain="+GC"				
/db_xref="taxon:102398"				
/clone="5-13"				
28..786				
/gene="mutant gamma1 34.5"				
BASE COUNT	72 a 392 c 282 g 78 t			
ORIGIN				
Query Match	0.1%; Score 18;	DB 1;	Length 824;	
Best Local Similarity	100.0%; Pred. No. 34;			
Matches 18;	Conservative 0;	Mismatches	0;	Indels 0;
Gaps	0;			
QY 132419	CGCCCCCGGGCGCGC	132436		
Db 373	CGCCCCCGGGCGCGC	356		
RESULT 42	AF251158/c	947 bp	DNA	linear VRL 12-DEC-2000
LOCUS	AF251158	947 bp	DNA	linear VRL 12-DEC-2000
DEFINITION	Human herpesvirus 1 gamma1 34.5 gene, complete cds.			
ACCESSION	AF251158			
VERSION	AF251158.1	GI:11640713		

KEYWORDS	Human herpesvirus 1
SOURCE	Human herpesvirus 1
ORGANISM	Human herpesvirus 1
REFERENCE	Alphaherpesvirinae; Simplexvirus.
AUTHORS	1 (bases 1 to 947)
TITLE	ling,J.-Y., Chen,T.-M. and Stroop,W.G.
JOURNAL	A gamma1 34.5 null mutant of herpes simplex virus type 1 strain +GGC
AUTHORS	1s neurovirulent
TITLE	Unpublished
REFERENCE	2 (bases 1 to 947)
AUTHORS	ling,J.-Y., Chen,T.-M. and Stroop,W.G.
JOURNAL	Submitted (03-APR-2000) Ophthalmology, Mail Slot: 523, University
FEATURES	of Arkansas for Medical Sciences, 4301 W. Mkrakham, Little Rock, AR
source	72205, USA
Location/Qualifiers	
1..947	
/organism="Human herpesvirus 1"	
/mol_type="genomic DNA"	
/strain="+GC"	
/db_xref="taxon:10298"	
151..909	
/codon_start=1	
/product="gamma1 34.5"	
/protein_id="AAG39340.1"	
/db_xref="GI:11640714"	
/translation="MARRRRRHRRRRRRPPPTGAVPTAOSQVTSFNPSEPAVRSAP	
AAAPPPASGPPSCSLRLQWLHVESASDDGDDWPSPPPEPAERPYAAP	
RPRPPGAGGGGANSHPSPRFLRLRYTAERLARLRRAAGEGAPPP	
PATPATPATPATPATPARVPRSPVVRHVLVYMASARLARAGSWAREBRADRAVFE	
RRRAEAENVIGPGLGPEARARALARAGANSV"	
BASE COUNT	93 a 444 c 312 g 98 t
ORIGIN	
Query Match	0.1%; Score 18; DB 1; Length 947;
Best Local Similarity	100.0%; Pred. No. 34;
Matches	18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	132419 CGCCCCCGGGCGCGCGC 132436
Db	496 CGCCCCCGGGCGCGCGC 479
IIIIIIIIIIIIIIIIIIII	
RESULT 43	
KSU52065	1047 bp DNA linear VRL 08-JAN-1997
LOCUS	Kaposi's sarcoma-associated herpes-like virus membrane glycoprotein
DEFINITION	Ox-2 homolog gene, complete cds.
ACCESSION	U52065
VERSION	U52065.1 GI:1765953
KEYWORDS	
SOURCE	
ORGANISM	Human herpesvirus 8 (Kaposi's sarcoma-associated herpesvirus -
	Human herpesvirus 8)
	Human herpesvirus 8
	viruses; dsDNA viruses, no RNA stage; Herpesviridae;
	Gammaherpesvirinae; Rhadinovirus.
REFERENCE	1 (bases 1 to 1047)
AUTHORS	Bohenzky,R.A., Russo,J.J., Moore,P.S. and Chang,Y.
TITLE	KSIV contains a homolog to Ox-2
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 1047)
AUTHORS	Bohenzky,R.A.
TITLE	Direct Submission
JOURNAL	Submitted (21-MAR-1996) Roy A. Bohenzky, Pathology, Columbia
	University College of Physicians and Surgeons, 630 W. 168th street,
	New York, NY 10032, USA
COMMENT	On Jan 8, 1997 this sequence version replaced gi:1654209.
FEATURES	
source	Location/Qualifiers
	1..1047
	/organism="Human herpesvirus 8"
	/mol_type="genomic DNA"
	/specific_host="Homo sapiens"

/db_xref="taxon:37296"
/clone="L54"
/cell_line="BC-1"
/clone_lib="Lambda FixII library L1 from body cavity based lymphoma cell line BC-1."
1..1047
/codon_start=1
/product="membrane glycoprotein OX-2 homolog"
/protein_id="AAB39927.1"
/db_xref="GI:1765954"
/translation="MHTFFDGRGRVGGVYSYFLIGARGRTAIKTEGVSAION
LPPVLPVAGTGVAVPVCAPEWTPPSASRGSMSLFI SLEWATIMLALCAVGA
RVQPMRGSAAITCALTPRADIVSVTKRQLPGPVNATVSHSYVVOYORHAN
ITCPGLMSTLVILHNLAVDEGCYLCIFNSFGQVSCACLEVSPPTGHVONSTE
DADVTCLATGRPPVNTWAAPMNNASSTOEPTDSGLTVAMRTVRLPRGDWTPSE
GICLTWGNESISIPASIGGPLAHDLPAAGTLGAVAILTVGLFGIFALHCRKRGCG
ASPTSDMDPLSTQ"

BASE COUNT 205 a 314 c 281 g 247 t

ORIGIN

Query Match
Best Local Similarity 100.0%; Score 18; DB 1; Length 1047;
Pred. No. 34;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 123181 TACCTGTATCTTTAAC 123198
|||||
Db 550 TACCTGTATCTTTAAC 567

RESULT 44
AF347327 1175 bp RNA linear VRL 12-JUN-2002
LOCUS HIV-1 isolate 981681 from Germany pol protein (pol) gene, partial
DEFINITION cds.
ACCESSION AF347327
VERSION AF347327.1 GI:13604763
KEYWORDS Human immunodeficiency virus 1 (HIV-1)
SOURCE Human immunodeficiency virus 1
ORGANISM
Virus; Retroviruses; Retroviridae; Lentivirus; Primate
Lentivirus group.
1 (bases 1 to 1175)
Beerenwinkler, N., Schmidt, B., Walter, H., Kaiser, R., Lengauer, T.,
Hoffmann, D., Korn, K. and Selbig, J.
Diversity and complexity of HIV-1 drug resistance: a bioinformatics
approach to predicting phenotype from genotype
Proc. Natl. Acad. Sci. U.S.A. 99 (12), 8271-8276 (2002)

JOURNAL
MEDLINE
PUBMED
22056123
12060770
2 (bases 1 to 1175)
Schmidt, B., Walter, H., Moschik, G., Paatz, C., Werwein, M.,
Schwengel, E. and Korn, K.
Recovery of HIV-1 pol gene sequences by direct sequencing of
amplification products derived from plasma samples
Unpublished
3 (bases 1 to 1175)
Schmidt, B., Walter, H., Moschik, G., Paatz, C., Werwein, M.,
Schwengel, E. and Korn, K.
Direct Submission
Submitted (08-FEB-2001) German National Reference Center for
Retroviruses, Institute of Clinical and Molecular Virology,
Schlossgarten 4, Erlangen 91054, Germany
Location/Qualifiers
1..1175
/organism="Human immunodeficiency virus 1"
/viflon
/mol_type="genomic RNA"
/isolate="981681"
/db_xref="taxon:11676"
/country="Germany"
/gene="pol"
/feature="pol"
CDS

/gene="pol"
/codon_start=1
/product="pol protein"
/protein_id="AAK32404.1"
/db_xref="GI:13604764"
/translation="PQITLMQRPRLTIKIGGOLKEALLDTGADDTVLESTELPRMKNP
KMIIGIGGIFKRVQYEQIPEXICGHVXSTVLVGPVNIIGXNIMTXIGCTLNPIIS
PIETVGVKLIKPGMDGPKVXQWPLTEERIKALVEICELEKEGKISKIGPENYNTPIF
AKKKNSTRMXXKLMDERELNRKTXDQWEOQLGPHAGLOKKSQVYXLDVDAVFAVP
LDKDFKRYAFTIPRXNNETPGIKKQYANVLPGQWGSPPXPCOSMTKILIXRRKRPD
XYITQXHDLCGSDLXIXYQHRHEDMLXHLGNGFYXPREKHQREPPFLMNGYEXH
PKMTYOPITXXKESDWTYNDIOXLVGLKLNMA5QITPGIKVRQCLKLNGTVALTEXP"

BASE COUNT 425 a 198 c 242 g 273 t 37 others

ORIGIN

Query Match
Best Local Similarity 100.0%; Score 18; DB 1; Length 1175;
Pred. No. 34;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 132204 ACTTGACAGTCCCTTAG 132221
|||||
Db 641 ACTTGACAGTCCCTTAG 658

RESULT 45
HS1ICP345B/c
LOCUS HSIICP345B 1346 bp DNA linear VRL 02-AUG-1993
DEFINITION Herpes simplex virus type 1 infected-cell protein (ICP34.5) gene,
complete cds.
ACCESSION M33700
VERSION M33700.1 GI:330116
KEYWORDS Infected-cell protein 34.5; neurovirulence factor.
SOURCE Human herpesvirus 1
ORGANISM Human herpesvirus 1
Virus; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Simplexvirus.
1 (bases 1 to 1346)
Chou, J. and Roizman, B.
The herpes simplex virus 1 gene for ICP34.5, which maps in inverted
repeats, is conserved in several limited-passage isolates but not
in strain 17syn+
J. Virol. 64 (3), 1014-1020 (1990)

JOURNAL
MEDLINE
PUBMED
2154589
90156494
2154589
Original source text: Herpes simplex virus type 1 (strain MGH-10)
DNA.
Draft entry and computer-readable sequence for [1] kindly submitted
by J.Chou, 13-APR-1990.
Location/Qualifiers
1..1346
/organism="Human herpesvirus 1"
/mol_type="genomic DNA"
/db_xref="taxon:10298"
134..871
/note="Infected-cell protein 34.5"
/codon_start=1
/protein_id="AAA45791.1"
/db_xref="GI:330117"
/translation="MARRRRRHRRGPRRPPGFTGAVPTAQSQVSTPNSSEPVRSAP
AAGPPSCSLRLKQWLHVESASDDDDDDMDSPDPAPAPARTAAAPRSPPP
GAGPGGATNPSHPPSRPRLPRLALRLVTAEHLRLRLRRGCGAGAPATPATP
ATPATPATPATPARVRSPPHVRVRLVWVASAARLARLRGSMAERADRARRRRVAEA
EAVIGPCLPPEARARLARAGAPANSV"

BASE COUNT 161 a 576 c 437 g 172 t

ORIGIN

Query Match
Best Local Similarity 100.0%; Score 18; DB 1; Length 1346;
Pred. No. 35;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 132419 CGCCCCCGGGCCGCGC 132436
|||||

Db 458 CCCCCCCCCCCCCC 441

Search completed: September 30, 2003, 03:36:52
Job time : 429 secs

CDS

OHPENVYVSVVPSVSGVLTGAIATSLIMCMFTICNGENSESTSYASQSYTOPSH
NORNTNCSRHITRNAAHOESIEELPNQHTSEIDSCQVLELVKNAVADPQNTI
NEVMQYDVVVKNIQOTSEYEDNVHMDYSDIINPNFYSGILILEVEDEVYNELEN
OYHGILLENLHNEYNHNLNMIQYDWMLE"
complement (2692..3258)
/note="ORF 2: similar to Kaposi's sarcoma-associated
herpesvirus ORF 2"
/codon_start=1
/product="dihydrofolate reductase"
/protein_id="AAd21331.1"
/db_xref="GI:4494909"

CDS

/translation="MDITVNCIYAVDDELQIGKNGTMPRYLNNEMMYFOKMTSPV
YGEKRVYMGKRTSEIPEKRPVLRNIIISRLRPPHAFHFLATLDAFERY
OYKEEQLNTVWYIGKSVESLVNKCPLKYLITRIMESFQCDVFPSPINTEYTM
SEIPEKDTNFENEGIKRYEYKFNK"
3676..5613
/note="ORF 4: similar to Kaposi's sarcoma-associated
herpesvirus ORF 4"
/codon_start=1
/product="complement binding protein"
/protein_id="AAd21332.1"
/db_xref="GI:4494910"

CDS

/translation="MTFKLFLPLFLHAIYVHCDENCKPHEPTEYKVNTEKOLYS
GETALICRPGVNTKIITTECLONGTMSPPNCPDRKCPPTADLLNGAVHISGD
NALKRSNIYECNCGVDLIGSNVRECLIDPENNMDSNEVCIOICIRPANEHG
DYLPHQDYNNGDATTCKOSLYTLVSTTLVCTISNKNMSEFICMLVCESPIDN
GYIDIGLSRRNHGQITVYKCSGDIYVIGPELITCTNTWPELVYLVNPNPTM
PETMPEETPDYOKINLSTAKATTAPNAVTTVYVSEPKDVTQVCKPHEPMEVAEN
DEKYSVASVELICRPGFTKOSTVSECLNGTWTAPNACCHKCKPOTDOLLNGE
YIVTGEAFKGTNITVYKCNQYGLSMVRCMLKDKLIKVDMEKAPICDEICK
PPOTTNKHYKHYKDYQYLDVYVSCNRDESLVDNMTCTISNMNKPPECEITC
SAPNIAHKLILGSSSVYKYGQSVTICGETGTLIGSEITCKDSSMDPLTCVPAV
SMSPOTPEKTPETPTEPEAKRPTPVNGHTTPKPPNPPIAPPMKMKRHVLY
LEFASVLSLFLVLAALYCCFLK"
6045..9443
/note="ORF 6: similar to Kaposi's sarcoma-associated
herpesvirus ORF 6"
/codon_start=1
/product="ssDNA binding protein"
/protein_id="AAd21333.1"
/db_xref="GI:4494911"

CDS

/translation="MASEKNGAGPLEDNOGSRAPIGAGCYVAYVSKODPFAEASILG
NRPSGVSVELPIYGLTVEHEPFLVKAAYKVVDTLAVKVCCHFEVYENHAST
FRPYDNGTGLICEARALFGYQOTIEPGRPHSTWNLBEPQDKREMLGYVTE
GKEKLRGCLVPANFOTOQOIAKQAFKPLDEDELPABGHMRPPEYTHKDSAYL
YDSLSTIAQALRLKDVTAIVIHATEKQPMODHYKIAKVOAKQESTLLPKTTDSSM
IVDSVVAELASLYGCMLECPQDACELNYSWPLFDGDSPEARVNALEKMSAOAV
HVAQGLFANASVLYLTQVQOAPRGOKGDVNVNSELFOHGDSEAFNLKENGSEAF
KGVPSNALDGSSFPYHLAASFPHLKICYMOFLQHKHKSSTNOAFNMVHYVGT
AANSEMTLCHGNTPATCLNTLFLYKLRPRAVTPPQRRDPYVYGTAGTNDLEILG
NPASFRDEBEGNPADHEPKYTYWOLCOTVTEKLSAIGITEHDHNVNLITNIOFLR
VFKGIDSLVDEVMKFNYSMTKNNNFREHVSXHIILQFCNVYMAQACAFPLVLY
KSLMILODILPCMIYEDONPAMGILPSEMLKMHQTLQNTFNACALDGVLTGCE
LKIYHRDMFCDFEDDAGSNGMLAPFKMQLARAMVVPKSIKINRIITSNMGSE
AVOSGEVFGTGRDTPYVAGPYMKFLNSLHRALEPDTALYLMHTISQNMVPYK
DVPEDELAELYSYKTNLSLAFETVLDVDPDSLARSIKNLNCAITLACQIOFYAT
TLHCLTPEVQTTIDETPFIHVLGSAIATPAVLAIRGIALVQVTAIRQPAAGRL
RPVITPVVNVKRYGVNGNNVNFHCGNLGYPAGVRGDRNLPBESSPEFKTARSAIRK
RHVMTPIIDRLIKRAAGOTISTEAEBSKRSVOALLEKDNPNLKSIIELIRHIG
KGCODLSEEDVQYLYGDYCMLTDEVLFTLINDIAOSGVPTIEDAGALIEDQDADDLQ
FVDSDDIATASCOPEBOLPTPSAGALLAGKKRKNALSLDL"
9468..11528
/note="ORF 7: similar to Kaposi's sarcoma-associated
herpesvirus ORF 7"
/codon_start=1
/product="transport protein"
/protein_id="AAd21334.1"
/db_xref="GI:4494912"

CDS

/translation="MLVNELSVLGDMEVTFHGRFSFVNLTQLQTEKGGVAVRVL
PESLDLQHFAAGLAVRLKLELPFSPCAVLLIPLDGGSDADARAAPGVLDSSRP
LTVWVNASGRHTIRFCLLFLKIDLERLAVTVFENGARREGTPKPCATESELPGR
LRVSGEASQTSFHSFVAVFPFANSVACILIRLAVPDSOAAHRDAISKYYTVSN
SGGVNCRASVHTLSRCKTQMOETIYARGPNAEYIVGQALDLPHTGEGVYVA
DAEKTIDPGSSAEVAVOLITFOOGAAKADLAFIYTGVAPELFTVYTPALLISGCTTHL
RLFNPNGTPTTIKDDTVLAAAPVVRVLSADDAADPLVASPTGALISNAFTIPVG
FPGVVASACHVTSIDNGVHERMN"
18520..19749
/note="ORF 11: similar to Kaposi's sarcoma-associated
herpesvirus ORF 11"

CDS

/translation="MDFPNYLGRGPRPHSHRGTDAPAPAGACAVOPPPVCELIPA
CLRTFAGAGMTIPVTIPPEPTYFENGARQDVLLANRSMTARDRPAVAPDQDSTIE
HAYDVETTVYADRCAEVPSRRQTDIIPSGVLYLKLGTEDGTSCVAVPFOQYFVA
KVPAGINTVTHILOALNKNTAGRAAGSESTRVNRKILKTYVABEHPVEIILSSGML
STSDRLVACGCEVYESVNDVRRVLDHGGFTTCGTCGATPRAILDAVARTALEFD
CSWDELVSQADRSWMPRIYAFIDEGEGGFTGAGTCAVAVIOISCVFTTEBAGP
NPNTLPSVGCDDIPPTDVLPEPSEYMLVSPFAMIRDEPVDLTGNTGNSNFDPL
ITRSQVNLNLNETYKTKTGSIEFVHPRGGGSPMSVSKITAGVPIQDMTOVCR
EKLSDYKIDLTVAQCIGGKEVSYDIPLFRRSGGRKAGSYCMDSVLMVL
LKMEPIHVEISEIKLAKIQARVLYLDOQQLRVSCLEAARENFTLPPVTPREGOG
YOGAVINPIGTFDEPVLAVDFASLYSIIQAHNLKTYMIGHDLHLHNPTRDDY
ETPVLGSPVHFVKKHRESLIGRLITVWLEKRAIRRTLAACDPSLTKTILDOOLA
IKVYCNAYGTVGASGLPCINIAEYVTLGKRLIMBESKYVALTIEDITRLRGRE
VTARGAFRRVYVGDLSLFTACDYSSEAVSAFCDDIARITADLPFPILKLEKTE
FKCLLLRKRKYIGVLLDNKVMGMDVDIRTACKFVQERKAILDLVHLDEPKAA
RLCKRPFAVEEGLPAGFKIYEVLNVAISLIDRNSVYPLEOITFSELSRPPCDYK
TTNPLHAVQGLKSRCELPQVDRIRIYVVDVAGSLSDSLAEHPDVVRQHQIPVAV
DLVYDKLHVGAANILQCLFGNNAOTVAIILNPLNVYKFLS"
17261..18511
/note="ORF 10: similar to Kaposi's sarcoma-associated
herpesvirus ORF 10"
/codon_start=1
/product="unknown"
/protein_id="AAd21337.1"
/db_xref="GI:4494915"

CDS

/translation="MLVNELSVLGDMEVTFHGRFSFVNLTQLQTEKGGVAVRVL
PESLDLQHFAAGLAVRLKLELPFSPCAVLLIPLDGGSDADARAAPGVLDSSRP
LTVWVNASGRHTIRFCLLFLKIDLERLAVTVFENGARREGTPKPCATESELPGR
LRVSGEASQTSFHSFVAVFPFANSVACILIRLAVPDSOAAHRDAISKYYTVSN
SGGVNCRASVHTLSRCKTQMOETIYARGPNAEYIVGQALDLPHTGEGVYVA
DAEKTIDPGSSAEVAVOLITFOOGAAKADLAFIYTGVAPELFTVYTPALLISGCTTHL
RLFNPNGTPTTIKDDTVLAAAPVVRVLSADDAADPLVASPTGALISNAFTIPVG
FPGVVASACHVTSIDNGVHERMN"
18520..19749
/note="ORF 11: similar to Kaposi's sarcoma-associated
herpesvirus ORF 11"

CDS

Query Match 77.5%; Score 31004; DB 1; Length 133719;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 40001; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 39900 AACACTATCAGACCCGGTCTACACCGAAACGGGGCTTAAGAAGCTGTTAACTCAGACA 39959
Db 39900 AAACACTATCAGACCCGGTCTACACCGAAACGGGGCTTAAGAAGCTGTTAACTCAGACA 39959
QY 39960 TGGTGCCATGTTCAAAAGCTTAAAGGATTAACCTGTTTCCCGCAAAATCAGACA 40019
Db 39960 TGGTGCCATGTTCAAAAGCTTAAAGGATTAACCTGTTTCCCGCAAAATCAGACA 40019
QY 40020 TCGCCGTCAAGGAAAGACAGTACGTCTCGGTTCTCCGACATGAGGGGCGGCTGT 40079
Db 40020 TCGCCGTCAAGGAAAGACAGTACGTCTCGGTTCTCCGACATGAGGGGCGGCTGT 40079
QY 40080 GTACAGAAACGTTTTTAAGGGGACAAATACGTATCTCTCATCGGGGACCAATTG 40139
Db 40080 GTACAGAAACGTTTTTAAGGGGACAAATACGTATCTCTCATCGGGGACCAATTG 40139
QY 40140 CCGGAGTCATGAGACACGAAAGATAATGGAAGATGTTAAACATGCTAGTACAG 40199
Db 40140 CCGGAGTCATGAGACACGAAAGATAATGGAAGATGTTAAACATGCTAGTACAG 40199
QY 40200 TTGACGGGGGCAATGTCGGGTCGGCTCTTACGCCAATTACGTTGTCAAGGGGCAAAATC 40259
Db 40200 TTGACGGGGGCAATGTCGGGTCGGGCTCTTACGCCAATTACGTTGTCAAGGGGCAAAATC 40259
QY 40260 TCGTAACCCGCGTACAGTACGTGCGGTATCGCAACGTTTGACCAAGTTCAAGAACGA 40319
Db 40260 TCGTAACCCGCGTACAGTACGTGCGGTATCGCAACGTTTGACCAAGTTCAAGAACGA 40319
QY 40320 TGGTGAACGTCCTCAACGGGACCGACGATGATGAGATGATGAGGACGGGGTGGCGAGC 40379
Db 40320 TGGTGAACGTCCTCAACGGGACCGACGATGATGAGATGATGAGGACGGGGTGGCGAGC 40379
QY 40380 GGCAGAGACTCCCTCGCCAAACACCGATGCGGGGCTGTTATCCAGATTGAGATTAAC 40439
Db 40380 GGCAGAGACTCCCTCGCCAAACACCGATGCGGGGCTGTTATCCAGATTGAGATTAAC 40439
QY 40440 TGGTGGCTTTGGAAAGATTACAGCAATGATACAGACAGCCAGTTTCCCTTCCGTTAA 40499
Db 40440 TGGTGGCTTTGGAAAGATTACAGCAATGATACAGACAGCCAGTTTCCCTTCCGTTAA 40499
QY 40500 ACAGGGGTATGACCTATCTATTTTCCCATTTGGGTGACATGCCCCGCTCAGT 40559
Db 40500 ACAGGGGTATGACCTATCTATTTTCCCATTTGGGTGACATGCCCCGCTCAGT 40559
QY 40560 ATTCAAGTCGGCCACAAATTAAAGGGGTGAGACCCAGCGGAACAATCCGTGAAACGT 40619
Db 40560 ATTCAAGTCGGCCACAAATTAAAGGGGTGAGACCCAGCGGAACAATCCGTGAAACGT 40619
QY 40620 GGAATTTAAATAAACAACGATCTGCTGAGTTTCAATTAACAAACGCGCTCAAGTCCA 40679
Db 40620 GGAATTTAAATAAACAACGATCTGCTGAGTTTCAATTAACAAACGCGCTCAAGTCCA 40679
QY 40680 TCGGTATCGCGGCATGACAAACCGATGCGGTGGGCAAGTTTGGGTGAGGCGTTTC 40739
Db 40680 TCGGTATCGCGGCATGACAAACCGATGCGGTGGGCAAGTTTGGGTGAGGCGTTTC 40739
QY 40740 CAGATCCCGGACAGTTACAGAGTACGAAAGATCTGACACCCCGCAACATGAAAC 40799
Db 40740 CAGATCCCGGACAGTTACAGAGTACGAAAGATCTGACACCCCGCAACATGAAAC 40799
QY 40800 TATACGGGCTGCTGATCAACTATTACAGGGGCAAAACGTTGACAGCTTCCGATGTG 40859
Db 40800 TATACGGGCTGCTGATCAACTATTACAGGGGCAAAACGTTGACAGCTTCCGATGTG 40859
QY 40860 CCTTAAAGGCGAGATGACCAACAGATGAGTGTGTGACCCCAACCTGCGACGAGACGCTTC 40919
Db 40860 CCTTAAAGGCGAGATGACCAACAGATGAGTGTGTGACCCCAACCTGCGACGAGACGCTTC 40919

QY 40920 GTTTGGAGGTTCAACCCGATGTTGATTTTTCGTCATCAGACAGCCCTGGTGGCAAGCCG 40979
Db 40920 GTTTGGAGGTTCAACCCGATGTTGATTTTTCGTCATCAGACAGCCCTGGTGGCAAGCCG 40979
QY 40980 CGTATAGGGGACCCACAGACATATGTGGTTAACTTCCACAAACCCCTGGGCCCAAGC 41039
Db 40980 CGTATAGGGGACCCACAGACATATGTGGTTAACTTCCACAAACCCCTGGGCCCAAGC 41039
QY 41040 AGTTTCAAAACAGCAGAGGCTGACATTTGACAGACGGGGCGGCTGGCTCAGCTGTGG 41099
Db 41040 AGTTTCAAAACAGCAGAGGCTGACATTTGACAGACGGGGCGGCTGGCTCAGCTGTGG 41099
QY 41100 ACCAGTCAACGATGAAATTAATCAAGATACGGGCTTTGACAGCTGTACCCACTACT 41159
Db 41100 ACCAGTCAACGATGAAATTAATCAAGATACGGGCTTTGACAGCTGTACCCACTACT 41159
QY 41160 GTTATGTCATCGAATGCTTCATTCACAGGACAGGAAACAAATTTTGTATTAATTCCTT 41219
Db 41160 GTTATGTCATCGAATGCTTCATTCACAGGACAGGAAACAAATTTTGTATTAATTCCTT 41219
QY 41220 TAATTCATTTAACCTTGAACCTTACTGAAACATGCGGAAACTGGCGTTATTAAACA 41279
Db 41220 TAATTCATTTAACCTTGAACCTTACTGAAACATGCGGAAACTGGCGTTATTAAACA 41279
QY 41280 GCTTCCCTATGCTGCAATTTATCTGCTACCTGSGCAACGGTATATTCTAAGAGACG 41339
Db 41280 GCTTCCCTATGCTGCAATTTATCTGCTACCTGSGCAACGGTATATTCTAAGAGACG 41339
QY 41340 TGTACGCCATTTACGAAAGTTTGGGGAATCTGTTGTTTGGACAGAGCCCTCTCGA 41399
Db 41340 TGTACGCCATTTACGAAAGTTTGGGGAATCTGTTGTTTGGACAGAGCCCTCTCGA 41399
QY 41400 AAATCGCGGGCCACAGAGTGTGGGGCGCAGGCCGCTCCGACATTAATGCTTTC 41459
Db 41400 AAATCGCGGGCCACAGAGTGTGGGGCGCAGGCCGCTCCGACATTAATGCTTTC 41459
QY 41460 AGGACCCCAATCTTTTGGCGCCCTTGTCTACATGACGTTTTTACCACTGCTCAGGC 41519
Db 41460 AGGACCCCAATCTTTTGGCGCCCTTGTCTACATGACGTTTTTACCACTGCTCAGGC 41519
QY 41520 AGTCCTCGGGACCCCATGCTACTATAGCCACAGAGGGTACGAAACGGAAATGACA 41579
Db 41520 AGTCCTCGGGACCCCATGCTACTATAGCCACAGAGGGTACGAAACGGAAATGACA 41579
QY 41580 GGGATAGCTATCAACAGTCAAGAGAAATGAGAACCTAGTCGATGATGTTAAACA 41639
Db 41580 GGGATAGCTATCAACAGTCAAGAGAAATGAGAACCTAGTCGATGATGTTAAACA 41639
QY 41640 TTTACGAGACCAAGAACACGCGGATCAGAGCGCCGACGTCCTTGAAGCTGCTCCT 41699
Db 41640 TTTACGAGACCAAGAACACGCGGATCAGAGCGCCGACGTCCTTGAAGCTGCTCCT 41699
QY 41700 TTTATGAAACGAAACGCAATGCTGCTGTGAAAAAGCTTTTATAGTGGTCTGC 41759
Db 41700 TTTATGAAACGAAACGCAATGCTGCTGTGAAAAAGCTTTTATAGTGGTCTGC 41759
QY 41760 CAGCTGTACCAAGGTCACGTCGCGGACATGAGGCGTGAATTTGACAAAGTGGCTTCG 41819
Db 41760 CAGCTGTACCAAGGTCACGTCGCGGACATGAGGCGTGAATTTGACAAAGTGGCTTCG 41819
QY 41820 CCTGAGCTCAACGGGCCAGTGTGCTGACGCTGTAACCCCGAGATGAGATTTTGG 41879
Db 41820 CCTGAGCTCAACGGGCCAGTGTGCTGACGCTGTAACCCCGAGATGAGATTTTGG 41879
QY 41880 ACCACTGGAAGACGGGACGCTCCGAGATGCTCAGAGCTTGGGATATACACCCACCG 41939
Db 41880 ACCACTGGAAGACGGGACGCTCCGAGATGCTCAGAGCTTGGGATATACACCCACCG 41939
QY 41940 TTGACATGATGGAACCTTTTGGACGCTTTCACCTGCGGTTTGTAAACCAAGGCT 41999
Db 41940 TTGACATGATGGAACCTTTTGGACGCTTTCACCTGCGGTTTGTAAACCAAGGCT 41999
QY 42000 CCGTGTGTGACTAGCGGGACCCGCGCACTGTTGACACTCAAGACGAGGAGAT 42059

Db	42000	CCCCGTTTGTACTAGAGGGGACCCCGCAACTTTGACCACTACACAGCAGGAGAT	42059
Oy	42060	ACGTGAGCCAGACTGCTCTGTTAAAGGGTTGCGCGCTTTGCTATCGAGATAGTCTC	42119
Db	42060	ACGTGAGCCAGACTGCTCTGTTAAAGGGTTGCGCGCTTTGCTATCGAGATAGTCTC	42119
Oy	42120	GTGAGCTTGGCGAAGACATGTTTACCGGGTGCCTTACCAAGCTGTACAGCATCCC	42179
Db	42120	GTGAGCTTGGCGAAGACATGTTTACCGGGTGCCTTACCAAGCTGTACAGCATCCC	42179
Oy	42180	TGGTGGCGGCCACAGCTCCACCGCTGTGTGCAATTTAGCTGAGCGGCTGCCGCCACG	42239
Db	42180	TGGTGGCGGCCACAGCTCCACCGCTGTGTGCAATTTAGCTGAGCGGCTGCCGCCACG	42239
Oy	42240	GGCTGCGGCTGCGTTTAAAGCTCCCGCGCCCTCATGAGCGCAGTACGAGAGTGGACA	42299
Db	42240	GGCTGCGGCTGCGTTTAAAGCTCCCGCGCCCTCATGAGCGCAGTACGAGAGTGGACA	42299
Oy	42300	AGTCCCAATGCTGGCTTACGCTTACACCTGCGCCATGACGCGCCACGCTGTGAGCACC	42359
Db	42300	AGTCCCAATGCTGGCTTACGCTTACACCTGCGCCATGACGCGCCACGCTGTGAGCACC	42359
Oy	42360	TGGCAGCATGACATGAAAGCTGTCCGCGCGGGGTTTATCTGCCACGCAAGACACAGA	42419
Db	42360	TGGCAGCATGACATGAAAGCTGTCCGCGCGGGGTTTATCTGCCACGCAAGACACAGA	42419
Oy	42420	TTACACCGGGCTTTGCGATGAGACCGCGCTCCGAACGATGAGTGTGGCGAGAACTTGC	42479
Db	42420	TTACACCGGGCTTTGCGATGAGACCGCGCTCCGAACGATGAGTGTGGCGAGAACTTGC	42479
Oy	42480	TATTTAGTGCAGGGCTTCGAGCTGCATGTTTATAGGCGAGCATTCGCTCGGG	42539
Db	42480	TATTTAGTGCAGGGCTTCGAGCTGCATGTTTATAGGCGAGCATTCGCTCGGG	42539
Oy	42540	AAGTCAGGGGCGAGCAGTCAAGTTTGAAGTGAATCATGATGTGTCATCGCTGAGCATGG	42599
Db	42540	AAGTCAGGGGCGAGCAGTCAAGTTTGAAGTGAATCATGATGTGTCATCGCTGAGCATGG	42599
Oy	42600	CGCTCGTTATTTTCAACATCAGCGCCGCCAGTTGCGGCGATTACCTCGGACATGG	42659
Db	42600	CGCTCGTTATTTTCAACATCAGCGCCGCCAGTTGCGGCGATTACCTCGGACATGG	42659
Oy	42660	GGCTGCTGCTGAGCAATGTTTCTCATGTTTCCCGGGGAGCTCGTACAGAGACAGACC	42719
Db	42660	GGCTGCTGCTGAGCAATGTTTCTCATGTTTCCCGGGGAGCTCGTACAGAGACAGACC	42719
Oy	42720	TCAAGCACTAGCTTAAACAAAAAGCGGATGCAAGATTCGGTGTCTCTGGCCAGATTG	42779
Db	42720	TCAAGCACTAGCTTAAACAAAAAGCGGATGCAAGATTCGGTGTCTCTGGCCAGATTG	42779
Oy	42780	GTGAGCCGCTGCTTACGTTGGGGGGGTGCGGCACTGCGAACATACCGGGTCTCAGCC	42839
Db	42780	GTGAGCCGCTGCTTACGTTGGGGGGGTGCGGCACTGCGAACATACCGGGTCTCAGCC	42839
Oy	42840	AOGGACACTGGCCAGCTGTAGATTTTGTGAGCCCGCTTACTGCAACGTTACTACTT	42899
Db	42840	AOGGACACTGGCCAGCTGTAGATTTTGTGAGCCCGCTTACTGCAACGTTACTACTT	42899
Oy	42900	TTCAAAACCCCAACAGTCCCGGGGAGCGGATCCTGTGATCTCGTGTACGGGTACA	42959
Db	42900	TTCAAAACCCCAACAGTCCCGGGGAGCGGATCCTGTGATCTCGTGTACGGGTACA	42959
Oy	42960	ACAAGAAAGCGCGAAGCTTGTCTTTGACCACTGCATCCCGGATTTCTGCTACGAT	43019
Db	42960	ACAAGAAAGCGCGAAGCTTGTCTTTGACCACTGCATCCCGGATTTCTGCTACGAT	43019
Oy	43020	ACCGCACTACGCTTAAACCAATGAGGAGTGTGACAGAGGCTCCCTGGAACAGTCTGTA	43079
Db	43020	ACCGCACTACGCTTAAACCAATGAGGAGTGTGACAGAGGCTCCCTGGAACAGTCTGTA	43079
Oy	43080	ACTCAACTCGCGCAGGTGCTGAGTGCAGGAGTGTACAGTCCGCTGTCAGTTTTC	43139
Db	43080	ACTCAACTCGCGCAGGTGCTGAGTGCAGGAGTGTACAGTCCGCTGTCAGTTTTC	43139
Oy	43140	ACAAGAGCTATTTTGGCTAAACAATCGGGCTGTGAACAACACTAGTACAGGATACGGG	43199
Db	43140	ACAAGAGCTATTTTGGCTAAACAATCGGGCTGTGAACAACACTAGTACAGGATACGGG	43199
Oy	43200	CCCGCTACAGGGAACGCGGGGAGCAGCGGAGCGGAGCGGAGCTGTGAGTGGGTCAACG	43259
Db	43200	CCCGCTACAGGGAACGCGGGGAGCAGCGGAGCGGAGCGGAGCTGTGAGTGGGTCAACG	43259
Oy	43260	GAACGATGTGTTTGTAGAACAAACGCTCCAGTTTCTCAAGAAAGCTTTCCACGCTCG	43319
Db	43260	GAACGATGTGTTTGTAGAACAAACGCTCCAGTTTCTCAAGAAAGCTTTCCACGCTCG	43319
Oy	43320	CCGCCAGTACAGGCTCTGCTGGAAGATATATGCAATATAGTCAACGACGCGCTG	43379
Db	43320	CCGCCAGTACAGGCTCTGCTGGAAGATATATGCAATATAGTCAACGACGCGCTG	43379
Oy	43380	TGCACATGGGACATTAATGATTTGAGGAAGTGGCCCTATGAAAGACTATTAAAGATCG	43439
Db	43380	TGCACATGGGACATTAATGATTTGAGGAAGTGGCCCTATGAAAGACTATTAAAGATCG	43439
Oy	43440	GAACAAAGTGCCTATTAGTTTACCTGACAGCGGTGTGAGCTAAGAGATGCGCTC	43499
Db	43440	GAACAAAGTGCCTATTAGTTTACCTGACAGCGGTGTGAGCTAAGAGATGCGCTC	43499
Oy	43500	GATAAGCAATCCTTGTCTCGGTGACGCTGTAGATTTATTCGCCGAGCATACAAATCTT	43559
Db	43500	GATAAGCAATCCTTGTCTCGGTGACGCTGTAGATTTATTCGCCGAGCATACAAATCTT	43559
Oy	43560	CAGTAAAGATAGATGATTTTGGCTGCGAGAGCGGCCACCGCTGACAAATATACAG	43619
Db	43560	CAGTAAAGATAGATGATTTTGGCTGCGAGAGCGGCCACCGCTGACAAATATACAG	43619
Oy	43620	GGCTGCTGCGGAAACCTGCTCTAGGAGATTCGCGGTGGATTTTATTCAGGCATAT	43679
Db	43620	GGCTGCTGCGGAAACCTGCTCTAGGAGATTCGCGGTGGATTTTATTCAGGCATAT	43679
Oy	43680	CACATTTTGGACAAATGCACTGCGCGGTGTGAAGAGTGTGCCAACAAGTTTACGG	43739
Db	43680	CACATTTTGGACAAATGCACTGCGCGGTGTGAAGAGTGTGCCAACAAGTTTACGG	43739
Oy	43740	CTAAGCGCATTTGATCCATGAGACATTAATCAATAAAGGCTGACCAACCGGCTTC	43799
Db	43740	CTAAGCGCATTTGATCCATGAGACATTAATCAATAAAGGCTGACCAACCGGCTTC	43799
Oy	43800	CATTGGATTACTACTAGAAATGTTAGTTATACCAACCGCTTTTGGCGCAAAAGATCG	43859
Db	43800	CATTGGATTACTACTAGAAATGTTAGTTATACCAACCGCTTTTGGCGCAAAAGATCG	43859
Oy	43860	ACCGTCTACTGAGTCTTACGGGTTTATGTTTCCCTGCCGTGTGCCAAGACA	43919
Db	43860	ACCGTCTACTGAGTCTTACGGGTTTATGTTTCCCTGCCGTGTGCCAAGACA	43919
Oy	43920	CTGGCTCAAAACAGTCTTACAGAGTGTGCTGCTTAAATATATACAGAGTGGCGAG	43979
Db	43920	CTGGCTCAAAACAGTCTTACAGAGTGTGCTGCTTAAATATATACAGAGTGGCGAG	43979
Oy	43980	ACGACGCCACCGAGCTCAACCTAGCCGAGGTGAGCGCTGTACAGACCAATATACCTTAC	44039
Db	43980	ACGACGCCACCGAGCTCAACCTAGCCGAGGTGAGCGCTGTACAGACCAATATACCTTAC	44039
Oy	44040	ATGGGTGCAACTACGCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG	44099
Db	44040	ATGGGTGCAACTACGCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG	44099
Oy	44100	CTGACGACGCTGCTTACCTGCTGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	44159
Db	44100	CTGACGACGCTGCTTACCTGCTGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	44159
Oy	44160	AGGCTACTGACCTATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	44219
Db	44160	AGGCTACTGACCTATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	44219
Oy	44220	AGGCTACTGACCTATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	44279
Db	44220	AGGCTACTGACCTATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	44279

Db	46380	GAACGGGCTTCATCCGCGCCCTCTATATCTTGAGAGCTGCTCTTACGGGACAGATCCA	46439
Oy	46440	ATTGTGACAGCGAAGAGTGCCTACGATTTTATGCACTGCTTGGAGGACGCGGCGCT	46499
Db	46440	ATTGTGACAGCGAAGAGTGCCTACGATTTTATGCACTGCTTGGAGGACGCGGCGCT	46499
Oy	46500	CCCCATTAGCTCCGTGGAAATGCGCCTTCCAAAAAAGATTAGTGCCTCCGTACC	46559
Db	46500	CCCCATTAGCTCCGTGGAAATGCGCCTTCCAAAAAAGATTAGTGCCTCCGTACC	46559
Oy	46560	TCTCATCATCTCTATATAGGAGAAATGCAAGCGGTAGACAGGGGACGCGACAGACG	46619
Db	46560	TCTCATCATCTCTATATAGGAGAAATGCAAGCGGTAGACAGGGGACGCGACAGACG	46619
Oy	46620	TCTTCGCAAGTTAAATCATCTTATGATCCGACATAGTAGTTCAACACGTTAAAGCA	46679
Db	46620	TCTTCGCAAGTTAAATCATCTTATGATCCGACATAGTAGTTCAACACGTTAAAGCA	46679
Oy	46680	TCTTTTCGCGGCGCTCTCAATTAAGTAAAAAACTAGTTGATTTGCAGATGAGTTAC	46739
Db	46680	TCTTTTCGCGGCGCTCTCAATTAAGTAAAAAACTAGTTGATTTGCAGATGAGTTAC	46739
Oy	46740	TTGAGGATATATAAATCGATTTGGCTCCTTTGGAAGCAATAACCCAGAAATCGGGGA	46799
Db	46740	TTGAGGATATATAAATCGATTTGGCTCCTTTGGAAGCAATAACCCAGAAATCGGGGA	46799
Oy	46800	GGGACCTCTTTTAAATGAAGTTCGCTCGATATATAGAGGTGAAAGCTCTGCCCC	46859
Db	46800	GGGACCTCTTTTAAATGAAGTTCGCTCGATATATAGAGGTGAAAGCTCTGCCCC	46859
Oy	46860	GGATCTCTAAAGGCAAGAAAAACAACAGAGTACGGCGGTATGGAGAACATACG	46919
Db	46860	GGATCTCTAAAGGCAAGAAAAACAACAGAGTACGGCGGTATGGAGAACATACG	46919
Oy	46920	CCTAAGGCAAAATCTCGGACCTGACTTCAACAGTGCAGCGCTTCTTACCGTCCC	46979
Db	46920	CCTAAGGCAAAATCTCGGACCTGACTTCAACAGTGCAGCGCTTCTTACCGTCCC	46979
Oy	46980	ATTAGAGATCTAATTTCACTGAGAGCTGACGCTTAAACCACTTACGCTATCTGATCA	47039
Db	46980	ATTAGAGATCTAATTTCACTGAGAGCTGACGCTTAAACCACTTACGCTATCTGATCA	47039
Oy	47040	GACGACATTAATTTGGAACGATTTCTTCTGCTTACCTGCTGGGACAGATGCTC	47099
Db	47040	GACGACATTAATTTGGAACGATTTCTTCTGCTTACCTGCTGGGACAGATGCTC	47099
Oy	47100	TCTTATACACAGATGCTGCAAAAGATGCAAAATGCGGCGTCAACACGCCAATATGTC	47159
Db	47100	TCTTATACACAGATGCTGCAAAAGATGCAAAATGCGGCGTCAACACGCCAATATGTC	47159
Oy	47160	GATTTTCATACGCTCTACTATATACAGTGTGTTGGATTGTAAGCGCTATCACGATGCG	47219
Db	47160	GATTTTCATACGCTCTACTATATACAGTGTGTTGGATTGTAAGCGCTATCACGATGCG	47219
Oy	47220	ACGGGGGACGCAATGCGTGCATCTGCTACCTCGGCAAAATTAAGTGTGATTTAACGG	47279
Db	47220	ACGGGGGACGCAATGCGTGCATCTGCTACCTCGGCAAAATTAAGTGTGATTTAACGG	47279
Oy	47280	GAATTCGGGTTTGGATATATGAGAGGATGTTGCTAGAGTCTCTCCAGAACCCCGCG	47339
Db	47280	GAATTCGGGTTTGGATATATGAGAGGATGTTGCTAGAGTCTCTCCAGAACCCCGCG	47339
Oy	47340	TACCCGAGCGCTTCATCGATCCGCTGCTGTCAACAGGCAAGGAAATCTTAAAGCG	47399
Db	47340	TACCCGAGCGCTTCATCGATCCGCTGCTGTCAACAGGCAAGGAAATCTTAAAGCG	47399
Oy	47400	ATATACAGGATCTTTGAGAGCGGTGTGAAATCTGAGGCAATATCTTACCGTTGCA	47459
Db	47400	ATATACAGGATCTTTGAGAGCGGTGTGAAATCTGAGGCAATATCTTACCGTTGCA	47459
Oy	47460	AGAAATGCAATTTGAATGCAATAGTAGATTAAATAGCGCTTAAACGAGTGGC	47519
Db	47460	AGAAATGCAATTTGAATGCAATAGTAGATTAAATAGCGCTTAAACGAGTGGC	47519
Db	47460	AGAAATGCAATTTGAATGCAATAGTAGATTAAATAGCGCTTAAACGAGTGGC	47519
Oy	47520	TTCCGGTATGAGCGACGGCGAAGGTGCGAGAGACTCCGGCGACATTTACATCCACA	47579
Db	47520	TTCCGGTATGAGCGACGGCGAAGGTGCGAGAGACTCCGGCGACATTTACATCCACA	47579
Oy	47580	TAAATATCTCATATATCTCCACTAAAACGGTATATGATATCTTATTTAAATGACGA	47639
Db	47580	TAAATATCTCATATATCTCCACTAAAACGGTATATGATATCTTATTTAAATGACGA	47639
Oy	47640	GAAATTAATAATACGACCATTTGTAATAATCATGACGCAAGGAAATGCGCATGCT	47699
Db	47640	GAAATTAATAATACGACCATTTGTAATAATCATGACGCAAGGAAATGCGCATGCT	47699
Oy	47700	CAACCGGCGATCCGTCGCGGTCAGTGCACAGGGTGTTCACGTGATCTTCCGAGAG	47759
Db	47700	CAACCGGCGATCCGTCGCGGTCAGTGCACAGGGTGTTCACGTGATCTTCCGAGAG	47759
Oy	47760	GTTTATCTCGCGCAACATATTTACGTGCGGTGACAGCGCGTTTTTTCACACACTTC	47819
Db	47760	GTTTATCTCGCGCAACATATTTACGTGCGGTGACAGCGCGTTTTTTCACACACTTC	47819
Oy	47820	GTTTATCTCGCGCAACATATTTACGTGCGGTGACAGCGCGTTTTTTCACACACTTC	47879
Db	47820	GTTTATCTCGCGCAACATATTTACGTGCGGTGACAGCGCGTTTTTTCACACACTTC	47879
Oy	47880	CACCGACCCGCGCGCGGAGAGTCCGTCGCGGCGGTGTCGCGATGAGTACT	47939
Db	47880	CACCGACCCGCGCGCGGAGAGTCCGTCGCGGCGGTGTCGCGATGAGTACT	47939
Oy	47940	GCCTCTGTTTACCAAAATGAAAAATTTATCCGTTGATGATGATATCTAAGGCCA	47999
Db	47940	GCCTCTGTTTACCAAAATGAAAAATTTATCCGTTGATGATGATATCTAAGGCCA	47999
Oy	48000	TACGCTGACTCTGGAAGCTCTGGAAGCTGGAAGTCTGTATATGCTTAAATGCGCG	48059
Db	48000	TACGCTGACTCTGGAAGCTCTGGAAGCTGGAAGTCTGTATATGCTTAAATGCGCG	48059
Oy	48060	TTACAGAAACGCAATGCGAGGTTTAAAGATTAAGTTTGAATGACGATGCGCGCT	48119
Db	48060	TTACAGAAACGCAATGCGAGGTTTAAAGATTAAGTTTGAATGACGATGCGCGCT	48119
Oy	48120	TGACGCTGAGGTTTCACTTAAACGCTTTAAAGAGGCTGTGATATCAACGCACTGC	48179
Db	48120	TGACGCTGAGGTTTCACTTAAACGCTTTAAAGAGGCTGTGATATCAACGCACTGC	48179
Oy	48180	TACGCAACCCGTCGCGCTGCAACCCCTTACAGATGTTGACGCGACTTACAGCTAG	48239
Db	48180	TACGCAACCCGTCGCGCTGCAACCCCTTACAGATGTTGACGCGACTTACAGCTAG	48239
Oy	48240	GGTACGGGACGACTACGTGACACACACCCTCGCTCGAAGCCCAAGTATGTAGGGG	48299
Db	48240	GGTACGGGACGACTACGTGACACACACCCTCGCTCGAAGCCCAAGTATGTAGGGG	48299
Oy	48300	ACAAATATCGCCCGGACGCGACCGAATGCGCAAAAGGATGCGGTAAGGCT	48359
Db	48300	ACAAATATCGCCCGGACGCGACCGAATGCGCAAAAGGATGCGGTAAGGCT	48359
Oy	48360	TGATTCGCGCTCCCAAAACAGCCAACTATCCAAAGAGCTGGGCGCAGGCGCTACGT	48419
Db	48360	TGATTCGCGCTCCCAAAACAGCCAACTATCCAAAGAGCTGGGCGCAGGCGCTACGT	48419
Oy	48420	TTTCTGCTCGCGCATATTTACGTGTGCTATATGATAAGAAATAGATACCAAGTG	48479
Db	48420	TTTCTGCTCGCGCATATTTACGTGTGCTATATGATAAGAAATAGATACCAAGTG	48479
Oy	48480	GCAGCGGCAAGATCCGCGCGCTTGCCGTACATTTGCTCGATCCGCTTACCTGTT	48539
Db	48480	GCAGCGGCAAGATCCGCGCGCTTGCCGTACATTTGCTCGATCCGCTTACCTGTT	48539
Oy	48540	AGAGGGCATTTGTTTAAAGAGCAAGCAAGATGCGTTTGCAGTTTAAAGAAAGC	48599
Db	48540	AGAGGGCATTTGTTTAAAGAGCAAGCAAGATGCGTTTGCAGTTTAAAGAAAGC	48599

OY	48600	GTGCAGGTGTCAGACATATACATTAAAGCAATTTTTCCGGTTTGTGATTAATAGGACAA	48659
Db	48600	GTGCAGGTGTCAGAACTATACATTAAAGCAATTTTTCCGGTTTGTGATTAATAGGACAA	48659
OY	48660	CGAAACAGTCGACTTAATAAGAGCAATTTATAGAGCGTGCCTGCTGATTAGAANCCA	48719
Db	48660	CGAAACAGTCGACTTAATAAGAGCAATTTATAGAGCGTGCCTGCTGATTAGAANCCA	48719
OY	48720	GGTGTCAAGAGAGACGCTTGGTAAAGGCGGCGCTTTTCGCAACGATAGTAACAGTA	48779
Db	48720	GGTGTCAAGAGAGACGCTTGGTAAAGGCGGCGCTTTTCGCAACGATAGTAACAGTA	48779
OY	48780	TTGGAAGGATGTTTTGGGATTAATGAGGACATGGCGCTCATPAAGCTGGGTACGGCTATAA	48839
Db	48780	TTGGAAGGATGTTTTGGGATTAATGAGGACATGGCGCTCATPAAGCTGGGTACGGCTATAA	48839
OY	48840	ACTACCAACATCGGAACCTTGCAATGGCCGACGTAACCTGGAGCTGGCTCCTGTGTACGA	48899
Db	48840	ACTACCAACATCGGAACCTTGCAATGGCCGACGTAACCTGGAGCTGGCTCCTGTGTACGA	48899
OY	48900	GGATATAACTGCGCAATTAATACCGGGAGCTACTGTTGGCTTAAGTGTCTCGCCACTACCT	48959
Db	48900	GGATATAACTGCGCAATTAATACCGGGAGCTACTGTTGGCTTAAGTGTCTCGCCACTACCT	48959
OY	48960	GACCGCCTGCTGCTCTCCGGGGGCTTTGTTATTAAAGGCGGCTACGACCTATACAG	49019
Db	48960	GACCGCCTGCTGCTCTCCGGGGGCTTTGTTATTAAAGGCGGCTACGACCTATACAG	49019
OY	49020	CGAGATTTATATGTTTGGGCTTGAGATATGGCCACCAGCCGTCGACATTCCTTAAT	49079
Db	49020	CGAGATTTATATGTTTGGGCTTGAGATATGGCCACCAGCCGTCGACATTCCTTAAT	49079
OY	49080	CGTTTTTAAACAGGAATGCATATGTTGGCAGACCCGGGTACGTCGCGCTTTGTTGGG	49139
Db	49080	CGTTTTTAAACAGGAATGCATATGTTGGCAGACCCGGGTACGTCGCGCTTTGTTGGG	49139
OY	49140	TATACACGCGACACATGCGCATTCCTCCGTTTTTGACCCGCGGTACTAAGCAAAATG	49199
Db	49140	TATACACGCGACACATGCGCATTCCTCCGTTTTTGACCCGCGGTACTAAGCAAAATG	49199
OY	49200	CGATGTCACCTAACTTTTTAAATGTTATGATCGTAATCATGAACCAAAAAGATTTGGCC	49259
Db	49200	CGATGTCACCTAACTTTTTAAATGTTATGATCGTAATCATGAACCAAAAAGATTTGGCC	49259
OY	49260	CGTGCGTTACCGTGTACATGAATGAGATATCTAGAATTTTTGTGCCACGGAATCTGTGC	49319
Db	49260	CGTGCGTTACCGTGTACATGAATGAGATATCTAGAATTTTTGTGCCACGGAATCTGTGC	49319
OY	49320	CCATTAAGGAGCGTCCGTGTAGGCGGACCTGTGTTAAATTCGTTTTGGTACCCCTTCTA	49379
Db	49320	CCATTAAGGAGCGTCCGTGTAGGCGGACCTGTGTTAAATTCGTTTTGGTACCCCTTCTA	49379
OY	49380	ATGCGCGGAGAGGAGGTTCCGATACCGGGCGGTTGAACCCACATCCGCGGAAAACTGTGC	49439
Db	49380	ATGCGCGGAGAGGAGGTTCCGATACCGGGCGGTTGAACCCACATCCGCGGAAAACTGTGC	49439
OY	49440	CCGGGCTAAACAAAACAGAAATTTATATACATTCGCAAAACAGTGCCTCAAGAGACATAC	49499
Db	49440	CCGGGCTAAACAAAACAGAAATTTATATACATTCGCAAAACAGTGCCTCAAGAGACATAC	49499
OY	49500	CAGATGCCATTAAGGGGAAAGAGATTCCACCAAAATAATCCGTTTTTGTGTTGACGGAG	49559
Db	49500	CAGATGCCATTAAGGGGAAAGAGATTCCACCAAAATAATCCGTTTTTGTGTTGACGGAG	49559
OY	49560	GGGGGTTTTGGCACTGTCTCTCTGTGATTTATAGTGCCTGTCCGCACTGCACA	49619
Db	49560	GGGGGTTTTGGCACTGTCTCTCTGTGATTTATAGTGCCTGTCTCCGCACTGCACA	49619
OY	49620	CAGTTCCGTCCCTGGCCAGAAATCGTTGGGCTTCTTACACAGTGCATTAAGACACGTGTA	49679
Db	49620	CAGTTCCGTCCCTGGCCAGAAATCGTTGGGCTTCTTACACAGTGCATTAAGACACGTGTA	49679
OY	49680	AAATTTGTACGGGGGCCACGTAACAGGTAACCCGATATGCGGATATACAGCCACCCTGACT	49739
Db	49680	AAATTTGTACGGGGGCCACGTAACAGGTAACCCGATATGCGGATATACAGCCACCCTGACT	49739
OY	49740	CGCAAGGACGTCACCTCGCTGCGCCCTGCTTATCTCGTGGGGGCGAGGGCGGGGG	49799
Db	49740	CGCAAGGACGTCACCTCGCTGCGCCCTGCTTATCTCGTGGGGGCGAGGGCGGGGG	49799
OY	49800	ATGTCCTGTTACCGGACAGGTTAATCTTTTGGGCGCTGCTCTTTGACCCCAAGGCTGCC	49859
Db	49800	ATGTCCTGTTACCGGACAGGTTAATCTTTTGGGCGCTGCTCTTTGACCCCAAGGCTGCC	49859
OY	49860	CCAAGTGAACCAAGCTGCGTTTTAAAGAAACCCACGCGCGGTACCGATAGAGACGCCA	49919
Db	49860	CCAAGTGAACCAAGCTGCGTTTTAAAGAAACCCACGCGCGGTACCGATAGAGACGCCA	49919
OY	49920	TGTCGGGGGTCACGCGCGGAAAGGACCGAGGTGCAACCCCACTTCGCTACCGTGGGCGCTCA	49979
Db	49920	TGTCGGGGGTCACGCGCGGAAAGGACCGAGGTGCAACCCCACTTCGCTACCGTGGGCGCTCA	49979
OY	49980	TTGCGCTGCGGATTTAGCCAGTCGCGGTATGCTATACGGCTGCGCAAGACTTAAAAAGA	50039
Db	49980	TTGCGCTGCGGATTTAGCCAGTCGCGGTATGCTATACGGCTGCGCAAGACTTAAAAAGA	50039
OY	50040	TCTGCTTACGTTCTTAATTAAGCAGTGCACACATCAGCGAATCGCGCCGCTCCGGG	50099
Db	50040	TCTGCTTACGTTCTTAATTAAGCAGTGCACACATCAGCGAATCGCGCCGCTCCGGG	50099
OY	50100	GCTCGGCTACAGATGCTTCGTTTTCTGTTTATGTTACAGTTCTTCGGGGAAACCA	50159
Db	50100	GCTCGGCTACAGATGCTTCGTTTTCTGTTTATGTTACAGTTCTTCGGGGAAACCA	50159
OY	50160	CCTGATTAACGTTGGCGATGACCTCGAGAGAAACGGCATTTGGGAGCTGTTTTGGTGGG	50219
Db	50160	CCTGATTAACGTTGGCGATGACCTCGGAGAAACGGCATTTGGGAGCTGTTTTGGTGGG	50219
OY	50220	CACGTAACCCAGTGAACGTTTTTCAACCGACAGAGAAAGACGCTGATTAATGGCCACAC	50279
Db	50220	CACGTAACCCAGTGAACGTTTTTCAACCGACAGAGAAAGACGCTGATTAATGGCCACAC	50279
OY	50280	GATCATGTTTTTCCCTGACGAGCGGGATTAACAAAACGCTGGCTTCGCTTAAACGT	50339
Db	50280	GATCATGTTTTTCCCTGACGAGCGGGATTAACAAAACGCTGGCTTCGCTTAAACGT	50339
OY	50340	CTGTAAACAGTCGCTCCGCTGTTTCAATTAACCAAGTGTGCTTAAACGTTGCAATTA	50399
Db	50340	CTGTAAACAGTCGCTCCGCTGTTTCAATTAACCAAGTGTGCTTAAACGTTGCAATTA	50399
OY	50400	CTGGTGTGCTTTTTGGGGTCTTTGATTAACGCGATTAATTAACGTTGCATGATTA	50459
Db	50400	CTGGTGTGCTTTTTGGGGTCTTTGATTAACGCGATTAATTAACGTTGCATGATTA	50459
OY	50460	TTGTTGTTAAAGGAGCTCAAGCAACAAACCCGGGACGTAATCTCCATTTAAAAATGA	50519
Db	50460	TTGTTGTTAAAGGAGCTCAAGCAACAAACCCGGGACGTAATCTCCATTTAAAAATGA	50519
OY	50520	CGACAGGTTGGCTAAAAACTGCCGCGATTCGTCATTAACGGGGCACTTAGAGAAAGCTTC	50579
Db	50520	CGACAGGTTGGCTAAAAACTGCCGCGAGTTCTGCATTAACGGGGCACTTAGAGAAAGCTTC	50579
OY	50580	GTCGGTCCGTTGGGCGGATTTGGTATTTCCATGTACGTGCTCTTGGGCTTGGCATTTTGGAC	50639
Db	50580	GTCGGTCCGTTGGGCGGATTTGGTATTTCCATGTACGTGCTCTTGGGCGTTCGCAATTTGGAC	50639
OY	50640	CCGACAAACATGTTTGTTTAAAGTAGTTTGTAGATTCTCGTGTTAACCGGGCAACAGTAGC	50699
Db	50640	CCGACAAACATGTTTGTTTAAAGTAGTTTGTAGATTCTCGGTAAACCGGGCAACAGTAGC	50699
OY	50700	GTCGCTAGAATAATCGGGGCTTTCACCAAGTAGGGGCGGCAATGGGCTTCTTGAACCTGCG	50759
Db	50700	GTCGCTAGAATAATCGGGGCTTTCACCAAGTAGGGGCGGCAATGGGCTTCTTGAACCTGCG	50759
OY	50760	GTAACGTTTAACATATGCTCTTAAAAACAATTAATATGTATTAACCGGCTGAATTAATCTTC	50819

QY	49680	AAATTTTACGGGGGCCACAGTACAGTTAACCCGATATGCGGATACACGCCACTGACT	49739
Db	49680	AAATTTTACGGGGGCCACAGTACAGTTAACCCGATATGCGGATACACGCCACTGACT	49739
QY	49740	CGCAAGGACCTACCCCTGCGCCGCTTATCTCGTGGGGGCAAGGCGGGGGG	49739
Db	49740	CGCAAGGACCTACCCCTGCGCCGCTTATCTCGTGGGGGCAAGGCGGGGGG	49739
QY	49800	ATGTCCTGCTTACCGGACAGCTTAATCTTTTGGGCGCTGCTTTTGACCCCAAGCCTCC	49859
Db	49800	ATGTCCTGCTTACCGGACAGCTTAATCTTTTGGGCGCTGCTTTTGACCCCAAGCCTCC	49859
QY	49860	CCAAAGTGACCAAGCTGCTTTAAAGAACCACGCCCGGATACCGATAGAGAGCCA	49919
Db	49860	CCAAAGTGACCAAGCTGCTTTAAAGAACCACGCCCGGATACCGATAGAGAGCCA	49919
QY	49920	TGTCGGGGGCTACGGCCGGAAGGAGACGAGGTGCAACCACTTCGTAACGCTGGGCGCTCA	49979
Db	49920	TGTCGGGGGCTACGGCCGGAAGGAGACGAGGTGCAACCACTTCGTAACGCTGGGCGCTCA	49979
QY	49980	TTGCGCTGCGGGATTTAGCAGTACGCGGTGATATGCTATACGGCTGCCAGACTTAAAAAGA	50039
Db	49980	TTGCGCGTGGGATTTAGCCAGTACGCGGTGATATGCTATACGGCTGCCAGACTTAAAAAGA	50039
QY	50040	TCCTCTTACGTTCTTATTTAAGACACGCGCACATCAGCAACTCGCGCGCGCTCCGG	50099
Db	50040	TCCTCTTACGTTCTTATTTAAGACACGCGCACATCAGCAACTCGCGCGCGCTCCGG	50099
QY	50100	GCCTGCGGTACAGATGGTTCGGTTTCCCTTTATGTTACAGTTCTTGCGCGGAACCA	50159
Db	50100	GCCTGCGGTACAGATGGTTCGGTTTCCCTTTATGTTACAGTTCTTGCGCGGAACCA	50159
QY	50160	CCTGGATAGCGTGCGACATCTGCGGAACAGCATTTGCGCAGCTGTTTGGTGGGCG	50219
Db	50160	CCTGGATAGCGTGCGACATCTGCGGAACAGCATTTGCGCAGCTGTTTGGTGGGCG	50219
QY	50220	CAGGTAAACCAAGTAAAGCTTTTCAACCCGAGAGAAAGCGTGAATAGGCGACAC	50279
Db	50220	CAGGTAAACCAAGTAAAGCTTTTCAACCCGAGAGAAAGCGTGAATAGGCGACAC	50279
QY	50280	GATCCATGTTTCCCGTAGACAGCGGGGATTAACAAAAGCGTTCCTGCTTAAACGT	50339
Db	50280	GATCCATGTTTCCCGTAGACAGCGGGGATTAACAAAAGCGTTCCTGCTTAAACGT	50339
QY	50340	CTGTAAACAGCTGCTGCTGTTTCAATAAACCAAGTGTGCTTAAACGTGGCAATTA	50399
Db	50340	CTGTAAACAGCTGCTGCTGTTTCAATAAACCAAGTGTGCTTAAACGTGGCAATTA	50399
QY	50400	CTGTGTGTCTTTTCCGGGCTCTTGTATGACGCGGATTAATAAAGCGTGTGATGTTAA	50459
Db	50400	CTGTGTGTCTTTTCCGGGCTCTTGTATGACGCGGATTAATAAAGCGTGTGATGTTAA	50459
QY	50460	TTTGTGTTGAAGGGCTCAAGGCAACAAACCCCGGGCAGCTAACCTCCATTTAAAAATGA	50519
Db	50460	TTTGTGTTGAAGGGCTCAAGGCAACAAACCCCGGGCAGCTAACCTCCATTTAAAAATGA	50519
QY	50520	CGACAGGTGGCTTAAAAATGCGCGAGTTCTGCATTAACGGGGCACTTAGGAAAAGCTTC	50579
Db	50520	CGACAGGTGGCTTAAAAATGCGCGAGTTCTGCATTAACGGGGCACTTAGGAAAAGCTTC	50579
QY	50580	GTCGGGTCCGTTGGGCGCATTTGATTCATGTACTGTGCTTGGCGCTTTGCCATTTTGGAC	50639
Db	50580	GTCGGGTCCGTTGGGCGCATTTGATTCATGTACTGTGCTTGGCGCTTTGCCATTTTGGAC	50639
QY	50640	CCGACACATGTTTGTTAAGGTAGTTTGTGAATCTCTCGGTTAACCGGGGCAACGTAAC	50699
Db	50640	CCGACACATGTTTGTTAAGGTAGTTTGTGAATCTCTCGGTTAACCGGGGCAACGTAAC	50699
QY	50700	GTGCGCTGAATATTCGGGGCTTTTCCCAACGTAAGGGGCGCGCATGAGGTTCTTGAACCTCTCGG	50759
Db	50700	GTGCGCTGAATATTCGGGGCTTTTCCCAACGTAAGGGGCGCGCATGAGGTTCTTGAACCTCTCGG	50759
QY	50760	GTAGCTTTGAAGATTAATCGTCTAATAACAGAACTATATGCAATTAACCGCGGTGAATATTC	50819

D	50760	GTACGTTGAAGATATATGCTGTAAACGAACTATATGCACTTAAACCGGTGAATACTCC	50819
Q	50820	CAGCATGGGTGGGCATTGCTGTGGTCTTGTCTGTGCCGATATTAATACGGCGGTG	50879
D	50820	CAAGCATGGGTGGGCATTGCTGTGGTCTTGTCTGTGCCGATTAATACGGCGGTG	50879
Q	50880	CCGAACACGATTTTCGCAACACCGCTCCGTACACACGGCAAGTATTTTGAACAGCTTC	50939
D	50880	CCGAACACGATTTTCGCAACACCGCTCCGTACACACGGCAAGTATTTTGAACAGCTTC	50939
Q	50940	CGCATAGCTGTAAACAACATGTTCCCTCAAGTTTTTGAATAACGGGACCCCGAAC	50999
D	50940	CGCATAGCTGTAAACAACATGTTCCCTCAAGTTTTTGAATAACGGGACCCCGAAC	50999
Q	51000	GGAAAGCGGCTGTTAAAGCGGTTCAGTTAGCTTTAGCACTGTGTACCAACATCCGGG	51059
D	51000	GGAAAGCGGCTGTTAAAGCGGTTCAGTTAGCTTTAGCACTGTGTACCAACATCCGGG	51059
Q	51060	ACAGTTTAACTAGTTGAACACCTCTCTAATAGTTTTCTTCGGTATCCAAAGCTTCGCC	51119
D	51060	ACAGTTTAACTAGTTGAACACCTCTCTAATAGTTTTCTTCGGTATCCAAAGCTTCGCC	51119
Q	51120	GGAATCGGCGCGGTTTANAGCTGTCCGCACACCGGAAGGTTTACCTTTGAACACATTCA	51179
D	51120	GGAATCGGCGCGGTTTANAGCTGTCCGCACACCGGAAGGTTTACCTTTGAACACATTCA	51179
Q	51180	CCTCCAAACATACACACGATCGACGCTGTCTGGGGGATACGACACATGTTAACAA	51239
D	51180	CCTCCAAACATACACACGATCGACGCTGTCTGGGGGATACGACACATGTTAACAA	51239
Q	51240	CGAGACACGTGCGTTAAACGTTAAAGCAAGTTCCTCGAATTACACAGGCTGCTTTTTA	51299
D	51240	CGAGACACGTGCGTTAAACGTTAAAGCAAGTTCCTCGAATTACACAGGCTGCTTTTTA	51299
Q	51300	TCGCGCGATGAGACGACGAAATGTTGGCGCTCAAGTTAGGAAGAACAGATGGT	51359
D	51300	TCGCGCGATGAGACGACGAAATGTTGGCGCTCAAGTTAGGAAGAACAGATGGT	51359
Q	51360	TAAATAGCTGTAGAGGGCTTGTCAAAATCCACAGACCTGGAAAGGTTTAGACCCGTGA	51419
D	51360	TAAATAGCTGTAGAGGGCTTGTCAAAATCCACAGACCTGGAAAGGTTTAGACCCGTGA	51419
Q	51420	TGCTTTACGCTCATATGAGGCTTGTCTTACGTTCCGGTCCGTCTGTGGGAAACAGA	51479
D	51420	TGCTTTACGCTCATATGAGGCTTGTCTTACGTTCCGGTCCGTCTGTGGGAAACAGA	51479
Q	51480	GTGCTATATGAAAGCAATTTTGGATGAAAGGACCATTACTCTTACCGCACATATGTA	51539
D	51480	GTGCTATATGAAAGCAATTTTGGATGAAAGGACCATTACTCTTACCGCACATATGTA	51539
Q	51540	TGCCCCCAAAAGACGTAATGACTTTTGTCCATCATATGTAATTAAGTAAATTTTTT	51599
D	51540	TGCCCCCAAAAGACGTAATGACTTTTGTCCATCATATGTAATTAAGTAAATTTTTT	51599
Q	51600	ATACGTGAACCCCGGTGGGGCTTGTGAACGTAACGCTCCCGCGCTTCGAGCGCTCGC	51659
D	51600	ATACGTGAACCCCGGTGGGGCTTGTGAACGTAACGCTCCCGCGCTTCGAGCGCTCGC	51659
Q	51660	GTGGGGCGACCATCGCTGCTTCGGGGAGCTGAAAGCGGATGACGATACCTGTCGCC	51719
D	51660	GTGGGGCGACCATCGCTGCTTCGGGGAGCTGAAAGCGGATGACGATACCTGTCGCC	51719
Q	51720	AAAGTGATTTGTGTACCTGTACCGGTACAGCAAAAGATACATTTCCATGTATGAACACA	51779
D	51720	AAAGTGATTTGTGTACCTGTGTACCGGTGTACAGCAAAAGATACATTTCCATGTATGAACACA	51779
Q	51780	CGTGGGCGAATCATCCGATTAAGCGGAGAGCGGTGCAGATATTAACGCTTACGTTCC	51839
D	51780	CGTGGGCGAATCATCCGATTAAGCGGAGAGCGGTGCAGATATTAACGCTTACGTTCC	51839
Q	51840	GGCTCAACGGTGCACGAGTGGGGAGATTTTGTATATCCCTGTACAAATTTGAAG	51899
D	51840	GGCTCAACGGTGCACGAGTGGGGAGATTTTGTATATCCCTGTACAAATTTGAAG	51899
Q	51900	GCTCTAGCATATATAAGGAACATGCGCTCGGCACACTATAAAAAATGTAATTAAGT	51959
D	51900	GCTCTAGCATATATAAGGAACATGCGCTCGGCACACTATAAAAAATGTAATTAAGT	51959
Q	51960	CGAGCTCGAGTGGAAATCAACAAAAAATCTGCATCTCCGATTTTGAAGGTTGGGG	52019
D	51960	CGAGCTCGAGTGGAAATCAACAAAAAATCTGCATCTCCGATTTTGAAGGTTGGGG	52019
Q	52020	CCGACAGTGCCTGTTTAAACGCGCAGTATTAAGGAACACGGGAATCGCTGCGGTACA	52079
D	52020	CCGACAGTGCCTGTTTAAACGCGCAGTATTAAGGAACACGGGAATCGCTGCGGTACA	52079
Q	52080	ACAGCCTAAAAAAGAGGAGATCTGGGACCGTTTCGAAACGGTAGAAACGTCGCTGC	52139
D	52080	ACAGCCTAAAAAAGAGGAGATCTGGGACCGTTTCGAAACGGTAGAAACGTCGCTGC	52139
Q	52140	GTGAAAAACAAAGCGAATTTGGATTCTAAGGGGTTTAAAGAAAAAATTTGAAGAT	52199
D	52140	GTGAAAAACAAAGCGAATTTGGATTCTAAGGGGTTTAAAGAAAAAATTTGAAGAT	52199
Q	52200	TTGACGCTGGGGGAGCGGGTTCCGACCTCAAGGACGAGCTGTACGGAACGTGGAGA	52259
D	52200	TTGACGCTGGGGGAGCGGGTTCCGACCTCAAGGACGAGCTGTACGGAACGTGGAGA	52259
Q	52260	TTCTAGGTACGCTTGCAATGATCTGTTCCGTTGGGAAAGAGTCCCCAAAGAGACACA	52319
D	52260	TTCTAGGTACGCTTGCAATGATCTGTTCCGTTGGGAAAGAGTCCCCAAAGAGACACA	52319
Q	52320	TTATTTAGTGGAAATGAGACCGTCCGACAGTGGCCCAAAAGCCCTGTATCCCAT	52379
D	52320	TTATTTAGTGGAAATGAGACCGTCCGACAGTGGCCCAAAAGCCCTGTATCCCAT	52379
Q	52380	CCCAAGGTTCAGACTACGTCGACAAACAGATCTCCCAATTAACGCTCATTTAAACA	52439
D	52380	CCCAAGGTTCAGACTACGTCGACAAACAGATCTCCCAATTAACGCTCATTTAAACA	52439
Q	52440	CGTAAGCAGTCCGCCAAGTAAAGATCTTAACACTGGGGCACTGTATGTACACAGCG	52499
D	52440	CGTAAGCAGTCCGCCAAGTAAAGATCTTAACACTGGGGCACTGTATGTATACACAGCG	52499
Q	52500	ACGAGTGGACCGCGCTGCTCGGAGCGGCTGTATGGTGGTGGGTCATGCTCTCC	52559
D	52500	ACGAGTGGACCGCGCTGCTCGGAGCGGCTGTATGGTGGTGGGTCATGCTCTCC	52559
Q	52560	GGCGGCTGGTTAAGCATTTTGGACCGCGGCTGAGTCTTTTACGAGTGCAATTTTAAC	52619
D	52560	GGCGGCTGGTTAAGCATTTTGGACCGCGGCTGAGTCTTTTACGAGTGCAATTTTAAC	52619
Q	52620	GATATAGTACGGCCCGCGGAGAAACATCCCTGAAACCGGGGGGTGACCGTATACA	52679
D	52620	GATATAGTACGGCCCGCGGAGAAACATCCCTGAAACCGGGGGGTGACCGTATACA	52679
Q	52680	TGTTTCTTAGAGCGCGGTACCATGTGCGGCTCGATATTCGCGAGTTAAC	

OY	52980	AAACTGGGTTCTGTCAGCACACGTAACATTTTAAAGCACCGGCACAGATTTATCTGAAG	53039
Db	52980	AAACTCGGGTTCCTGTCAGCACACGTAACATTTTAAAGCACCGGCACAGATTTATCTGAAG	53039
OY	53040	CACATTTACGGGGCGTCGTCTCCTACCCGTCCTGCTGTCGTGGCGCGGGGGCCCG	53099
Db	53040	CACATTTACGGGGCGTCGTCTCCTACCCGTCCTGCTGTCGTGGCGCGGGGGCCCG	53099
OY	53100	CAGGCGCATATGCTAAATCAGCCGTTTCCAAATACCTCCACAACCTGGCTCCAAATTTGAC	53159
Db	53100	CAGGCGCATATGCTAAATCAGCGGTTTCCAAATACCTCCACAACCTGGCTCCAAATTTGAC	53159
OY	53160	ATATTCCTCCCTGGGTTATAGTTTGTACGATGCTATGAGAATATCTTAGCCAGCTGAC	53219
Db	53160	ATATTCCTCCCTGGGTTATAGTTTGTACGATGCTATGAGAATATCTTAGCCAGCTGAC	53219
OY	53220	CCATTTTCCCGACAGAGGAGGCGTTGGGGGAGCGTCTCCGGAATCCGCCACCATTTGTTCC	53279
Db	53220	CCATTTTCCCGACAGAGGAGGCGTTGGGGGAGCGTCTCCGGAATCCGCCACCATTTGTTCC	53279
OY	53280	TATTTGCGTTGCATAGTGCCACAGAGTAATCATGCCCCGAGATTTTTCGTGGCTGGGAC	53339
Db	53280	TATTTGCGTTGCATAGTGCGCCACAGAGTAATCATGCCCCGAGATTTTTCGTGGCGGAC	53339
OY	53340	GTTCACACTGCATTTTAGGCAATGATGCTATGCGCACGCGCCACGCTATTCCTCGTAGAGAA	53399
Db	53340	GTTCACACTGCATTTTAGGCAATGATGCTATGCGCACGCGCCACGCTATTCCTCGTAGAGAA	53399
OY	53400	GCGTCACAGGCGGTTTTTTTGGCCAAACAGTAGTAGTTTATATAGGGCGCAATACAAAGAGAT	53459
Db	53400	GCGTCACAGGCGGTTTTTTTGGCCAAACAGTAGTAGTTTATATAGGGCGCAATACAAAGAGAT	53459
OY	53460	GCGTTTACAAAACCCATCTCTCGGGCTGTGAATCTCAAACCTTAACCTAGTTCTCCAGAG	53519
Db	53460	GCGTTTACAAAACCCATCTCTCGGGCTGTGAATCTCAAACCTTAACCTAGTTCTCCAGAG	53519
OY	53520	CTGTTGGTCAAGGCACTACTTTAGTCATTCGCGAAATCGCGAGATCATGATTTTTCCTC	53579
Db	53520	CTGTTGGTCAAGGCACTACTTTAGTCATTCGCGAAATCGCGAGATCATGATTTTTCCTC	53579
OY	53580	AGATGACCCGATGTTTCAGGAGATGGCGCTTCTCCATCATGATGAGCAGACGGCTCCT	53639
Db	53580	AGATGACCCGATGTTTCAGGAGATGGCGCTTCTCCATCATGATGAGCAGACGGCTCCT	53639
OY	53640	CTCGAAATATAGCCTGGCCCAACTTTTAAACATGAGCAGTAAGGGCGCTTTTAAAGCA	53699
Db	53640	CTCGAAATATAGCCTGGCCCAACTTTTAAACATGAGCAGTAAGGGCGCTTTTAAAGCA	53699
OY	53700	TAAACAAAAGAAATAAGATGCGGCTATACGTTTCGTATTAATTTTATCTATTCGC	53759
Db	53700	TAAACAAAAGAAATAAGATGCGGCTATACGTTTCGTATTAATTTTATCTATTCGC	53759
OY	53760	CAAGGTGGGAGTTTTTATGGGCAACACGACGTCAGATTTTACGTACTTGGGTGT	53819
Db	53760	CAAGGTGGGAGTTTTTATGGGCAACACGACGTCAGATTTTACGTACTTGGGTGT	53819
OY	53820	CAGGGGAGGCGCTGACGCGCCTGTTCGGAAGTATACGACGCGTGCTTAAACATGACCC	53879
Db	53820	CAGGGGAGGCGCTGACGCGCCTGTTCGGAAGTATACGACGCGTGCTTAAACATGACCC	53879
OY	53880	GCACGATTCGACACACAGCTGTGTGCTATTTGATAGAACAGTTCACGGCGCCAAAACATCAA	53939
Db	53880	GCACGATTCGACACACAGCTGTGTGCTATTTGATAGAACAGTTCACGGCGCCAAAACATCAA	53939
OY	53940	TTCCTTGTGGAGGCTCTGAGGAGCGGATATATTTGCTGTCGTCAAAATTTCACTGGGCCAT	53999
Db	53940	TTCCTTGTGGAGGCTCTGAGGAGCGGATATATTTGCTGTCGTCAAAATTTCACTGGGCCAT	53999
OY	54000	AAAAACAACAATTCGTCCAAAAAATTTTAAACCCGTGGCCTATATGTCAAACATCATTT	54059
Db	54000	AAAAACAACAATTCGTCCAAAAAATTTTAAACCCGTGGCCTATATGTCAAACATCATTT	54059

QY	54060	TGTAGCGGGCCCGCTGCGCTTTGGACTGCGTTGCCAGAAAGTGTTAAAAAGATACGTGC	54119
Db	54060	TGTAGCGGGCCCGCTGCGCTTTGGACTGCGTTGCCAGAAAGTGTTAAAAAGATACGTGC	54119
QY	54120	GAGTTGCTCATCCAGGGGAGCGACGTGTAAGAACTACGGATTCAAGAGAGTCCT	54179
Db	54120	GAGTTGCTCATCCAGGGGAGCGACGTGTAAGAACTACGGATTCAAGAGAGTCCT	54179
QY	54180	CAACGGGGTTTTGGGGTCTCTTGGATTGGAAATTAACGTACAGTCTGCACCCAAAGA	54239
Db	54180	CAACGGGGTTTTGGGGTCTCTTGGATTGGAAATTAACGTACAGTCTGCACCCAAAGA	54239
QY	54240	CGGTTTGGAGTTCCACCCAGACTGCAAAATCTATGAATTAATATCCGGTTTAAGTACAC	54299
Db	54240	CGGTTTGGAGTTCCACCCAGACTGCAAAATCTATGAATTAATATCCGGTTTAAGTACAC	54299
QY	54300	TTTTTCCAAATGGACTGTGACCCGATTTAACCTGGTATGCTAAACTTTATCAAGAACCC	54359
Db	54300	TTTTTCCAAATGGACTGTGACCCGATTTAACCTGGTATGCTAAACTTTATCAAGAACCC	54359
QY	54360	CAGCATGCAGACGCTTAAAGGGTTTTTGTACTCATATCTAAACCGGAGTCGATTTGT	54419
Db	54360	CAGCATGCAGACGCTTAAAGGGTTTTTGTACTCATATCTAAACCGGAGTCGATTTGT	54419
QY	54420	CGGAGAGGACAGGCTCCCAAGTGAATCGGACTATCTTGTGGCATATGACAAAGATGGGA	54479
Db	54420	CGGAGAGGACAGGCTCCCAAGTGAATCGGACTATCTTGTGGCATATGACAAAGATGGGA	54479
QY	54480	GGTGTGCCGGGAAAAAGAGACGCTTAACCTCAGACACCACTACGTATTAAGTAATGGAT	54539
Db	54480	GGTGTGCCGGGAAAAAGAGACGCTTAACCTCAGACACCACTACGTATTAAGTAATGGAT	54539
QY	54540	GATTCAACAATCTACGGCGCCTTCTATGTATATATGTGAGATCCGAGAAACCGG	54599
Db	54540	GATTCAACAATCTACGGCGCCTTCTATGTATATATGTGAGATCCGAGAAACCGG	54599
QY	54600	AGGCAAAATTAATTAAGCTCATGTGAGCCCAACCTATTATTAACGTCAGGCAATCC	54659
Db	54600	AGGCAAAATTAATTAAGCTCATGTGAGCCCAACCTATTATTAACGTCAGGCAATCC	54659
QY	54660	GTAATTATTACAGTGTGCTCCAGTCTCTGTTGTACAGAGATACATCAGTCTCCAA	54719
Db	54660	GTAATTATTACAGTGTGCTCCAGTCTCTGTTGTACAGAGATACATCAGTCTCCAA	54719
QY	54720	GGGAATTAATTTGGGAACCCAGAAAACTTTATAGGACTGGCTTTTTAGAAAAAG	54779
Db	54720	GGGAATTAATTTGGGAACCCAGAAAACTTTATAGGACTGGCTTTTTAGAAAAAG	54779
QY	54780	GCAGTTTCAAGACCGAGCTGTGCACGATCGGTGAATTTGCCCGTTGGATCCACAGT	54839
Db	54780	GCAGTTTCAAGACCGAGCTGTGCACGATCGGTGAATTTGCCCGTTGGATCCACAGT	54839
QY	54840	AGAGATACGACCCCTTTAATGTGACACCGGTGATTTTCCACGTGGCCAAACCA	54899
Db	54840	AGAGATACGACCCCTTTAATGTGACACCGGTGATTTTCCACGTGGCCAAACCA	54899
QY	54900	ACGTGGTAACGAGCGACGCAATTCGGCGGCTAGTGTGTTGAAGGATTTCCCGAGCT	54959
Db	54900	ACGTGGTAACGAGCGACGCAATTCGGCGGCTAGTGTGTTGAAGGATTTCCCGAGCT	54959
QY	54960	ACCATGGGATTATCTCTCTGTGTGCAACAGCCCCACCACACCGTAGATGTGAAGGG	55019
Db	54960	ACCATGGGATTATCTCTCTGTGTGCAACAGCCCCACCACACCGTAGATGTGAAGGG	55019
QY	55020	GAGCCCATAGATGTATCCAAAGAAATTCGATCTATTATAGGAAGAAAGCATGTCTTGG	55079
Db	55020	GAGCCCATAGATGTATCCAAAGAAATTCGATCTATTATAGGAAGAAAGCATGTCTTGG	55079
QY	55080	TTTAACGGCAGATGGAGCTGCCCGGGGGCGGTGTACAAAACCCAAACCAAGCATCCAAA	55139
Db	55080	TTTAACGGCAGATGGAGCTGCCCGGGGGCGGTGTACAAAACCCAAACCAAGCATCCAAA	55139
QY	55140	CATAAAAACAATTAATGTGCAGATTTTGTTTAAGCATTCGTATCTTTATGTGAGTGGGGT	55199

Db	55140	CAATAAAACAATAATTTGTCAGATTTTGTTTAAGCATTCGTATCTTTATTTGAGTGGGCT	55199	
Qy	55200	GGATGGTGGGGGTGGGAAGGGAATGGGATTGAGGGGAGATGAATGCTGAATCATATA	55259	
Db	55200	GGATGGTGGGGGTGGGAAGGGAATGGGATTGAGGGGAGATGAATGCTGAATCATATA	55259	
Qy	55260	TGTATTTTGGATATGTCATCTCTGTAATGCGTCTCAGCTCTTCTTCTGTTTCATATTAACGCT	55319	
Db	55260	TGTATTTTGGATATGTCATCTCTGTAATGCGTCTCAGCTCTTCTTCTGTTTCATATTAACGCT	55319	
Qy	55320	TCAGTTCGGGGAGTACTTAATCTTGTGCTTCCTTCCTTAGGGCTTGAGGAAGGGTG	55379	
Db	55320	TCAGTTCGGGGAGTACTTAATCTTGTGCTTCCTTCCTTAGGGCTTGAGGAAGGGTG	55379	
Qy	55380	CGFATTTGGGGGACCTTTGCGCACCATTTCCAACTCGTTTCTGATTAATTTCTTAAGATGATG	55439	
Db	55380	CGFATTTGGGGGACCTTTGCGCACCATTTCCAACTCGTTTCTGATTAATTTCTTAAGATGATG	55439	
Qy	55440	CTAGATGCAAGTGTGCGGAATCATAGAGATGTTCAAGCGCTATGACTTTGTCCAGGCTGG	55499	
Db	55440	CTAGATGCAAGTGTGCGGAATCATAGAGATGTTCAAGCGCTATGACTTTGTCCAGGCTGG	55499	
Qy	55500	CAGATATGAATACCTTGTGCTGTCAGACGAGGGAAGAAGCAATCAGGTAACTGACAA	55559	
Db	55500	CAGATATGAATACCTTGTGCTGTCAGACGAGGGAAGAAGCAATCAGGTAACTGACAA	55559	
Qy	55560	AAACGCCAACGTAGAATCCGATCTGCTTGTAGTACTTTACTAGAAATAGTCTGTGT	55619	
Db	55560	AAACGCCAACGTAGAATCCGATCTGCTTGTAGTACTTTACTAGAAATAGTCTGTGT	55619	
Qy	55620	TGATTTACCAAGCTTTGTGAAGGACAAAAACAATTTATTAACCAAGACAAATATCGG	55679	
Db	55620	TGATTTACCAAGCTTTGTGAAGGACAAAAACAATTTATTAACCAAGACAAATATCGG	55679	
Qy	55680	AAACGAGATATAGAACTGTTTCCATAGCCATCATGCTTCGAGGGAGGAATTAACA	55739	
Db	55680	AAACGAGATATAGAACTGTTTCCATAGCCATCATGCTTCGAGGGAGGAATTAACA	55739	
Qy	55740	TCTCCATGGCTATTAAAGACAGATTAAGTGGCGCAATCGTTTCCGTAACGCACA	55799	
Db	55740	TCTCCATGGCTATTAAAGACAGATTAAGTGGCGCAATCGTTTCCGTAACGCACA	55799	
Qy	55800	GGGTGCTAGCAAGCTATTTCCAGGAATCTGCTGCTTAAGACGGGTGAGAACCCAGTGG	55859	
Db	55800	GGGTGCTAGCAAGCTATTTCCAGGAATCTGCTGCTTAAGACGGGTGAGAACCCAGTGG	55859	
Qy	55860	CCGAAATGCAGATATCATAGCTGAGCTGAGTAAAGCATAGCAAAAAATGTATACAT	55919	
Db	55860	CCGAAATGCAGATATCATAGCTGAGCTGAGTAAAGCATAGCAAAAAATGTATACAT	55919	
Qy	55920	ATACAAACGAGGCTAAAAGTATGTGTGTACGACAGAAACGGATTAATTAATCTGATGG	55979	
Db	55920	ATACAAACGAGGCTAAAAGTATGTGTGTGTACGACAGAAACGGATTAATTAATCTGATGG	55979	
Qy	55980	TCACAGGCTCAAAATATACATTAATAACTACACGTGGAGGCTTGTGACACGATCCATG	56039	
Db	55980	TCACAGGCTCAAAATATACATTAATAACTACACGTGGAGGCTTGTGACACGATCCATG	56039	
Qy	56040	TCTGAGGCTGTCATTTGTTCGCTGACGCGCTTGGCTTGAATATGGCCAGATGG	56099	
Db	56040	TCTGAGGCTGTCATTTGTTCGCTGACGCGCTTGGCTTGAATATGGCCAGATGG	56099	
Qy	56100	CCACAGCATAGTAAACACAGAGATATCCGTCACACAAAAAGCCACAGATGTAGACAA	56159	
Db	56100	CCACAGCATAGTAAACACAGAGATATCCGTCACACAAAAAGCCACAGATGTAGACAA	56159	
Qy	56160	ACATTTTGGTGGTTCCTCAAAAAACAAGTGGCGCTAGATGTTTAGACAACCTTCCAGCG	56219	
Db	56160	ACATTTTGGTGGTTCCTCAAAAAACAAGTGGCGCTAGATGTTTAGACAACCTTCCAGCG	56219	
Qy	56220	TTAGGTTTAACGCGCTAGTGTGACCAACGTGTTAAATAGACGGAATCCAAGTCCG	56279	
Db	56220	TTAGGTTTAACGCGCTAGTGTGACCAACGTGTTAAATAGACGGAATCCAAGTCCG	56279	

Db	56220	TTAGGTTTAACGCGCTAGTGTGACCAACGTGTTAAAGTACGACGGAATCCAAGTCCG	56279	
Qy	56280	GGAAATGTGGCGGTCAAGTGGCACTACCGCTGACATTAATAAATAGTCCAGAAATPACCA	56339	
Db	56280	GGAAATGTGGCGGTCAAGTGGCACTACCGCTGACATTAATAAATAGTCCAGAAATPACCA	56339	
Qy	56340	GTAAGTTTACCATGACGATTAAGATTAACGATCCGTCGCTGAATTTTTCATAGTTCAAA	56399	
Db	56340	GTAAGTTTACCATGACGATTAAGATTAACGATCCGTCGCTGAATTTTTCATAGTTCAAA	56399	
Qy	56400	GAATCTGCTCGGGGGGCTTGGCAACTACAGTAATTAATGACAAAGTGGCTTACATGT	56459	
Db	56400	GAATCTGCTCGGGGGGCTTGGCAACTACAGTAATTAATGACAAAGTGGCTTACATGT	56459	
Qy	56460	TACGGAATTTAAATAGGCTCCGTTTAAATATACATCTGTGCAAAAGGATTTGAGCCAC	56519	
Db	56460	TACGGAATTTAAATAGGCTCCGTTTAAATATACATCTGTGCAAAAGGATTTGAGCCAC	56519	
Qy	56520	GGCACCATTGAACGCCCGGAGGTGGCAGTCAAGGACATGTTTGCACATATCGCTGAT	56579	
Db	56520	GGCACCATTGAACGCCCGGAGGTGGCAGTCAAGGACATGTTTGCACATATCGCTGAT	56579	
Qy	56580	AGCAGCACAGCGCGAGAAATTAATTAATCTGGAGTTTCAATTACTTGTATGTAACAA	56639	
Db	56580	AGCAGCACAGCGCGAGAAATTAATTAATCTGGAGTTTCAATTACTTGTATGTAACAA	56639	
Qy	56640	TGCGGAATTCAGGAGAGTCCGATATCTATTTGTACCGAAACATTAAGCAATACGAC	56699	
Db	56640	TGCGGAATTCAGGAGAGTCCGATATCTATTTGTACCGAAACATTAAGCAATACGAC	56699	
Qy	56700	TGGGGAATTAATACCGGCAATTAACCGTACGACCGCTCATTAATAGACAGCGCGTAT	56759	
Db	56700	TGGGGAATTAATACCGGCAATTAACCGTACGACCGCTCATTAATAGACAGCGCGTAT	56759	
Qy	56760	TATATGACAGTGGGAATCCGTAAGTGTACGGAATCCCATGTTCAATTTGTTAAGTGC	56819	
Db	56760	TATATGACAGTGGGAATCCGTAAGTGTACGGAATCCCATGTTCAATTTGTTAAGTGC	56819	
Qy	56820	CAGCCCGGTGCGGTTAAGCTAAGGTCACAGACCGCAATATGTAATAGTGGTGGCA	56879	
Db	56820	CAGCCCGGTGCGGTTAAGCTAAGGTCACAGACCGCAATATGTAATAGTGGTGGCA	56879	
Qy	56880	CGAGGCTTGATCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	56939	
Db	56880	CGAGGCTTGATCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	56939	
Qy	56940	ACTATGACTTATGTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTG	56999	
Db	56940	ACTATGACTTATGTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTG	56999	
Qy	57000	ATGTTTCTCACTGTTTACATTTCAACATTTGAATTTGATTTGATTTGATTTGATTTG	57059	
Db	57000	ATGTTTCTCACTGTTTACATTTCAACATTTGAATTTGATTTGATTTGATTTGATTTG	57059	
Qy	57060	TACTATAGGCGATTCAGTGGCCAGCAATGCCAAAAAGGGCAAGATGGCGCATTTGGGT	57119	
Db	57060	TACTATAGGCGATTCAGTGGCCAGCAATGCCAAAAAGGGCAAGATGGCGCATTTGGGT	57119	
Qy	57120	ATTTCTGATATCTTTAATTTGCAATCTCGTGAATTAACAAGTTGCCGGCAGAAATACAC	57179	
Db	57120	ATTTCTGATATCTTTAATTTGCAATCTCGTGAATTAACAAGTTGCCGGCAGAAATACAC	57179	
Qy	57180	TTGAGTATGCGCCAGCAATTTACGTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	57239	
Db	57180	TTGAGTATGCGCCAGCAATTTACGTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	57239	
Qy	57240	GGGGCCCTGGCGGAATTTTAAAGGCGCTGACAAATTAAGTTTGGGACCGGGAAGGC	57299	
Db	57240	GGGGCCCTGGCGGAATTTTAAAGGCGCTGACAAATTAAGTTTGGGACCGGGAAGGC	57299	
Qy	57300	GTAAGGCAACGTTTAACGTAGTGTGCTGGGGGCGCACTCCGAGAGGAACCCCTTCCCG	57359	
Db	57300	GTAAGGCAACGTTTAACGTAGTGTGCTGGGGGCGCACTCCGAGAGGAACCCCTTCCCG	57359	

OY	57360	CCCTACTTTTCCGCGTTTCCACACGTCGCCGTGCTGTTTGGAAAGACGCGGAAGGCTGCAC	57419
Db	57360	CCCTACTTTTCCGCGTTTCCACACGTCGCCGTGCTGTTTGGAAAGACGCGGAAGGCTGCAC	57419
OY	57420	GTAACCGCGGTCCAAAGACACTCCAAAGCACAAAATTGGCGTACACTGGGCCCCGTTTAA	57479
Db	57420	GTAACCGCGGTCCAAAGACACTCCAAAGCACAAAATTGGCGTACACTGGGCCCCGTTTAA	57479
OY	57480	GATTTCATCTTAGGGGATCAGCTTCTCATACCTGGCATTTTCACCTAAAAGCGAGTACC	57539
Db	57480	GATTTCATCTTAGGGGATCAGCTTCTCATACCTGGCATTTTCACCTAAAAGCGAGTACC	57539
OY	57540	GTACCCGTTGTTGGCGCGCTTGGTGGGAGATGTTAACTGACGTCCTCGCAGACGACA	57599
Db	57540	GTACCCGTTGTTGGCGCGCTTGGTGGGAGATGTTAACTGACGTCCTCGCAGACGACA	57599
OY	57600	GAAAGCGTTCCCGCATATGCGACGCCACATTCATATGTAAATCATAAATTTTCATCACG	57659
Db	57600	GAAAGCGTTCCCGCATATGCGACGCCACATTCATATGTAAATCATAAATTTTCATCACG	57659
OY	57660	TTGTGCGACGACCTAAAAATGCCACCGCTGGCTTGTAAAAATGAGTTAGAAATACATAGCA	57719
Db	57660	TTGTGCGACGACCTAAAAATGCCACCGCTGGCTTGTAAAAATGAGTTAGAAATACATAGCA	57719
OY	57720	ACCATCTGTTCACGACCACTTCCGCTCTTCATCAAGAGGAATACACCGGTACTTGCC	57779
Db	57720	ACCATCTGTTCACGACCACTTCCGCTCTTCATCAAGAGGAATACACCGGTACTTGCC	57779
OY	57780	ACCATCTGTTCACGACCACTTCCGCTCTTCATCAAGAGGAATACACCGGTACTTGCC	57779
Db	57780	ACCATCTGTTCACGACCACTTCCGCTCTTCATCAAGAGGAATACACCGGTACTTGCC	57779
OY	57840	GTAATTCATCAAGGCTCCCAAGCTCAGCGCAGCTGTAAGTGTTTCTGCCCATCACTAAAT	57899
Db	57840	GTAATTCATCAAGGCTCCCAAGCTCAGCGCAGCTGTAAGTGTTTCTGCCCATCACTAAAT	57899
OY	57900	AGTTGCCGTAGGAAACAATGTTACGAAGGTTAAAAATACACGTCTATTCTTTCACAG	57959
Db	57900	AGTTGCCGTAGGAAACAATGTTACGAAGGTTAAAAATACACGTCTATTCTTTCACAG	57959
OY	57960	AACGACAAAAGTCGTGACCCGCTTGAAGGCGATTTGGAGTCCCGGTACAGAAACTT	58019
Db	57960	AACGACAAAAGTCGTGACCCGCTTGAAGGCGATTTGGAGTCCCGGTACAGAAACTT	58019
OY	58020	CCCAACCCGCTGACCTGAGCTCAAGTGTGAGGCTGCTCCGCGTCCGTTTAAAAATAC	58079
Db	58020	CCCAACCCGCTGACCTGAGCTCAAGTGTGAGGCTGCTCCGCGTCCGTTTAAAAATAC	58079
OY	58080	CAGCGCGGGGTTTGTATGCCGGGACTGGCAAGACCCCAACGAGGAAGAAACCGGGACT	58139
Db	58080	CAGCGCGGGGTTTGTATGCCGGGACTGGCAAGACCCCAACGAGGAAGAAACCGGGACT	58139
OY	58140	CGTGGCTGGACTGTCTAGTGAAGAGGCGAGCTGTTGCTTAAACACTCAGTGTACCGA	58199
Db	58140	CGTGGCTGGACTGTCTAGTGAAGAGGCGAGCTGTTGCTTAAACACTCAGTGTACCGA	58199
OY	58200	TTGGGCGCTGCGGGGTATCTTAACCAACCTTTTGCACAACGCGGTGTGTTAATTTT	58259
Db	58200	TTGGGCGCTGCGGGGTATCTTAACCAACCTTTTGCACAACGCGGTGTGTTAATTTT	58259
OY	58260	GGCGTGGTGCACGCGGTGGGTAAATGGCGGCCCATATGGCTCCCGTACCGAGTGA	58319
Db	58260	GGCGTGGTGCACGCGGTGGGTAAATGGCGGCCCATATGGCTCCCGTACCGAGTGA	58319
OY	58320	GTTGTACGCTCCACAGTGTGTGTCACAAGAGGTGAGACCAATCTGTTGTAAGGAAT	58379
Db	58320	GTTGTACGCTCCACAGTGTGTGTCACAAGAGGTGAGACCAATCTGTTGTAAGGAAT	58379
OY	58380	GGCGGTTACCGGTTGACGTTGATTTATGTACTACTACAGAGGACATATGTGTTT	58439
Db	58380	GGCGGTTACCGGTTGACGTTGATTTATGTACTACTACAGAGGACATATGTGTTT	58439

QY	58440	GTGTTGTCTCCACGGGGAGGGTACGAGAGTCAACCGGACAAATATACGACAATTAGAGA	58439
Db	58440	GTGTTGTCTCCACGGGGAGGGTACGAGAGTCAACCGGACAAATATACGACAATTAGAGA	58439
QY	58500	AGTTGAAGAAGTACTATGTTTATTTTAAACAGAGTCGTCTGGGGATCGCTGTAGGC	58559
Db	58500	AGTTGAAGAAGTACTATGTTTATTTTAAACAGAGTCTGTCTGGGGATCGCTGTAGGC	58559
QY	58560	TGTTTATTTGAAAAATATTTTAAATACGCATGCGTTATGAAAGTGTGTGTAATAATTGTC	58619
Db	58560	TGTTTATTTGAAAAATATTTTAAATACGCATGCGTTATGAAAGTGTGTGTAATAATTGTC	58619
QY	58620	CGCAATAAATATGTTAAAGTCTCCGGTGGCCCTCTTCTTCTCCAACTCTCTGTTA	58679
Db	58620	CGCAATAAATATGTTAAAGTCTCCGGTGGCCCTCTTCTTCTCCAACTCTCTGTTA	58679
QY	58680	GACGAAAGATTTCCAAATAAATGGGTTTCAGTAACCTTCACTGTCGCTGGGTTTGT	58739
Db	58680	GACGAAAGATTTCCAAATAAATGGGTTTCAGTAACCTTCACTGTCGCTGGGTTTGT	58739
QY	58740	CCAACAGCTTATGAGATTGGAACCCACTAGGGGGGGAACGCGCAAAATGCTTTGGGGTG	58799
Db	58740	CCAACAGCTTATGAGATTGGAACCCACTAGGGGGGGAACGCGCAAAATGCTTTGGGGTG	58799
QY	58800	GGTTTAACTCGTGGTATGCGCCCAAGTGCAGCGTATCATCTTCGATCCCATATACAA	58859
Db	58800	GGTTTAACTCGTGGTATGCGCCCAAGTGCAGCGTATCATCTTCGATCCCATATACAA	58859
QY	58860	ACGGGAAATCATTAACAGTATACCTCTGTGTAGTACTGGCCGGGTCAACGGGGACA	58919
Db	58860	ACGGGAAATCATTAACAGTATACCTCTGTGTAGTACTGGCCGGGTCAACGGGGACA	58919
QY	58920	GGATAAATGATAGGGGGGGCTTATGTAATTTCCAGATAGAAAGAAATGACAGAGTT	58979
Db	58920	GGATAAATGATAGGGGGGGCTTATGTAATTTCCAGATAGAAAGAAATGACAGAGTT	58979
QY	58980	CTGTTAGCGTCGCGCTCGCCGGCTTAAACAGCTGCACGCGGTGCAGAAAAACGTGGGAT	59039
Db	58980	CTGTTAGCGTCGCGCTCGCCGGCTTAAACAGCTGCACGCGGTGCAGAAAAACGTGGGAT	59039
QY	59040	ATATGTCAGTCCGTCGATCATGTCCTGTGTGACACAGCAGCAAAAGACAAACCCAG	59099
Db	59040	ATATGTCAGTCCGTCGATCATGTCCTGTGTGACACAGCAGCAAAAGACAAACCCAG	59099
QY	59100	TAAAGTTGCGCAGTGAAGCCGTGTGTGCGCAGCTGCAGCGCTTAATCAGGAAGCTTATGTC	59159
Db	59100	TAAAGTTGCGCAGTGAAGCCGTGTGTGCGCAGCTGCAGCGCTTAATCAGGAAGCTTATGTC	59159
QY	59160	GTCCTCGAACACACAGCTTAAAGCGTATTTGGAAGCCATGCAAAATGCTATTTTATGTA	59219
Db	59160	GTCCTCGAACACACAGCTTAAAGCGTATTTGGAAGCCATGCAAAATGCTATTTTATGTA	59219
QY	59220	CTTCCAAATCATGTCGGGAAAAACTGGATATTTATAGGGCCCTCTGGACGAGCAATTCG	59279
Db	59220	CTTCCAAATCATGTCGGGAAAAACTGGATATTTATAGGGCCCTCTGGACGAGCAATTCG	59279
QY	59280	TTTCAGGATTAACCCCTCAGATCGGTGCTCCCCCTTAAGAGCTTCAGTATTTGGT	59339
Db	59280	TTTCAGGATTAACCCCTCAGATCGGTGCTCCCCCTTAAGAGCTTCAGTATTTGGT	59339
QY	59340	CCATGCGTTCCAGGCTGGCTAAATTTGTCGCAATATTTGTGGCCATGTATATATAC	59399
Db	59340	CCATGCGTTCCAGGCTGGCTAAATTTGTCGCAATATTTGTGGCCATGTATATATAC	59399
QY	59400	ACAGACAGCTGCTGTCCACATACAGCTGTGTGCAATATCTGTGTAACCTTAAGGAAATG	59459
Db	59400	ACAGACAGCTGCTGTCCACATACAGCTGTGTGCAATATCTGTGTAACCTTAAGGAAATG	59459
QY	59460	AGAGAGTGTATATAGGTCATGAGATCAATTTGGGATTAATAGCTAAACGGGCT	59519
Db	59460	AGAGAGTGTATATAGGTCATGAGATCAATTTGGGATTAATAGCTAAACGGGCT	59519
QY	59520	AAGAAATGAAAACCGTGTCTGCGAGTAGGCGATGCTGTTGCGTCCCGCTGATTTGTGC	59579
Db	59520	AAGAAATGAAAACCGTGTCTGCGAGTAGGCGATGCTGTTGCGTCCCGCTGATTTGTGC	59579

Db	59520	AAGAGAAATGAAACCGTCTCTCGAGTAGAGCGATGCTCGTTCCTGCTCCCTGATTGTTCG	59579
Oy	59580	ACCAGGGGTGAGAGTTGTACGTTTGAACAATTTCCCTTCCACAGCGTAAGTAGCTCT	59639
Db	59580	ACCAGGGGTGAGAGTTGTACGTTTGAACAATTTCCCTTCCACAGCGTAGTAGCTCT	59639
Oy	59640	TTGAGCAATCTCCATAAACGGAGGAGCGATTGTAAAAAAAGCGTTTACTACGAGACTG	59699
Db	59640	TTGAGCAATCTCCATAAACGGAGGAGCGATTGTAAAAAAAGCGTTTACTACGAGACTG	59699
Oy	59700	CCTTAGGAGATGATCGATTCGAGTAGAGTTAATGGTTGGGTGCGCAGACCGGATAAGCC	59759
Db	59700	CCTTAGGAGATGATCGATTCGAGTAGAGTTAATGGTTGGGTGCGCAGACCGGATAAGCC	59759
Oy	59760	TGCAACGATTTCTGAGTAGTAATTAATATCGTGTCTGGGCTTCCTCTGTGTAA	59819
Db	59760	TGCAACGATTTCTGAGTAGTAATTAATATCGTGTCTGGGCTTCCTCTGTGTAA	59819
Oy	59820	CTCTGAACCACTGGGTTTCATATGATTCATTTTACGTAGTGTCTCGTCTTCTTC	59879
Db	59820	CTCTGAACCACTGGGTTTCATATGATTCATTTTACGTAGTGTCTCGTCTTCTTC	59879
Oy	59880	TCAAGGTTAGAATTTGATTCGAACTGCTGTTGATCTGTGATCTGTCAGAGCAATTTGAACAGC	59939
Db	59880	TCAAGGTTAGAATTTGATTCGAACTGCTGTTGATCTGTGATCTGTCAGAGCAATTTGAACAGC	59939
Oy	59940	GTAATTTGAACCTGTTTCCGAGACCCGGGTGCTACTTTCGTAACCGGTCCCAAGACG	59999
Db	59940	GTAATTTGAACCTGTTTCCGAGACCCGGGTGCTACTTTCGTAACCGGTCCCAAGACG	59999
Oy	60000	TTGTTTTTGTCCACAAATGTTTTTGAGAGACGTCGTGAGCAAAATCTCAACAGCTCTGT	60059
Db	60000	TTGTTTTTGTCCACAAATGTTTTTGAGAGACGTCGTGAGCAAAATCTCAACAGCTCTGT	60059
Oy	60060	ATGCGCGCTACATGTTTTGTCTCCGCGAGCTTTATACAGCAAGTTTAGAGAGTCCCTCTTG	60119
Db	60060	ATGCGCGCTACATGTTTTGTCTCCGCGAGCTTTATACAGCAAGTTTAGAGAGTCCCTCTTG	60119
Oy	60120	GGGTGCGTTTTTTAGACAGATTGCTTAAGCGAGCCAAATATGCTTTATACATGCTGTG	60179
Db	60120	GGGTGCGTTTTTTAGACAGATTGCTTAAGCGAGCCAAATATGCTTTATACATGCTGTG	60179
Oy	60180	CACGTGCTACCGACAGCGCTTTTATAGAGCGCGGTATTTAGTAATCTGACATTAATTGCG	60239
Db	60180	CACGTGCTACCGACAGCGCGCTTTTATAGAGCGCGGTATTTAGTAATCTGACATTAATTGCG	60239
Oy	60240	TGCTCCGGGTCGTGTGATGTCATATGCGGGTAATTAACCGGTACAGAGGCTATCA	60299
Db	60240	TGCTCCGGGTCGTGTGATGTCATATGCGGGTAATTAACCGGTACAGAGGCTATCA	60299
Oy	60300	AAGCGACGCGTCATTTGTAATTAATTAAGCGCGTAAGAACCACTTCAGCTTTATATCTTT	60359
Db	60300	AAGCGACGCGTCATTTGTAATTAATTAAGCGCGTAAGAACCACTTCAGCTTTATATCTTT	60359
Oy	60360	TGCTGTATGATGCGGAGATTAAGACCGCTTATCTCCGTTAAATCTCACAGACCTCTGCGG	60419
Db	60360	TGCTGTATGATGCGGAGATTAAGACCGCTTATCTCCGTTAAATCTCACAGACCTCTGCGG	60419
Oy	60420	TAGTCTGGAATATTAATAGACATCGGTCAATTAATCGAGTAATCTCTGTGCGAGT	60479
Db	60420	TAGTCTGGAATATTAATAGACATCGGTCAATTAATCGAGTAATCTCTGTGCGAGT	60479
Oy	60480	TTGTGCGAATTCGCGATATCGTAACGTCCTCCGGAAGCGTAACGTTTTTCCATCTGTTGA	60539
Db	60480	TTGTGCGAATTCGCGATATCGTAACGTCCTCCGGAAGCGTAACGTTTTTCCATCTGTTGA	60539
Oy	60540	CAGTGTGTTTATTCCTGCGATGCTGTGCGGCGGTGCGCCTTGACAAATAGGCAAC	60599
Db	60540	CAGTGTGTTTATTCCTGCGATGCTGTGCGGCGGTGCGCCTTGACAAATAGGCAAC	60599
Oy	60600	AACCCAAAGGCGACACCCAGTCGACGTATCGTTCGTAACGATAAAGACGTCTGCTGTG	60659
Db	60600	AACCCAAAGGCGACACCCAGTCGACGTATCGTTCGTAACGATAAAGACGTCTGCTGTG	60659
Oy	60660	AGTACCTGATTAATAGTGTTCAGTAACAGTGTGATGACATGTTAGACGAAGGTACGTGCC	60719
Db	60660	AGTACCTGATTAATAGTGTTCAGTAACAGTGTGATGACATGTTAGACGAAGGTACGTGCC	60719
Oy	60720	CACGATTCGAAAGCTAGACCGGTTTGAATTCGCGGTAGGTGCTCGACACCGGCCAACG	60779
Db	60720	CACGATTCGAAAGCTAGACCGGTTTGAATTCGCGGTAGGTGCTCGACACCGGCCAACG	60779
Oy	60780	GTCCTTGAAGGTGCTCGAAGTTGTGTCAGTCCCTTTTAAAGCGTTGTCTATGTGACCTC	60839
Db	60780	GTCCTTGAAGGTGCTCGAAGTTGTGTCAGTCCCTTTTAAAGCGTTGTGTATGTGACGCTC	60839
Oy	60840	CCCAATTCGCGTCTTTGACAGGTGTATGAACAGTGTCTTCCAAAGATCCCTGGATTTGCA	60899
Db	60840	CCCAATTCGCGTCTTTGACAGGTGTATGAACAGTGTCTTCCAAAGATCCCTGGATTTGCA	60899
Oy	60900	AGACTGGAGTGTAGCTTTGACCGCAAGATAGCGCTACTTCCCGTATGAGATCTCGAAA	60959
Db	60900	AGACTGGAGTGTAGCTTTGACCGCAAGATAGCGCTACTTCCCGTATGAGATCTCGAAA	60959
Oy	60960	AGCGAATGAGAGATTCCTCGATGAGACCAACACGTGCAACCAATTCGGGGTTTCATC	61019
Db	60960	AGCGAATGAGAGATTCCTCGATGAGACCAACACGTGCAACCAATTCGGGGTTTCATC	61019
Oy	61020	TTGACATGACGTCGATGCAAAAGTCAGGGGTGTGTGATGACGTGACGTGCGCTGTCA	61079
Db	61020	TTGACATGACGTCGATGCAAAAGTCAGGGGTGTGTGATGACGTGACGTGCGCTGTCA	61079
Oy	61080	AATATTAACATACAGCCACCGGAATAGGTTGTGTACAGCTGAGCTTCGATCCGGCTGAA	61139
Db	61080	AATATTAACATACAGCCACCGGAATAGGTTGTGTACAGCTGAGCTTCGATCCGGCTGAA	61139
Oy	61140	GACTCGGGCGCTTGTGCGCTTACGTTTATCTAATTAACGGAACGTCTGCTGTGG	61199
Db	61140	GACTCGGGCGCTTGTGCGCTTACGTTTATCTAATTAACGGAACGTCTGCTGTGG	61199
Oy	61200	AAAAGTACAGCATATCGGCCCTGTACCAAAATTTAACTGCTGATACAGGGCGCGAC	61259
Db	61200	AAAAGTACAGCATATCGGCCCTGTACCAAAATTTAACTGCTGATACAGGGCGCGAC	61259
Oy	61260	ACCATAGCGCGACAGAACTATTCGCGCTCCCTTAAGAGCTTGTGCCACGATCTTCAAC	61319
Db	61260	ACCATAGCGCGACAGAACTATTCGCGCTCCCTTAAGAGCTTGTGTGCCACGATCTTCAAC	61319
Oy	61320	GCTTTGCGCTTAAAGAGCGGACACATCAATATAGCGGTAGAAAGCTATCAGACCGGA	61379
Db	61320	GCTTTGCGCTTAAAGAGCGGACACATCAATATAGCGGTAGAAAGCTATCAGACCGGA	61379
Oy	61380	GCCGTAATCCATAGAGCAATTTACAGACAGAGCTATGAGATTTGGCCGTTTATGTG	61439
Db	61380	GCCGTAATCCATAGAGCAATTTACAGACAGAGCTATGAGATTTGGCCGTTTATGTG	61439
Oy	61440	GACATTAATGAAGAGTTATGGGGAATAAACCAATGGATGTACGSGGCTATATCCAAAC	61499
Db	61440	GACATTAATGAAGAGTTATGGGGAATAAACCAATGGATGTACGSGGCTATATCCAAAC	61499
Oy	61500	GCGAATTTTGAACCCCTCGAGAAATAGCCGAGACCGTGTTAATGACCTTCATAATAT	61559
Db	61500	GCGAATTTTGAACCCCTCGAGAAATAGCCGAGACCGTGTTAATGACCTTCATAATAT	61559
Oy	61560	GTAATGAGAGAGCGCGGAACCTGTCTCTTATACATATCACACACCGTGTCTTTTAC	61619
Db	61560	GTAATGAGAGAGCGCGGAACCTGTCTCTTATACATATCACACACCGTGTCTTTTAC	61619
Oy	61620	TGCTTCCTTAAACAGCTGAGGCTAAATACCCCTTTTACCGGCAAGGGGCGTTCCGTGATA	61679
Db	61620	TGCTTCCTTAAACAGCTGAGGCTAAATACCCCTTTTACCGGCAAGGGGCGTTCCGTGATA	61679
Oy	61680	GTAATGCTGCGTTGCGCAACGACAGACAAAGCGTTTCACTCAATTAACACAGCGGAC	61739
Db	61680	GTAATGCTGCGTTGCGCAACGACAGACAAAGCGTTTCACTCAATTAACACAGCGGAC	61739

QY	61740	CAAAAGACGAGATATGCTGCTGGAGAACATCTTAACATTCATGATAGGAGAAAGGTC	61799	QY	82820	YCCCCTTCAGAACGATCTCAACGGGCGTGTGGCGTTCGATCAACGCTGTGAATCTGATAA	82879
Db	61740	CAAAAGACGAGATATGCTGCTGGAGAACATCTTAACATTCATGATAGGAGAAAGGTC	61799	Db	82820	TCCCCTTCAGAACGATCTCAACGGGCGTGTGGCGTTCGATCAACGCTGTGAATCTGATAA	82879
QY	61800	GTAATCTGATACGTACACTTGTGGAGAAACTGGGCGCTGTTTATAAACCAACAGCGTCG	61859	QY	62880	ATTAAAGGGGACACGTTTTTACCGGATAGGGTTCGGTCCGTGCATGAGGTTTTGGCACTACGT	62939
Db	61800	GTAATCTGATACGTACACTTGTGGAGAAACTGGGCGCTGTTTATAAACCAACAGCGTCG	61859	Db	62880	ATTAAAGGGGACACGTTTTTACCGGATAGGGTTCGGTCCGTGCATGAGGTTTTGGCACTACGT	62939
QY	61860	ACCGATCTGCAGTTGCGGACACCTCTTAAGATTAATCTTCCCATCTCCGAC	61919	QY	62940	GATGACCTCAGAAAGAAGATGGCCCTCCGTGCTGTCAGAGACTTACGCGTTTATCCG	62999
Db	61860	ACCGATCTGCAGTTGCGGACACCTCTTAAGATTAATCTTCCCATCTCCGAC	61919	Db	62940	GATGACCTCAGAAAGAAGATGGCCCTCCGTGCTGTCAGAGACTTACGCGTTTATCCG	62999
QY	61920	GAACTCATGACTACGTACGTAGACAGATTTGTGCTTCTTAAGTAAGATTATGATCTTTA	61979	QY	63000	TGCTTAGAGATTAACATAACAAATTGACCGAAACCATGAGAGAGCGGAGCGTTTCCAA	63059
Db	61920	GAACTCATGACTACGTACGTAGACAGATTTGTGCTTCTTAAGTAAGATTATGATCTTTA	61979	Db	63000	TGCTTAGAGATTAACATAACAAATTGACCGAAACCATGAGAGAGCGGAGCGTTTCCAA	63059
QY	61980	GAATACATATGGCTGGACCCGACTCTTTTGTACATAGCGAGTAAGGGGATCTACAA	62039	QY	63060	GTGTGCTGTGGCGGGGACATATGGGGGACACTCAAAATTTAGCCATGACCAATGCTAAAGCA	63119
Db	61980	GAATACATATGGCTGGACCCGACTCTTTTGTACATAGCGAGTAAGGGGATCTACAA	62039	Db	63060	GTGTGCTGTGGCGGGGACATATGGGGGACACTCAAAATTTAGCCATGACCAATGCTAAAGCA	63119
QY	62040	AACCTACACACATGCTTAACGCTAGGGGGCGATACAGGGGACAGAACTCTTAACTG	62099	QY	63120	CAGGAATGTGTTGGAGGAGTAGCGGTAGTATTTGGGTGCCACAAAGACCTCCAGACA	63179
Db	62040	AACCTACACACATGCTTAACGCTAGGGGGCGATACAGGGGACAGAACTCTTAACTG	62099	Db	63120	CAGGAATGTGTTGGAGGAGTAGCGGTAGTATTTGGGTGCCACAAAGACCTCCAGACA	63179
QY	62100	CCCGTGTGTGCGAGGTGTTTGTAGAGCCGTTTGAAGAAATCAAGCGGCGCTACACTC	62159	QY	63180	AGCCACGTGATGTACCAATATCAGAGGCTGTTAACTCAAAATTTATTTGGTCAATGACAC	63239
Db	62100	CCCGTGTGTGCGAGGTGTTTGTAGAGCCGTTTGAAGAAATCAAGCGGCGCTACACTC	62159	Db	63180	AGCCACGTGATGTACCAATATCAGAGGCTGTTAACTCAAAATTTATTTGGTCAATGACAC	63239
QY	62160	ACCAACCTCACCGTAGCGAGTGGGTGACAAAAACCTTTAGTTAAGTAATATATTCG	62219	QY	63240	AACCCCTTAAAAACCTCTCCGTACAGAGAACAGTGTGAACACCTCGCCAGACATTAATG	63299
Db	62160	ACCAACCTCACCGTAGCGAGTGGGTGACAAAAACCTTTAGTTAAGTAATATATTCG	62219	Db	63240	AACCCCTTAAAAACCTCTCCGTACAGAGAACAGTGTGAACACCTCGCCAGACATTAATG	63299
QY	62220	CAGTTTGTGACACAGAGATGTCCATAGTCGCCACGGAAATCCACTGAAAGCTTCCAGCCAG	62279	QY	63300	CGCGCCCTCCACAACCCAAACACAAACCCATCTACTTAATTAATTAATAACAAAGCAAAATG	63359
Db	62220	CAGTTTGTGACACAGAGATGTCCATAGTCGCCACGGAAATCCACTGAAAGCTTCCAGCCAG	62279	Db	63300	CGCGCCCTCCACAACCCAAACACAAACCCATCTACTTAATTAATTAATAACAAAGCAAAATG	63359
QY	62280	GTTACCTTTATCACCAGTTTGTAAAAACAGCCAGCTGTCTTTAAATGGAAAAACAAA	62339	QY	63360	GAAAAATGTGTTTTTATTCAGTCCAACACAGGCGCAGGATATGTTGTATTTCCACACA	63419
Db	62280	GTTACCTTTATCACCAGTTTGTAAAAACAGCCAGCTGTCTTTAAATGGAAAAACAAA	62339	Db	63360	GAAAAATGTGTTTTTATTCAGTCCAACACAGGCGCAGGATATGTTGTATTTCCACACA	63419
QY	62340	AAATGCAATATGTGGGTTTTCAGAGTACGTACTTGTAGTTCAAAAGAAATCCTAGACAGGAA	62399	QY	63420	CCGGGGGGGTGGCGGCGCATAGTTTGACGACAGAAACGCCCGGCGCTTGGGTTTGAAG	63479
Db	62340	AAATGCAATATGTGGGTTTTCAGAGTACGTACTTGTAGTTCAAAAGAAATCCTAGACAGGAA	62399	Db	63420	CCGGGGGGGTGGCGGCGCATAGTTTGACGACAGAAACGCCCGGCGCTTGGGTTTGAAG	63479
QY	62400	CTCTTCGTGAGAGCGCATTCGCAAGACCGTCCGGAATACGTATACGGTTTTCTTAAACAGC	62459	QY	63480	TAGCCCGCGCCCGCTGGTGTGAGGTCATACGTCTTTAGGGCCCTGAGTTGTAACAAAT	63539
Db	62400	CTCTTCGTGAGAGCGCATTCGCAAGACCGTCCGGAATACGTATACGGTTTTCTTAAACAGC	62459	Db	63480	TAGCCCGCGCCCGCTGGTGTGAGGTCATACGTCTTTAGGGCCCTGAGTTGTAACAAAT	63539
QY	62460	CTACTGTCACAGCGCATGTACTGCTTTCACGCGGTACGCGGCGTACGTACACAGCAAA	62519	QY	63540	AAATTCACGTGTCATACCGGTTCGACGTCCCTGCTGACGCGCGGCTCTTGCAGGCGGCAC	63599
Db	62460	CTACTGTCACAGCGCATGTACTGCTTTCACGCGGTACGCGGCGTACGTACACAGCAAA	62519	Db	63540	AAATTCACGTGTCATACCGGTTCGACGTCCCTGCTGACGCGCGGCTCTTGCAGGCGGCAC	63599
QY	62520	TATCTGCAAGAAGCTAAAAATTTGCAACCCCTCCGCGCGCTCTGGCAACCGGCGTGTAGAC	62579	QY	63600	GAACACCGCGGCTTTGTAAGGTATCTGCAATCTGCTGCTGTCTGAAGATGAACACAGT	63659
Db	62520	TATCTGCAAGAAGCTAAAAATTTGCAACCCCTCCGCGCGCTCTGGCAACCGGCGTGTAGAC	62579	Db	63600	GAACACCGCGGCTTTGTAAGGTATCTGCAATCTGCTGCTGTCTGAAGATGAACACAGT	63659
QY	62580	CTTCAAAACGTTTCTGAAAGTAAACCTGGAAGACACATCTTCTACCAAGTGTGACGT	62639	QY	63660	CAATTCACATGAGTGGCGCCGCTGCTATCGGCGGTGTGATTCCTCAACAG	63719
Db	62580	CTTCAAAACGTTTCTGAAAGTAAACCTGGAAGACACATCTTCTACCAAGTGTGACGT	62639	Db	63660	CAATTCACATGAGTGGCGCCGCTGCTATCGGCGGTGTGATTCCTCAACAG	63719
QY	62640	CCCCCGCACCCGGGGGATACACTCCCTCCAGGTTTGGTGCACAGTACTGGGCCCTA	62699	QY	63720	AGCCTGCGTGCACCTTGTGCTGCTATTCGTAATTAATTTGGTCTCTTCCGCAAGTTG	63779
Db	62640	CCCCCGCACCCGGGGGATACACTCCCTCCAGGTTTGGTGCACAGTACTGGGCCCTA	62699	Db	63720	AGCCTGCGTGCACCTTGTGCTGCTATTCGTAATTAATTTGGTCTCTTCCGCAAGTTG	63779
QY	62700	AAGGACGTGTTGCGCTCCAGAAATAAAGTGGCGTGTGCTGTTGGCGGGAGATTGAG	62759	QY	63780	ATTCACAAACACAGGTTCTTCTTCAATCGGAAGACCATCGGCCCTCTGCGGTGATCTAG	63839
Db	62700	AAGGACGTGTTGCGCTCCAGAAATAAAGTGGCGTGTGCTGTTGGCGGGAGATTGAG	62759	Db	63780	ATTCACAAACACAGGTTCTTCTTCAATCGGAAGACCATCGGCCCTCTGCGGTGATCTAG	63839
QY	62760	AAGGAAACGTTTTCCGGTTTTACGTTTAACTGCTTAAGGAGGACGAGGATTGACTTTGTC	62819	QY	63840	ATATATACCTGACACAGCGGCGGAGGCGCGGTGGCGGAAAAGCGCTGACGTTCTCCGCCAC	63899
Db	62760	AAGGAAACGTTTTCCGGTTTTACGTTTAACTGCTTAAGGAGGACGAGGATTGACTTTGTC	62819	Db	63840	ATATATACCTGACACAGCGGCGGAGGCGCGGTGGCGGAAAAGCGCTGACGTTCTCCGCCAC	63899
				QY	63900	TTTTCATCAGTGTGCTGTAGTATCTATTAATAAATTCGCTTCCGCTGCTGATGATG	63959

Db 63900 TTTTCATCAGTGTCTCTGTAGTCACTATATAAAAAATCGTCTTGTGCTGATTCAGATG 63959
QY 63960 ACTGGGGTGGGGGTGTTGGCAGTAACCAACCGCAACGGGCGCGGACCAACAAAGCGG 64019
Db 63960 ACTGGGGTGGGGGTGTTGGCAGTAACCAACCGCAACGGGCGCGGACCAACAAAGCGG 64019
QY 64020 TCAATGGCGGGGGCGGCTGGTGTGTGGGACCTTCGAAATGATGACGTAGTA 64079
Db 64020 TCAATGGCGGGGGCGGCTGGTGTGTGGGACCTTCGAAATGATGACGTAGTA 64079
QY 64080 GCGGCGCGCTGGTTAAAGGACTCACCGTCCGCTGGCGGATCTATCTAGTGGGG 64139
Db 64080 GCGGCGCGCTGGTTAAAGGACTCACCGTCCGCTGGCGGATCTATCTAGTGGGG 64139
QY 64140 AAGAGACCGGCGGTTCTGTTCTTCATCCACATCACTGATGATGCGTCTCGAATGAG 64199
Db 64140 AAGAGACCGGCGGTTCTGTTCTTCATCCACATCACTGATGATGCGTCTCGAATGAG 64199
QY 64200 ACTCGGTTCTGCTGGCGTTTGTGGAGTAGTGGGAGGGAATCTTGGTCAAAAACATCT 64259
Db 64200 ACTCGGTTCTGCTGGCGTTTGTGGAGTAGTGGGAGGGAATCTTGGTCAAAAACATCT 64259
QY 64260 CAGGTGCACTGATGATCACTACGAGGGGCGCTCCGACCGGGCGGTACCGGACCCCG 64319
Db 64260 CAGGTGCACTGATGATCACTACGAGGGGCGCTCCGACCGGGCGGTACCGGACCCCG 64319
QY 64320 TACGGGACCCCGGGAACAAAAACGTTGTTCTCTTTTCTAGGTGCCCCGGGAATCG 64379
Db 64320 TACGGGACCCCGGGAACAAAAACGTTGTTCTCTTTTCTAGGTGCCCCGGGAATCG 64379
QY 64380 GCAAGCATCTCTGGGAGTGGCGGGGCGGCTCTGACGGGTGCGATGAAGACATAGCCATG 64439
Db 64380 GCAAGCATCTCTGGGAGTGGCGGGGCGGCTCTGACGGGTGCGATGAAGACATAGCCATG 64439
QY 64440 CCGAAACGTTCACTCTATAAAGCACTGCTATCCCGCATCACTATATATTCAGTCAAC 64499
Db 64440 CCGAAACGTTCACTCTATAAAGCACTGCTATCCCGCATCACTATATATTCAGTCAAC 64499
QY 64500 GGCACCCCTCCGATTCGTAGTATGATATGTCGCAAGTTTAAAAATGGTTGACGCTAG 64559
Db 64500 GGCACCCCTCCGATTCGTAGTATGATATGTCGCAAGTTTAAAAATGGTTGACGCTAG 64559
QY 64560 AAACGTGGGGGGAAGCAACCGGTTGCGCGGGGGGTAGCCAGGGGAGAGCGAATGGG 64619
Db 64560 AAACGTGGGGGGAAGCAACCGGTTGCGCGGGGGGTAGCCAGGGGAGAGCGAATGGG 64619
QY 64620 CCGCTTGAGAGAGATGCTGTCTGCTGTTTATCAGCGCTGCTGTATAGCCTTTCT 64679
Db 64620 CCGCTTGAGAGAGATGCTGTCTGCTGTTTATCAGCGCTGCTGTATAGCCTTTCT 64679
QY 64680 TCCCCACAGCATAAAAACGCACTCTGAGGCTTGAGAAAGGACACTTATATGAGCT 64739
Db 64680 TCCCCACAGCATAAAAACGCACTCTGAGGCTTGAGAAAGGACACTTATATGAGCT 64739
QY 64740 GGTGAACCAATCCCAAGGTTGGCGTGTGACCCCGCTTCCCTTTTCCACCTGAG 64799
Db 64740 GGTGAACCAATCCCAAGGTTGGCGTGTGACCCCGCTTCCCTTTTCCACCTGAG 64799
QY 64800 AATGGGTTTAAAAAGCAGACTCCCGTTTGGCCCAACAGTCTTAACACCCCGTGAAGAG 64859
Db 64800 AATGGGTTTAAAAAGCAGACTCCCGTTTGGCCCAACAGTCTTAACACCCCGTGAAGAG 64859
QY 64860 ACGGATGAACCCAGGTACAGTATGGCTATCTCTTTAAAAATATTTTGAAGCTTGAGG 64919
Db 64860 ACGGATGAACCCAGGTACAGTATGGCTATCTCTTTAAAAATATTTTGAAGCTTGAGG 64919
QY 64920 TATCTAGTATGTCGGAAGCAACGCTAAAGGCTAGTCCGCTTGACCCGATGAGTAAG 64979
Db 64920 TATCTAGTATGTCGGAAGCAACGCTAAAGGCTAGTCCGCTTGACCCGATGAGTAAG 64979
QY 64980 ATCCGTGGCAAGATACGACTTTATATCTCTCCGTTTGGCAACATATAGACACACAT 65039
Db 64980 ATCCGTGGCAAGATACGACTTTATATCTCTCCGTTTGGCAACATATAGACACACAT 65039

Db 64980 ATCCGTGGCAAGATACGACTTTATATCTCTCCGTTTGGCAACATATAGACACACAT 65039
QY 65040 AATTCTATCTATGCGGATGAATTAATCAAGGTTACGTTGCTCATATCCATAACGGCTTCA 65099
Db 65040 AATTCTATCTATGCGGATGAATTAATCAAGGTTACGTTGCTCATATCCATAACGGCTTCA 65099
QY 65100 CAGAGCCGGAGGCTTCTGTTTAAAAATGGAGAAATTTAAAAATTCAGGCTAGATG 65159
Db 65100 CAGAGCCGGAGGCTTCTGTTTAAAAATGGAGAAATTTAAAAATTCAGGCTAGATG 65159
QY 65160 GCTAATGACAACTTGTGTGTGGAGGTTCTTTAACAATCTGCTGGATTTTACTCCA 65219
Db 65160 GCTAATGACAACTTGTGTGTGGAGGTTCTTTAACAATCTGCTGGATTTTACTCCA 65219
QY 65220 AACTATGTTTAAAGCAACCCCTCATTAATCCCGCTGTGTAAATTAATCTAGTAA 65279
Db 65220 AACTATGTTTAAAGCAACCCCTCATTAATCCCGCTGTGTAAATTAATCTAGTAA 65279
QY 65280 CGTGAACCTTTGTACTTCTGCTGTGAAGAAATCCACAGAGTGGCCGCTATAGCAGTT 65339
Db 65280 CGTGAACCTTTGTACTTCTGCTGTGAAGAAATCCACAGAGTGGCCGCTATAGCAGTT 65339
QY 65340 CCGCTTCACTACCGTTTATGTAAGGCTTCAAACTCGGCTAAAAACTATCAAGACTA 65399
Db 65340 CCGCTTCACTACCGTTTATGTAAGGCTTCAAACTCGGCTAAAAACTATCAAGACTA 65399
QY 65400 TATTCATATATTAACAATGAGCTCTCTCTGCGGACACTGTATATTAATCTGTAC 65459
Db 65400 TATTCATATATTAACAATGAGCTCTCTCTGCGGACACTGTATATTAATCTGTAC 65459
QY 65460 AAATGCTTATAAAAACGCCCTAAGGTAAATCCATTTACATATTTCTGTGGTAGAG 65519
Db 65460 AAATGCTTATAAAAACGCCCTAAGGTAAATCCATTTACATATTTCTGTGGTAGAG 65519
QY 65520 CGATCAGCTTATATGCAATGTTGCTGTACACAGCCCTGAGACATTAAGCTAAATTTGTT 65579
Db 65520 CGATCAGCTTATATGCAATGTTGCTGTACACAGCCCTGAGACATTAAGCTAAATTTGTT 65579
QY 65580 AAATGAAAAAGCAATCTCAAAAGCGCTCGGGAATATTAAGTCACTAAGGTATATT 65639
Db 65580 AAATGAAAAAGCAATCTCAAAAGCGCTCGGGAATATTAAGTCACTAAGGTATATT 65639
QY 65640 TTCAACATGAGATTCTCTCAAAAGCCGGTACCAACATGTATTTAAAAAATCCACATGTA 65699
Db 65640 TTCAACATGAGATTCTCTCAAAAGCCGGTACCAACATGTATTTAAAAAATCCACATGTA 65699
QY 65700 ATAAATAACTTAAGGTATACATCTTCATGTTTATATCAATATATGAACGCTAATGC 65759
Db 65700 ATAAATAACTTAAGGTATACATCTTCATGTTTATATCAATATATGAACGCTAATGC 65759
QY 65760 TGTACTTATATATATGATATGATATGATATGCAATACAGTCAAGGTAAATATTAAAG 65819
Db 65760 TGTACTTATATATATGATATGATATGATATGCAATACAGTCAAGGTAAATATTAAAG 65819
QY 65820 CATTAATGCAAACTCAATTAATTAACAAAAATGACGCTTCGGAATATCCGCCAGCT 65879
Db 65820 CATTAATGCAAACTCAATTAATTAACAAAAATGACGCTTCGGAATATCCGCCAGCT 65879
QY 65880 GTTAAACCGAAAAATACAGAAATGACTACAAACACACCTGAAACCAATTTTATCTCAA 65939
Db 65880 GTTAAACCGAAAAATACAGAAATGACTACAAACACACCTGAAACCAATTTTATCTCAA 65939
QY 65940 CATATGCAACATATTTCAAGGTTAACACCATGTTTAAATATGCAAGATGACATTTT 65999
Db 65940 CATATGCAACATATTTCAAGGTTAACACCATGTTTAAATATGCAAGATGACATTTT 65999
QY 66000 TAGCTAAGTCTCTCAAAAGCAATTTCTCTTCAATGATGATGATCAATCACTGCTTCC 66059
Db 66000 TAGCTAAGTCTCTCAAAAGCAATTTCTCTTCAATGATGATGATCAATCACTGCTTCC 66059
QY 66060 GTGTTATGTCGGAATATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 66119
Db 66060 GTGTTATGTCGGAATATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 66119

QY	66120	AGGGCTGTAAAAATATCATCAGTCAATCAAGCTGTAATGTCAGAGAGTGTGTTCTAAT	66179
Db	66120	AGGGCTGTAAAAATATCATCAGTCAATCAAGCTGTAATGTCAGAGAGTGTGTTCTAAT	66179
QY	66180	TTTAAGCCCATCCAAATGCTAGTGGGTGACATTTGGGCAAGACCCCTAAATTTGGCA	66239
Db	66180	TTTAAGCCCATCCAAATGCTAGTGGGTGACATTTGGGCAAGACCCCTAAATTTGGCA	66239
QY	66240	CGCTCCACACAAAACGGAAGGATGCATTTATCGTTTACAGAGGGGACGATATATTAATTTT	66299
Db	66240	CGCTCCACACAAAACGGAAGGATGCATTTATCGTTTACAGAGGGGACGATATTTATTTT	66299
QY	66300	ATTAACATCAGAAACCGGACCCGTCATAGCAGCATATGTCCATTAGATTGGAGTCGTG	66359
Db	66300	ATTAACATCAGAAACCGGACCCGTCATAGCAGCATATGTCCATTAGATTGGAGTCGTG	66359
QY	66360	ACACTGGTTGAATTTGACGGTGAATAAATATTTGCTGTCCATGCGCACTATTTT	66419
Db	66360	ACACTGGTTGAATTTGACGGTGAATAAATATTTGCTGTCCATGCGCACTATTTT	66419
QY	66420	AACCCACAGAGGGGCGAATTAACAGGGGTCCCGGCGCTTAAGGCCGCGAATGGCGAGCA	66479
Db	66420	AACCCACAGAGGGGCGAATTAACAGGGGTCCCGGCGCTTAAGGCCGCGAATGGCGAGCA	66479
QY	66480	CGGCTCATTTGCCATTTTCCAGATTTGTTAAATCTGTTCGAAATACGAGTCTAATAATCAG	66539
Db	66480	CGGCTCATTTGCCATTTTCCAGATTTGTTAAATCTGTTCGAAATACGAGTCTAATAATCAG	66539
QY	66540	TATACGACGACAAAGTTCCAAACAGAGGCAACGGGCTGGTTTCCACCCGGGACATCCCG	66599
Db	66540	TATACGACGACAAAGTTCCAAACAGAGGCAACGGGCTGGTTTCCACCCGGGACATCCCG	66599
QY	66600	CTCACAACCCCGAAGCTCTAGGAGACGCAATCAAAAGCCTTGACAGAAATTCGGAAC	66659
Db	66600	CTCACAACCCCGAAGCTCTAGGAGACGCAATCAAAAGCCTTGACAGAAATTCGGAAC	66659
QY	66660	GAAACCTAGTTCTGAGACACCATCTGTTATTAATCTGCGGTTAAGAGACGAGCGCCACA	66719
Db	66660	GAAACCTAGTTCTGAGACACCATCTGTTATTAATCTGCGGTTAAGAGAGCAGCGCCACA	66719
QY	66720	CACGTGCTGTGAGAGATTCACGCTTAGGAGGCGCTCAGGCTTGCGTGAACGAGCCGCTAGC	66779
Db	66720	CACGTGCTGTGAGAGATTCACGCTTAGGAGGCGCTCAGGCTTGCGTGAACGAGCCGCTAGC	66779
QY	66780	TGCCTGGCGGCGCTCGCGCACCTTTGACACGCGCACGCGCATGTTCCAGAGCGAGGAGAG	66839
Db	66780	TGCCTGGCGGCGCTCGCGCACCTTTGACACGCGCACGCGCATGTTCCAGAGCGAGGAGAG	66839
QY	66840	CGCTCTTTGCAAGTCGCGCCCATATCTGGCCATATGAGAGATTCGCTCGCGTGAATCTTTTAG	66899
Db	66840	CGCTCTTTGCAAGTCGCGCCCATATCTGGCCATATGAGAGATTCGCTCGCGTGAATCTTTTAG	66899
QY	66900	TGCATATATATCTGTGGTGAACAAACCTCAGCTCTGTTAAAGGGGAATTAAGTCCGTT	66959
Db	66900	TGCATATATATCTGTGGTGAACAAACCTCAGCTCTGTTAAAGGGGAATTAAGTCCGTT	66959
QY	66960	CTTTCTATGCTTTTCTCTGAACTATAGTTACATCTTTAAGTATTAACAAAGACGCTAAA	67019
Db	66960	CTTTCTATGCTTTTCTCTGAACTATAGTTACATCTTTAAGTATTAACAAAGACGCTAAA	67019
QY	67020	AACCCAGAGTGTGACACCTTTTAAAAAATCGAAAAAGGACCGGATGGCTATATCCGCG	67079
Db	67020	AACCCAGAGTGTGACACCTTTTAAAAAATCGAAAAAGGACCGGATGGCTATATCCGCG	67079
QY	67080	TTTTCAGTGTGTTCAAGGTAGTACAGAGTATCTCAGTTAGACTCTGTCCCTGTTA	67139
Db	67080	TTTTCAGTGTGTTCAAGGTAGTACAGAGTATCTCAGTTAGACTCTGTCCCTGTTA	67139
QY	67140	ACACCCTTAATCTGGAATGGAACAGCCATGACACCGTGAATCTTGATGTCTCTTAAA	67199
Db	67140	ACACCCTTAATCTGGAATGGAACAGCCATGACACCGTGAATCTTGATGTCTCTTAAA	67199

QY	67200	CTAACCCCGAAGACAGCTAAATATCCAAATGACTGTACACCCCTTACCCCAAGCCAGCCGCC	67259
Db	67200	CTAACCCCGAAGACAGCTAAATATCCAAATGACTGTACACCCCTTACCCCAAGCCAGCCGCC	67259
QY	67260	GTACTATTAGACCGAGGGGTGAGTAAACACGGTATCTCTTTAAAAACCATCTGAGAGTTTG	67319
Db	67260	GTACTATTAGACCGAGGGGTGAGTAAACACGGTATCTCTTTAAAAACCATCTGAGAGTTTG	67319
QY	67320	TAAAGTAAACAGCTCGTGTATTTTACAGACGCCCTGTCTATAAATGGATACCGACGACAT	67379
Db	67320	TAAAGTAAACAGCTCGTGTATTTTACAGACGCCCTGTCTATAAATGGATACCGACGACAT	67379
QY	67380	CAGGTATTTAACTTTTATTATTCAGAGTTACAGAGGGCGGTGTTTACAAGTGTGTAGGTG	67439
Db	67380	CAGGTATTTAACTTTTATTATTCAGAGTTACAGAGGGCGGTGTTTACAAGTGTGTAGGTG	67439
QY	67440	GGACCATATCCCGCATGGGAATGGGTGTATGAAATCACACTAGTACGTACGGATCAGGTG	67499
Db	67440	GGACCATATCCCGCATGGGAATGGGTGTATGAAATCACACTAGTACGTACGGATCAGGTG	67499
QY	67500	CTCTGTCTACTTTACTAGTCCGATGACCTAAATTTGGCGTGTATAGCTGTACCAAC	67559
Db	67500	CTCTGTCTACTTTACTAGTCCGATGACCTAAATTTGGCGTGTATAGCTGTACCAAC	67559
QY	67560	AAAAACTGCCGTGCGCTTGTAGAGCTGTATGACAAGCTTTATCTGTCCAAATAG	67619
Db	67560	AAAAACTGCCGTGCGCTTGTAGAGCTGTATGACAAGCTTTATCTGTCCAAATAG	67619
QY	67620	CTTGTCTTTAAAAATGCACTGTGTATCTTATGACAGTGGTCCAAAAACCAAG	67679
Db	67620	CTTGTCTTTAAAAATGCACTGTGTATCTTATGACAGTGGTCCAAAAACCAAG	67679
QY	67680	ATTTAAAAACACGTTTAACTACGCTGTCTCTGTAGTCTCTGTATATACCTCCCTCAACAG	67739
Db	67680	ATTTAAAAACACGTTTAACTACGCTGTCTCTGTAGTCTCTGTATATACCTCCCTCAACAG	67739
QY	67740	AAAAATTTTAAACCAACTCGCCAGAGTCTGAAACGATGGTAGCGACAGGTGCGTGA	67799
Db	67740	AAAAATTTTAAACCAACTCGCCAGAGTCTGAAACGATGGTAGCGACAGGTGCGTGA	67799
QY	67800	AGTGTATATATCTCCCTTACGCTCCCTTTGAAGGTTTTGGTTATACCCGACATGTGACA	67859
Db	67800	AGTGTATATATCTCCCTTACGCTCCCTTTGAAGGTTTTGGTTATACCCGACATGTGACA	67859
QY	67860	TAGGCACACAGCTCAGGGGGAGGTGCGATGCTGAGGGGGGTAAACAATTCTGTGGCGTGGG	67919
Db	67860	TAGGCACACAGCTCAGGGGGAGGTGCGATGCTGAGGGGGGTAAACAATTCTGTGGCGTGGG	67919
QY	67920	GTACTCCAGTTTATAGATCTCCGCGACGAGACGCTACGAGTCTTCTGTCAAATCTTACGCA	67979
Db	67920	GTACTCCAGTTTATAGATCTCCGCGACGAGACGCTACGAGTCTTCTGTCAAATCTTACGCA	67979
QY	67980	GCCCGCATTCACACGAGGGGAGTACTGATTAATTAAGTCCCGCAATCTATCTGCTAT	68039
Db	67980	GCCCGCATTCACACGAGGGGAGTACTGATTAATTAAGTCCCGCAATCTATCTGCTAT	68039
QY	68040	TTTGTGAGAGCTCCTTTAGACAGTAAACCATGTGTCTCCGACACTGCGGTACATGTAACCG	68099
Db	68040	TTTGTGAGAGCTCCTTTAGACAGTAAACCATGTGTCTCCGACACTGCGGTACATGTAACCG	68099
QY	68100	CTCTCTCTGTCTGTGTGATGACACCTGGAGTATCTTACAGAGGTATAGGCGCCGTTTC	68159
Db	68100	CTCTCTCTGTCTGTGTGATGACACCTGGAGTATCTTACAGAGGTATAGGCGCCGTTTC	68159
QY	68160	CACCTTAAAGGTGCGCCTGTGTGAGAGCGGATTTGCGGGCATGTGACGCTCAGTGTCTAT	68219
Db	68160	CACCTTAAAGGTGCGCCTGTGTGAGAGCGGATTTGCGGGCATGTGACGCTCAGTGTCTAT	68219
QY	68220	TTTACCAACATATCATGCGCAGTGGCGGATGTGTGAACTGTGACATATGATTTAAAAAGATG	68279
Db	68220	TTTACCAACATATCATGCGCAGTGGCGGATGTGTGAACTGTGACATATGATTTAAAAAGATG	68279
QY	68280	GTCCTTTCCCGTAAATGCGCACTCATGTGCTGTTTAAACGTTACAGAGGTGTTAAAAAACT	68339

Db	68280	GTCTTCCCGTAATGGGAGCATCATGGCGGTGTTTAACGTACACAGGGTTAAAAAAT	68339
QY	68340	CAGAAGTCTCGGTGACAACTTTTGCAGACTCTCCGAAACGGCTCAGGGATAGCTGTA	68399
Db	68340	CAGAAGTCTCGGTGACAACTTTTGCAGACTCTCCGAAACGGCTCAGGGATAGCTGTA	68399
QY	68400	CCAGCGGCTCTCTTTAAACAGAGATACGTCAAAAAACATGACCCACGTGACCTTAA	68459
Db	68400	CCAGCGGCTCTCTTTAAACAGAGATACGTCAAAAAACATGACCCACGTGACCTTAA	68459
QY	68460	TAACTCACAGAAAGATCTGTGATGATTTGTAATGAATGTCCCTCCCTGGTCCAT	68519
Db	68460	TAACTCACAGAAAGATCTGTGATGATTTGTAATGAATGTCCCTCCCTGGTCCAT	68519
QY	68520	CTCCGGCTCATGGCGGATCTGAAATCTTTAACTGTTCTGTCTTACCGGGTCCCG	68579
Db	68520	CTCCGGCTCATGGCGGATCTGAAATCTTTAACTGTTCTGTCTTACCGGGTCCCG	68579
QY	68580	GGTTAAAAACCGGGGGCCGCCACCTGATACTGCCGTGCGCAGAAATGCGCCAGAGCAT	68639
Db	68580	GGTTAAAAACCGGGGGCCGCCACCTGATACTGCCGTGCGCAGAAATGCGCCAGAGCAT	68639
QY	68640	CTGAGAAATTTCTACCGAGAGGGCCCTTGTGTACCGAAAGATTTTATAGCTCTGC	68699
Db	68640	CTGAGAAATTTCTACCGAGAGGGCCCTTGTGTATCCGAAAGATTTTATAGCTCTGC	68699
QY	68700	CTGCAGCGGGGTGTTTATACCGCCACAGTGGCCAGAGTTCTGCACAGCTGTACCGGA	68759
Db	68700	CTGCAGCGGGGTGTTTATACCGCCACAGTGGCCAGAGTTCTGCACAGCTGTACCGGA	68759
QY	68760	AATGAAAGCCAACTGTTTGGGGGCGTGGGCTCTCTCAATGTTTGCAGGCGGCTATCAT	68819
Db	68760	AATGAAAGCCAACTGTTTGGGGGCGTGGGCTCTCTCAATGTTTGCAGGCGGCTATCAT	68819
QY	68820	GGCATATGGCCAGCTCGGCTCCTCGTCACTTATATACCGTGAATGCCAGAGGAAACTGGA	68879
Db	68820	GGCATATGGCCAGCTCGGCTCCTCGTCACTTATATACCGTGAATGCCAGAGGAAACTGGA	68879
QY	68880	ACTTAGACTCAAAACACTGTGCAAACTGTTTTCACCCATCTTCTCTCAAGATCTT	68939
Db	68880	ACTTAGACTCAAAACACTGTGCAAACTGTTTTCACCCATCTTCTCTCAAGATCTT	68939
QY	68940	AGCCCTTATCAGCTACTGTGGCCAAAGGGAAGTGTCTGTGACATTTATTTACATCAC	68999
Db	68940	AGCCCTTATCAGCTACTGTGGCCAAAGGGAAGTGTCTGTGACATTTATTTACATCAC	68999
QY	69000	CGGTACGCGCGAAGAGAGGGCCCTCTCGACTGTGAATCTAGAGGGATACGCTGC	69059
Db	69000	CGGTACGCGCGAAGAGAGGGCCCTCTCGACTGTGAATCTAGAGGGATACGCTGC	69059
QY	69060	GGGAAGCAAGCTTGTCCCGGATTCCTTAATCTGCCAGTATGCGAAGCGGGCTTCTCCC	69119
Db	69060	GGGAAGCAAGCTTGTCCCGGATTCCTTAATCTGCCAGTATGCGAAGCGGGCTTCTCCC	69119
QY	69120	GGCAACCCCTGTTGACTCGTATGATGCTTAGAAATTCAGAAATATCTCAGGGCCCC	69179
Db	69120	GGCAACCCCTGTTGACTCGTATGATGCTTAGAAATTCAGAAATATCTCAGGGCCCC	69179
QY	69180	ACCCCTGAGTCAATTTGTCTACAAACAGCACCCCACTGTGCTCAGTCACTAGTCAGAT	69239
Db	69180	ACCCCTGAGTCAATTTGTCTACAAACAGCACCCCACTGTGCTCAGTCACTAGTCAGAT	69239
QY	69240	TATTAGCCCAACCCAGGGGCTTGTCCCGCCCAATTTTATATGACAGCTGGAAGCGGT	69299
Db	69240	TATTAGCCCAACCCAGGGGCTTGTCCCGCCCAATTTTATATGACAGCTGGAAGCGGT	69299
QY	69300	GTCACAGAGATTTACACACAGGCAACAGAGCCTATTTTGGCGCGGCACTAACCGGTTTC	69359
Db	69300	GTCACAGAGATTTACACACAGGCAACAGAGCCTATTTTGGCGCGGCACTAACCGGTTTC	69359
QY	69360	GACATCTGGGCCCTTGGCCCGCATATGCATGTTTCCCAAGTTGGCGGACGTCGCGCA	69419
Db	69360	GACATCTGGGCCCTTGGCCCGCATATGCATGTTTCCCAAGTTGGCGGACGTCGCGCA	69419

D	b	69360	GACATCTGCGGGCCCCCTGAGCCCGCATATGCATGTTTCCCAAGTTGCCGGACGCTTCGGCA	69419
O	y	69420	GGTGGAGGGGTCTCGCGGGCTCGATTGCGGGAAACAGCATGCTTCCGACGCCGCGTT	69479
D	b	69420	GGTGGAGGGGTCTCGCGGGCTCGATTGCGGGAAACAGCATGCTTCCGACGCCGCGTT	69479
O	y	69480	ACGCGCCATATGTCGCCGCAAGAGATGGAACGGTAGACACAGTTGGGAACGTCCTCGT	69539
D	b	69480	ACGCGCCATATGTCGCCGCAAGAGATGGAACGGTAGACACAGTTGGGAACGTCCTCGT	69539
O	y	69540	AAAAAGGTCCACATGGAGAGCGCGCGATACGCTCCAGCGGTTAAATATCAATATAGA	69599
D	b	69540	AAAAAGGTCCACATGGAGAGCGCGCGATACGCTCCAGCGGTTAAATATCAATATAGA	69599
O	y	69600	CTTAACCTCCCGCTCAGAGGGTCCGGCCAGAGTCCGGCCGATATCCGACACACTCCAGATC	69659
D	b	69600	CTTAACCTCCCGCTCAGAGGGTCCGGCCAGAGTCCGGCCGATATCCGACACACTCCAGATC	69659
O	y	69660	CCGCATGGCGGGCGGCTCTCCGCCCTTCCGCCAAGCCGCGACACTCCCGCTAAGAG	69719
D	b	69660	CCGCATGGCGGGCGGCTCTCCGCCCTTCCGCCAAGCCGCGACACTCCCGCTAAGAG	69719
O	y	69720	AAACACACCCAGGAGAGTGGCAGACAAACATCGAAGGGGAGCTTGGGGGGCGCC	69779
D	b	69720	AAACACACCCAGGAGAGTGGCAGACAAACATCGAAGGGGAGCTTGGGGGGCGCC	69779
O	y	69780	AACAGTAAACACACCTTCCCGGGAGCGTCCGGATGCGCTTCCGAGCAGGGCTATT	69839
D	b	69780	AACAGTAAACACACCTTCCCGGGAGCGTCCGGATGCGCTTCCGAGCAGGGCTATT	69839
O	y	69840	CGATTATATGAAAGCTCCACGATGTAAACCGCAACGATCTGGACCCAAAACGACGA	69899
D	b	69840	CGATTATATGAAAGCTCCACGATGTAAACCGCAACGATCTGGACCCAAAACGACGA	69899
O	y	69900	CGAATCTGAGCGGGCTATCCTAAGAGCCGTATGAGATACAGTCCCGCCGCGCATGA	69959
D	b	69900	CGAATCTGAGCGGGCTATCCTAAGAGCCGTATGAGATACAGTCCCGCCGCGCATGA	69959
O	y	69960	TTCCCTCCACGAACTCGGACATGAGAGATTTCCAGAGGTTAGTCCGCATCTAG	70019
D	b	69960	TTCCCTCCACGAACTCGGACATGAGAGATTTCCAGAGGTTAGTCCGCATCTAG	70019
O	y	70020	CGGCGACGATCGCTTGAAGAATGACCCCAAGCAGAGATCACACACGAGACATC	70079
D	b	70020	CGGCGACGATCGCTTGAAGAATGACCCCAAGCAGAGATCACACACGAGACATC	70079
O	y	70080	CCACGCAACCCGGCGGATGTCTAACCGTAAAAATATCACGGTGGAAAGTCCCTGGTG	70139
D	b	70080	CCACGCAACCCGGCGGATGTCTAACCGTAAAAATATCACGGTGGAAAGTCCCTGGTG	70139
O	y	70140	CGACAAAATAGACTTCAAACTTAACCATTTTCTGCTATTTCCGGGACACTAAAAAAT	70199
D	b	70140	CGACAAAATAGACTTCAAACTTAACCATTTTCTGCTATTTCCGGGACACTAAAAAAT	70199
O	y	70200	GTCGCGAGTGGGCACAATTTTAAATCTGTGAATATGTCATCTTCTCAAGTTCTGTC	70259
D	b	70200	GTCGCGAGTGGGCACAATTTTAAATCTGTGAATATGTCATCTTCTCAAGTTCTGTC	70259
O	y	70260	CTAAGAAATTCACATCCAGTTTCAATATCAATATAAGACACGCTTTGTTTCGGGAATC	70319
D	b	70260	CTAAGAAATTCACATCCAGTTTCAATATCAATATAAGACACGCTTTGTTTCGGGAATC	70319
O	y	70320	TTGGGCTTTTATCTTGAAGGCCCCCTAAAAACATGCGCTGTGGAAACACAAACCA	70379
D	b	70320	TTGGGCTTTTATCTTGAAGGCCCCCTAAAAACATGCGCTGTGTGGAAACACAAACCA	70379
O	y	70380	AGAGACCCCAAGTCTTGAATTTATGCCATTAAGATCTCCACGGTGGAAACACACGAGGA	70439
D	b	70380	AGAGACCCCAAGTCTTGAATTTATGCCATTAAGATCTCCACGGTGGAAACACACGAGGA	70439
O	y	70440	TGGAATTCACAAACCTGTGTCTGACGCGCAGGATCTGCTCGGGCTTATATCTATAGG	70499
D	b	70440	TGGAATTCACAAACCTGTGTCTGACGCGCAGGATCTGCTCGGGCTTATATCTATAGG	70499

QY	70300	AGAAATAACGGCCCGCTTTTCCCAATAATAATGACAAATGACAGACAAATACCGGAGACGCTG	70559
Db	70500	AGAAATAACGGCCCGCTTTTCCCAATAATAATGACAAATGACAGACAAATACCGGAGACGCTG	70559
QY	70560	AAACCTTCGGCAGCTACGCTGCGCGGAGCGCTTTTCTGGCGCTTCTGTGTCAAGGAGCT	70619
Db	70560	AAACCTTCGGCAGCTACGCTGCGCGGAGCGCTTTTCTGGCGCTTCTGTGTCAAGGAGCT	70619
QY	70620	ATGGAACAACACACCGAGAGAGGGCGCTGTCTTAAAGACCGTCCCGCTCCGCTAAACGCT	70679
Db	70620	ATGGAACAACACACCGAGAGAGGGCGCTGTCTTAAAGACCGTCCCGCTCCGCTAAACGCT	70679
QY	70680	CGCGTCGACATAATTCACGCGGGCTCGAGGCGCTGTGTGGCCGACGAAGGACACCTCACAG	70739
Db	70680	CGCGTCGACATAATTCACGCGGGCTCGAGGCGCTGTGTGGCCGACGAAGGACACCTCACAG	70739
QY	70740	GGGCACTATGCCGATATCTGACCGGATAGGCAAGACAGGTGGCGCTGACATATACATATCTCA	70799
Db	70740	GGGCACTATGCCGATATCTGACCGGATAGGCAAGACAGGTGGCGCTGACATATACATATCTCA	70799
QY	70800	AGGTGATTCGCGGGCTGTCGCAAAAAAACAAGACCCCTTCGACACCATCTCTCTCTTC	70859
Db	70800	AGGTGATTCGCGGGCTGTCGCAAAAAAACAAGACCCCTTCGACACCATCTCTCTCTTC	70859
QY	70860	GTTGCTATTCCTTTGATGTTTAAACAGTATGCTGTTTATATTAACCCCTGCCATAGCCCG	70919
Db	70860	GTTGCTATTCCTTTGATGTTTAAACAGTATGCTGTTTATATTAACCCCTGCCATAGCCCG	70919
QY	70920	AACGGAACCTGTGCGATGCGATATTAACGCAACACACGACAGTACAGATGGACGCG	70979
Db	70920	AACGGAACCTGTGCGATGCGATATTAACGCAACACACGACAGTACAGATGGACGCG	70979
QY	70980	CAAAACGCGCGGCGACAGTGCAGAACCTCAGAGAAAAATTAAGCCCAACGCTGCACAACAG	71039
Db	70980	CAAAACGCGCGGCGACAGTGCAGAACCTCAGAGAAAAATTAAGCCCAACGCTGCACAACAG	71039
QY	71040	TACAAATAAGCAAAATTTAGTAATTTGTAATTTTAAAGTTTCCGAGGTTTCCCGCTGCGCT	71099
Db	71040	TACAAATAAGCAAAATTTAGTAATTTGTAATTTTAAAGTTTCCGAGGTTTCCCGCTGCGCT	71099
QY	71100	GCGGACACCGTCCGCTCTTAAATGGAATACCTCTCCTAACAGACGCTATTCCAAACAG	71159
Db	71100	GCGGACACCGTCCGCTCTTAAATGGAATACCTCTCCTAACAGACGCTATTCCAAACAG	71159
QY	71160	GAGCTGGAAGATTAACACAGCACTGACCCGCTCAGCCGCTCAACAGCAAGCCCTTCAA	71219
Db	71160	GAGCTGGAAGATTAACACAGCACTGACCCGCTCAGCCGCTCAACAGCAAGCCCTTCAA	71219
QY	71220	AAGCAGCGCATCTTTTACAGAAAGATGATATTTATGATGTGCAAAAAACGGGAACGATAA	71279
Db	71220	AAGCAGCGCATCTTTTACAGAAAGATGATATTTATGATGTGCAAAAAACGGGAACGATAA	71279
QY	71280	AAAAGCAGCGCATGATTTTAAGCCACCTCGGGTTACTAGTTTAAACCTCCCTAATGATTT	71339
Db	71280	AAAAGCAGCGCATGATTTTAAGCCACCTCGGGTTACTAGTTTAAACCTCCCTAATGATTT	71339
QY	71340	CTATTTCACCCCTTCATAATAAATTTTAAATACGTTTGGGGGTTTGCATTTCCGTCT	71399
Db	71340	CTATTTCACCCCTTCATAATAAATTTTAAATACGTTTGGGGGTTTGCATTTCCGTCT	71399
QY	71400	TAAACATATTAACAAATCTCATTTTGGGAATTAAGATTTATGGGATTAAGGATTTAAATTTT	71459
Db	71400	TAAACATATTAACAAATCTCATTTTGGGAATTAAGATTTATGGGATTAAGGATTTAAATTTT	71459
QY	71460	TTTGTGATCATGCGATTTGGGAACATACGCTGCGGATGAGAGGTATGCTCATGAGCTGCG	71519
Db	71460	TTTGTGATCATGCGATTTGGGAACATACGCTGCGGATGAGAGGTATGCTCATGAGCTGCG	71519
QY	71520	TGGCGTGAGATTGCACGGGGACGCTCGGTGTGCCAACTGCGACCTGACAGATGGGAAT	71579
Db	71520	TGGCGTGAGATTGCACGGGGACGCTCGGTGTGCCAACTGCGACCTGACAGATGGGAAT	71579

QY	71580	ACGAGGCGGATACAGGACTACCTGGAAGAATGCGCGCAAACTGAAGGCTGGGGAGCC	71635
Db	71580	ACGAGGCGGATACAGGACTACCTGGAAGAATGCGCGCAAACTGAAGGCTGGGGAGCC	71639
QY	71640	TGGACGGTCCGGACAGACAAGAGGGCTGTGAACCAAGCAACACCGAAGCGTAATATAT	71699
Db	71640	TGGACGGTCCGGACAGACAAGAGGGCTGTGAACCAAGCAACACCGAAGCGTAATATAT	71699
QY	71700	CGATTAAGACCTTAACGTTGTACATCAATCAGGTCAAAAATAAGAGCCCTGGGACAGCACGA	71759
Db	71700	CGATTAAGACCTTAACGTTGTACATCAATCAGGTCAAAAATAAGAGCCCTGGGACAGCACGA	71759
QY	71760	GGGCGGAATCATCAACAGCACTGCCAGCATCAAGCAGTTAAGCTCTCCGATTATCAA	71819
Db	71760	GGGCGGAATCATCAACAGCACTGCCAGCATCAAGCAGTTAAGCTCTCCGATTATCAA	71819
QY	71820	CCCCGGAATTGGGCGCAACAACCTCCCGGTATTAATAATGCACTCCGCGGAGTCACTACAG	71879
Db	71820	CCCCGGAATTGGGCGCAACAACCTCCCGGTATTAATAATGCACTCCGCGGAGTCACTACAG	71879
QY	71880	GTGGGACACCCCTGGAAAGCGCGCCCCACGCGTTTATTATGACACAAAGCATCTCA	71939
Db	71880	GTGGGACACCCCTGGAAAGCGCGCCCCACGCGTTTATTATGACACAAAGCATCTCA	71939
QY	71940	ACCACTGTGTCTCTCTCTTTAGAGCCATCCGTGGCGGTCAGACGCGATACCGAGC	71999
Db	71940	ACCACTGTGTCTCTCTCTTTAGAGCCATCCGTGGCGGTCAGACGCGATACCGAGC	71999
QY	72000	AGTCGGTTCGGGATCGGAACAGCGTCAAGCAAGATATGTAACCCCTGGCGCGCTTCCC	72059
Db	72000	AGTCGGTTCGGGATCGGAACAGCGTCAAGCAAGATATGTAACCCCTGGCGCGCTTCCC	72059
QY	72060	TCCTTCAAGCCAGACCCCTGCTCACAGGTCCGGGTACCCCTTGCCCGCAAGATAG	72119
Db	72060	TCCTTCAAGCCAGACCCCTGCTCACAGGTCCGGGTACCCCTTGCCCGCAAGATAG	72119
QY	72120	CAAGATACGCCGAGTGCAGAACTATGCAACAAAATTGACCGCAAGAATACACGCGC	72179
Db	72120	CAAGATACGCCGAGTGCAGAACTATGCAACAAAATTGACCGCAAGAATACACGCGC	72179
QY	72180	GTCGGTTCGACGAGTGCCTCGGTATGAGCGGTGACACGGGACCTCAACGTCGCGTACAGC	72239
Db	72180	GTCGGTTCGACGAGTGCCTCGGTATGAGCGGTGACACGGGACCTCAACGTCGCGTACAGC	72239
QY	72240	CCATTTCCTCCCTTGCGCGAAGCGCGTGGCACTGGTTCACCCCGTGGGGCTATGGCGGGA	72299
Db	72240	CCATTTCCTCCCTTGCGCGAAGCGCGTGGCACTGGTTCACCCCGTGGGGCTATGGCGGGA	72299
QY	72300	ATATTGGGCGCTCAGGATGCGCTTGTACAGATATATCAATATATGACATGAAGAATAC	72359
Db	72300	ATATTGGGCGCTCAGGATGCGCTTGTACAGATATATCAATATATGACATGAAGAATAC	72359
QY	72360	ACGACGCTTCACTCGGAATAAAGTTATTATTATTTTGGACACATGTCGCGGTGTAATTT	72419
Db	72360	ACGACGCTTCACTCGGAATAAAGTTATTATTATTTTGGACACATGTCGCGGTGTAATTT	72419
QY	72420	CTGGTCTCGAGCTGGGCGCGCTCTCTCTAGCGCCCGCGCGCTGGGAGGAGATTCCG	72479
Db	72420	CTGGTCTCGAGCTGGGCGCGCTCTCTCTAGCGCCCGCGCGCTGGGAGGAGATTCCG	72479
QY	72480	CCTCTGTGTGTTCTGCTCAATTGACACGTCACGCGGATACTAATTCGCGGAGGCGTCT	72539
Db	72480	CCTCTGTGTGTTCTGCTCAATTGACACGTCACGCGGATACTAATTCGCGGAGGCGTCT	72539
QY	72540	TCGCAATCGCCCGCGCGCTACAGGCGCTTGGCGGTGGCCGCTCACCTTACCTTCAACTTA	72599
Db	72540	TCGCAATCGCCCGCGCGCTACAGGCGCTTGGCGGTGGCCGCTCACCTTACCTTCAACTTA	72599
QY	72600	CGGGTTGGACAGTTACATAAGCGCAAGCGACGTGCAATTTTGGCTCTCTTTGGGTTG	72659
Db	72600	CGGGTTGGACAGTTACATAAGCGCAAGCGACGTGCAATTTTGGCTCTCTTTGGGTTG	72659
QY	72660	TTAAGATGACGGGGTCCGAGCCGAGCTGTGGGATCCCGAGAAATTTATCAGCTTTTGG	72719

Db	72650	TTAGAGATGACGGGTCGGAGCCGACCTGGTGGATCCGAGATTTATCAGCTTTTGG	72719	Db	73740	TGAGTTGTATTATAGATGTCACAGCTCAGACCCGCCAGCTCCCATTAATCGTGGGC	73799
Oy	72720	AGTCTCTGTTTTCACCGACAAATTTTTCACCTGAGCGGCTAACTCCCTCATTTGTACG	72779	Oy	73800	GCTGTGACCTGGCGCAAAAGGGGCTTACCGTGCAGCGACCAATGACCCAGTGTGG	73859
Db	72720	AGTCTCTGTTTTCACCGACAAATTTTTCACCTGAGCGGCTAACTCCCTCATTTGTACG	72779	Db	73800	GCTGTGACCTGGCGCAAAAGGGGCTTACCGTGCAGCGACCAATGACCCAGTGTGG	73859
Oy	72780	TCTTTTGGGGGCGCGCTGTGGGACCGCTGCAGACATGAGCGACTACTACGATTAC	72839	Oy	73860	TACATCTAGGTTTATTAACCTTACCAAGAGCCCAATGATATACCAACAAGCCGCA	73919
Db	72780	TCTTTTGGGGGCGCGCTGTGGGACCGCTGCAGACATGAGCGACTACTACGATTAC	72839	Db	73860	TACATCTAGGTTTATTAACCTTACCAAGAGCCCAATGATATACCAACAAGCCGCA	73919
Oy	72840	AGAGTACAGGGGAGCTTAAATCTTACAGGGGCCCTGAGGCTCATCGGGCCGACG	72899	Oy	73920	TATGTCAGGTAGTGTATATCCACGAAGACCAAGCTCCCAAGGGGGGGAACATTTAGAT	73979
Db	72840	AGAGTACAGGGGAGCTTAAATCTTACAGGGGCCCTGAGGCTCATCGGGCCGACG	72899	Db	73920	TATGTCAGGTAGTGTATATCCACGAAGACCAAGCTCCCAAGGGGGGGAACATTTAGAT	73979
Oy	72900	GTTTCAACAAATTTAAAAACACATATATGTAGTACAGAAATGTTGCAACCGGACG	72959	Oy	73980	CCCGGTACAACTCGCGAGCACCCCTCCAGATATCGTGGCCCAAAATCAGTTTACCGACG	74039
Db	72900	GTTTCAACAAATTTAAAAACACATATATGTAGTACAGAAATGTTGCAACCGGACG	72959	Db	73980	CCCGGTACAACTCGCGAGCACCCCTCCAGATATCGTGGCCCAAAATCAGTTTACCGACG	74039
Oy	72960	AGAACAGATTGATCAGCCCATATCTCGAAAACTAGACAGCAGCGGCTGTAGTG	73019	Oy	74040	TGGCAGCGCTCCCAAAACCCACCGCTCAACTCCCGCCACACTCAAGCCAAACCGAAC	74099
Db	72960	AGAACAGATTGATCAGCCCATATCTCGAAAACTAGACAGCAGCGGCTGTAGTG	73019	Db	74040	TGGCAGCGCTCCCAAAACCCACCGCTCAACTCCCGCCACACTCAAGCCAAACCGAAC	74099
Oy	73020	TCCGCGGAGCAATCATAGTATATAAAGAGGGCGTTAGGAGGAGCGCGGAGGGGTTT	73079	Oy	74100	CGGAGACCGCCCGCGCCCAAGGGGTTGGGGTGGTCAAGGTTATATTTAAAAACATGG	74159
Db	73020	TCCGCGGAGCAATCATAGTATATAAAGAGGGCGTTAGGAGGAGCGCGGAGGGGTTT	73079	Db	74100	CGGAGACCGCCCGCGCCCAAGGGGTTGGGGTGGTCAAGGTTATATTTAAAAACATGG	74159
Oy	73080	GTAATCAGAGAGGCGCCCTCTCTAGTTCGAGAGGTGTGACGCTGGCGCACAC	73139	Oy	74160	CATTATTTTAAAGTTTATTTATTTTAAATAAACAATCCAAATTAACGTTAACATCAGCT	74219
Db	73080	GTAATCAGAGAGGCGCCCTCTCTAGTTCGAGAGGTGTGACGCTGGCGCACAC	73139	Db	74160	CATTATTTTAAAGTTTATTTATTTTAAATAAACAATCCAAATTAACGTTAACATCAGCT	74219
Oy	73140	GGCAGACACATATATAGCACGCCAACAGGGCTAAACGCGACACATTTGACCTGTCA	73199	Oy	74220	TGCGATCTGTATTTATTTTCTGCGACGATATATCCGACCGCCACACTGGGGCGTC	74279
Db	73140	GGCAGACACATATATAGCACGCCAACAGGGCTAAACGCGACACATTTGACCTGTCA	73199	Db	74220	TGCGATCTGTATTTATTTTCTGCGACGATATATCCGACCGCCACACTGGGGCGTC	74279
Oy	73200	TTCAAGCGCGGCTTCGCGAGGCAACCCCTCACTTGGACGCGGCTCTCTTATATATCT	73259	Oy	74280	GTTTGTCAATCACCGGATGGGAGGGTGGAGAGCGCTTGGTGTCTACAGCACATTA	74339
Db	73200	TTCAAGCGCGGCTTCGCGAGGCAACCCCTCACTTGGACGCGGCTCTCTTATATATCT	73259	Db	74280	GTTTGTCAATCACCGGATGGGAGGGTGGAGAGCGCTTGGTGTCTACAGCACATTA	74339
Oy	73260	ACGAGTTAAACATTATGCGAGAGTGAACCGCCCATACGGTTCCGTACGCTTTGACTCT	73319	Oy	74340	TTAATTTCCGAGCCGACGTGACAGATCATGAGATGAGCGATCGTGTGCCAGTTTTC	74399
Db	73260	ACGAGTTAAACATTATGCGAGAGTGAACCGCCCATACGGTTCCGTACGCTTTGACTCT	73319	Db	74340	TTAATTTCCGAGCCGACGTGACAGATCATGAGATGAGCGATCGTGTGCCAGTTTTC	74399
Oy	73320	GTAAGTTGAATATATACCAAAAAACAATCTATCTGTATAGCGTTACGCAACAATTTTC	73379	Oy	74400	ATTTCAGAGTGAACAGGCTCGTGGGCCGCTTATTCAAAAGCGGTGAAGGCGGCTC	74459
Db	73320	GTAAGTTGAATATATACCAAAAAACAATCTATCTGTATAGCGTTACGCAACAATTTTC	73379	Db	74400	ATTTCAGAGTGAACAGGCTCGTGGGCCGCTTATTCAAAAGCGGTGAAGGCGGCTC	74459
Oy	73380	CCGTCTGTGTAACACCGGAGAACCTCTAGTCTGTCCTGGGACTAAAAATTTATCCGCG	73439	Oy	74460	TCGTCCACCGTAATATCCCTATAGCCAGGAGCAACATGAGGCTTCCAGATTAACGTTCTGT	74519
Db	73380	CCGTCTGTGTAACACCGGAGAACCTCTAGTCTGTCCTGGGACTAAAAATTTATCCGCG	73439	Db	74460	TCGTCCACCGTAATATCCCTATAGCCAGGAGCAACATGAGGCTTCCAGATTAACGTTCTGT	74519
Oy	73440	CGCCCGAGTGGCATTTCTTCTCAGCGGAGCGCGAGCGATGAGGTGATTACACACCG	73499	Oy	74520	ATPACCTTACCTTAGATATTTGAATCTTAACCGTCTCTGCGACCCCGGGTACCTTA	74579
Db	73440	CGCCCGAGTGGCATTTCTTCTCAGCGGAGCGCGAGCGATGAGGTGATTACACACCG	73499	Db	74520	ATPACCTTACCTTAGATATTTGAATCTTAACCGTCTCTGCGACCCCGGGTACCTTA	74579
Oy	73500	GACTTATATGATCAAGGGATATGTGGAGAAATAAACTATCTGTTCTCAATAAGACTAAC	73559	Oy	74580	GCTTCCGCAAGGGGCGGTGCGACATCTCTGCTCTTCAATCTCCATATTCACCTCC	74639
Db	73500	GACTTATATGATCAAGGGATATGTGGAGAAATAAACTATCTGTTCTCAATAAGACTAAC	73559	Db	74580	GCTTCCGCAAGGGGCGGTGCGACATCTCTGCTCTTCAATCTCCATATTCACCTCC	74639
Oy	73560	AGGTCTGACACTTTACCGGGGAGAGTCAAGTCTCATCTCATGCGGTTTATGTACGCTT	73619	Oy	74640	GTCCTCCGAAGGGGCGGTGCGACATCTCTGCTCTTCAATCTCCATATTCACCTCC	74699
Db	73560	AGGTCTGACACTTTACCGGGGAGAGTCAAGTCTCATCTCATGCGGTTTATGTACGCTT	73619	Db	74640	GTCCTCCGAAGGGGCGGTGCGACATCTCTGCTCTTCAATCTCCATATTCACCTCC	74699
Oy	73620	CGCCCGGCGCCCTAAATATGCGGATGTAAGTCAACATTAATCTTGTGACGCTGAT	73679	Oy	74700	GGGGGACAGCCATATGCTATTTTGGTCCGCGAGTGTAGTAGCACTCGTTAAGAGATCT	74759
Db	73620	CGCCCGGCGCCCTAAATATGCGGATGTAAGTCAACATTAATCTTGTGACGCTGAT	73679	Db	74700	GGGGGACAGCCATATGCTATTTTGGTCCGCGAGTGTAGTAGCACTCGTTAAGAGATCT	74759
Oy	73680	TTGATGTTAGTGGCGCATATGACATATACCCCAACCGACAGAAACCCGTTTACGT	73739	Oy	74760	GGCAGGGGACATATTTGACATCCACGCGTCCAAACGACCTAAACCCGCAACAGCTCAA	74819
Db	73680	TTGATGTTAGTGGCGCATATGACATATACCCCAACCGACAGAAACCCGTTTACGT	73739	Db	74760	GGCAGGGGACATATTTGACATCCACGCGTCCAAACGACCTAAACCCGCAACAGCTCAA	74819
Oy	73740	TGATTTGTATTATTAAGTGCACAGCTCAGACCCCGCAGCTCCCACTAATCGTGGGCG	73799	Oy	74820	AACGACACGCGCGGCGCATTTGCCAACAAATGATGATAAATTAGGCAATTTCTC	74879
Db	73740	TGATTTGTATTATTAAGTGCACAGCTCAGACCCCGCAGCTCCCACTAATCGTGGGCG	73799	Db	74820	AACGACACGCGCGGCGCATTTGCCAACAAATGATGATAAATTAGGCAATTTCTC	74879

QY 74880 TACTAGTGAATATGCGCCGAAAGTAATTAAGGATATCTGACTGAAGCGCAAGCGGC 74939
Db 74880 TACTAGTGAATATGCGCCGAAAGTAATTAAGGATATCTGACTGAAGCGCAAGCGGC 74939
QY 74940 GTCCCTTTTTCGCTGCTCCACGATCGGGGCGACGCCCTTAATAATCTCCACATGCCGT 74999
Db 74940 GTCCCTTTTTCGCTGCTCCACGATCGGGGCGACGCCCTTAATAATCTCCACATGCCGT 74999
QY 75000 AATTAACTGTCGCTGCGCCGCAAGCGCCGACGGGGGGGCGCAAGGTTTACCGTGGAT 75059
Db 75000 AATTAACTGTCGCTGCGCCGCAAGCGCCGACGGGGGGGCGCAAGGTTTACCGTGGAT 75059
QY 75060 GGTGCTGAACCTACCGCGCGTGGCGAGTTTAATCTAATCTTAACAGGTGACGCCACCTTGGAC 75119
Db 75060 GGTGCTGAACCTACCGCGCGTGGCGAGTTTAATCTAATCTTAACAGGTGACGCCACCTTGGAC 75119
QY 75120 CTGGGATTAACATTAAGACCGCATTTGACCTGGCTCAACACCGAGGAAATACTCGAACCCAT 75179
Db 75120 CTGGGATTAACATTAAGACCGCATTTGACCTGGCTCAACACCGAGGAAATACTCGAACCCAT 75179
QY 75180 ATTAAAGCTACTGGCATGCAAAAGCGTCCGGCGACAGCAACCATGACTCGTTTAATC 75239
Db 75180 ATTAAAGCTACTGGCATGCAAAAGCGTCCGGCGACAGCAACCATGACTCGTTTAATC 75239
QY 75240 TAAAGTGGCTGGTTTCAGGGGCAAGTTCGTCGCGCCCTAAGAAAGTGTACAATAATGAC 75299
Db 75240 TAAAGTGGCTGGTTTCAGGGGCAAGTTCGTCGCGCCCTAAGAAAGTGTACAATAATGAC 75299
QY 75300 CCCATCCCCCTATTGATGATTAACGCTGCTGGGCTCGTTGAGGATCTGTTTGTACTGCGC 75359
Db 75300 CCCATCCCCCTATTGATGATTAACGCTGCTGGGCTCGTTGAGGATCTGTTTGTACTGCGC 75359
QY 75360 CGGACGCTTTTATTTTTCAGTCTCATATATGACGCGGAGACGCTGGTGACTTAAC 75419
Db 75360 CGGACGCTTTTATTTTTCAGTCTCATATATGACGCGGAGACGCTGGTGACTTAAC 75419
QY 75420 GAGGTATTCAGTCTCAGTCAAGTCAAGGCGCAGAGCTTGTACCGTAAACCTATGACGAAT 75479
Db 75420 GAGGTATTCAGTCTCAGTCAAGTCAAGGCGCAGAGCTTGTACCGTAAACCTATGACGAAT 75479
QY 75480 AGGGCGGCTATTCGCGGGGCTCAGATTCCTTTGGAATTTTCCAAATTTTGGGGTATCT 75539
Db 75480 AGGGCGGCTATTCGCGGGGCTCAGATTCCTTTGGAATTTTCCAAATTTTGGGGTATCT 75539
QY 75540 AAAATACAAAATGCAACAGGACGACGTGAGAGTCCAGGGCCATCGATCAAAACAATCACTC 75599
Db 75540 AAAATACAAAATGCAACAGGACGACGTGAGAGTCCAGGGCCATCGATCAAAACAATCACTC 75599
QY 75600 CATACGTGGGGGCTTGAATGCTGTACCTCAGGACCTGTACACTTCACTACCTGTCAT 75659
Db 75600 CATACGTGGGGGCTTGAATGCTGTACCTCAGGACCTGTACACTTCACTACCTGTCAT 75659
QY 75660 TTACAGATGCAATGACGACAGAGCTTCTGCTACTCTCTGTAACACGCTCAGTTTAC 75719
Db 75660 TTACAGATGCAATGACGACAGAGCTTCTGCTACTCTCTGTAACACGCTCAGTTTAC 75719
QY 75720 GACCCGCGCAAGGTTAAACCTCCGACGCTGTGTCGGGGCTTAAGGGGATTTTAAGGA 75779
Db 75720 GACCCGCGCAAGGTTAAACCTCCGACGCTGTGTCGGGGCTTAAGGGGATTTTAAGGA 75779
QY 75780 GCACGTATGCAATTAATTAAGCAAGCTTACGTAGTACTGATCAATTAACATTTTAAAC 75839
Db 75780 GCACGTATGCAATTAATTAAGCAAGCTTACGTAGTACTGATCAATTAACATTTTAAAC 75839
QY 75840 CGTACCGGCTCTCTCCCGACGGATAGAAACTTTCAGGAATAGCATGTCAATACTG 75899
Db 75840 CGTACCGGCTCTCTCCCGACGGATAGAAACTTTCAGGAATAGCATGTCAATACTG 75899
QY 75900 GTGTGACAAATCGAGAGACGTGGGGAATATGACTAGATTAATGACCAAGTATCCACA 75959
Db 75900 GTGTGACAAATCGAGAGACGTGGGGAATATGACTAGATTAATGACCAAGTATCCACA 75959

QY 75960 GCTGAATCTAACAAGATTTATCGGCTCTCCTTGAACCTAGCGGCCCTAGATCAGTATTC 76019
Db 75960 GCTGAATCTAACAAGATTTATCGGCTCTCCTTGAACCTAGCGGCCCTAGATCAGTATTC 76019
QY 76020 CGGAGGCCCAAGGAAACCTTTTACGTGTGGCTTCCGAAATTCACATACAGTGCGA 76079
Db 76020 CGGAGGCCCAAGGAAACCTTTTACGTGTGGCTTCCGAAATTCACATACAGTGCGA 76079
QY 76080 GTTTTGAATTAAGATATTTTGTCTAATGACGACGACTGTATAGACGCTACTGGAA 76139
Db 76080 GTTTTGAATTAAGATATTTTGTCTAATGACGACGACTGTATAGACGCTACTGGAA 76139
QY 76140 ACAAAACATTAATCGTCCCGCAAGACGCCAATTCGACAGGCCCTGACGATCAAGATCTCAC 76199
Db 76140 ACAAAACATTAATCGTCCCGCAAGACGCCAATTCGACAGGCCCTGACGATCAAGATCTCAC 76199
QY 76200 CTCCAGGATATTTTACGTGCGACCTGCGGCTATCTCTACCTTACATTTAAACAATTTCT 76259
Db 76200 CTCCAGGATATTTTACGTGCGACCTGCGGCTATCTCTACCTTACATTTAAACAATTTCT 76259
QY 76260 AGTTTACGCGCAGATATTTCAACCCAGCACTCCAGTTTATAGATGGGTGGATTT 76319
Db 76260 AGTTTACGCGCAGATATTTCAACCCAGCACTCCAGTTTATAGATGGGTGGATTT 76319
QY 76320 TGATCTAAAGGTAAACCGAGGTAGACGACTCTAAACGATATCTACAACATATGCGTAAC 76379
Db 76320 TGATCTAAAGGTAAACCGAGGTAGACGACTCTAAACGATATCTACAACATATGCGTAAC 76379
QY 76380 GCTGCGCAGGCTCATTTAGAAAGCTGCACTTAATAGTCCACTAAACCGAACCCACC 76439
Db 76380 GCTGCGCAGGCTCATTTAGAAAGCTGCACTTAATAGTCCACTAAACCGAACCCACC 76439
QY 76440 CGTGTATTTTAAAGTCGCGGCTCTCCAGCCGTAACCGCGCGGATGATATCTAGACAC 76499
Db 76440 CGTGTATTTTAAAGTCGCGGCTCTCCAGCCGTAACCGCGCGGATGATATCTAGACAC 76499
QY 76500 CGCGTCTGTACTGTGACGCAAAATAGGATGAGAAATTTGTAACCCCGTTTCCGAGCGG 76559
Db 76500 CGCGTCTGTACTGTGACGCAAAATAGGATGAGAAATTTGTAACCCCGTTTCCGAGCGG 76559
QY 76560 AATCTGTTGGTGGGGTCCGCTCACGCTGCTCCCTGACGCAATTTTAAACCGCGTGGT 76619
Db 76560 AATCTGTTGGTGGGGTCCGCTCACGCTGCTCCCTGACGCAATTTTAAACCGCGTGGT 76619
QY 76620 TAACTGGACACGCGGCTAGCCTCAGAGTATCTGGGATCTTAAGATTAAGAACCAT 76679
Db 76620 TAACTGGACACGCGGCTAGCCTCAGAGTATCTGGGATCTTAAGATTAAGAACCAT 76679
QY 76740 CCCGGGGGCGAGCTGTACAGGCTCTTAAATTAATTAATGTAACCCGGAAGTCCAGA 76799
Db 76740 CCCGGGGGCGAGCTGTACAGGCTCTTAAATTAATTAATGTAACCCGGAAGTCCAGA 76799
QY 76800 TAAATCGGCTATTTGAAAAACGCGTTTAAAGTTTCTAATCTGATCAACGCGCCCTGG 76859
Db 76800 TAAATCGGCTATTTGAAAAACGCGTTTAAAGTTTCTAATCTGATCAACGCGCCCTGG 76859
QY 76860 AGACTCTGTACCAAAAACGCGCACCTGCTAGCGATCACTGACGAAAAAGAGGCTT 76919
Db 76860 AGACTCTGTACCAAAAACGCGCACCTGCTAGCGATCACTGACGAAAAAGAGGCTT 76919
QY 76920 TCTAGAAAACCAAAACGAATTAATCTTCCAAAACATCAACGACCTGCGCGAAAAAT 76979
Db 76920 TCTAGAAAACCAAAACGAATTAATCTTCCAAAACATCAACGACCTGCGCGAAAAAT 76979
QY 76980 TGAGGAAACCAACAGAAAAACCATTAATGATTGGGACGACCGGAGTGGCCAAAAC 77039
Db 76980 TGAGGAAACCAACAGAAAAACCATTAATGATTGGGACGACCGGAGTGGCCAAAAC 77039
QY 77040 ACAGGATACCATACAGGCTTTCTTCCGATGACCGGATCGGCAATTTGCACTGTGAG 77099

|||||
Db 77040 ACACGATACCATACACGCTTTCTTCGGATGATGACCGCATGCGCAATTTTGCAATCTGTGAG 77099
QY 77100 CTTCAATGCACCTCCGGAGACACATTTATACAGTTAAACCAAAAAAGAAACAACTTTT 77159
Db 77100 CTTCAATGCACCTCCGGAGACACATTTATACAGTTAAACCAAAAAAGAAACAACTTTT 77159
QY 77160 CTGTATTAATCAATTAAGACCAACACACATGAGACAGTCCGTATTTTAAACCTTACA 77219
Db 77160 CTGTATTAATCAATTAAGACCAACACACATGAGACAGTCCGTATTTTAAACCTTACA 77219
QY 77220 TTCCCAAAAAAGAGAGGTACGGTGCCTTTATGATCAGTGGTGTGCGCAAAAG 77279
Db 77220 TTCCCAAAAAAGAGAGGTACGGTGCCTTTATGATCAGTGGTGTGCGCAAAAG 77279
QY 77280 TAATCATTAATAGCCCAACTGCACATTTTCATTTATGTAACCATTAACCGGACGTAGA 77339
Db 77280 TAATCATTAATAGCCCAACTGCACATTTTCATTTATGTAACCATTAACCGGACGTAGA 77339
QY 77340 GACACGAATTAATATCATCCGTATGGCCAGCTCTCCGGCTACTTTGTTAAATTTAAAC 77399
Db 77340 GACACGAATTAATATCATCCGTATGGCCAGCTCTCCGGCTACTTTGTTAAATTTAAAC 77399
QY 77400 GCGTAACCCCAAAAAACATCTGGAGAGTTTGTGCGAAGCGTAACATGGACAG 77459
Db 77400 GCGTAACCCCAAAAAACATCTGGAGAGTTTGTGCGAAGCGTAACATGGACAG 77459
QY 77460 GCAATGCTGAGCCTGGATATCATGAAGATATTTTGAAGAGTGAAGAGACCCCTGTGCG 77519
Db 77460 GCAATGCTGAGCCTGGATATCATGAAGATATTTTGAAGAGTGAAGAGACCCCTGTGCG 77519
QY 77520 TCTTACGACTCCCATTTAAACCCGACATTATCAACGCGCTTTTATATGATTTACAT 77579
Db 77520 TCTTACGACTCCCATTTAAACCCGACATTATCAACGCGCTTTTATATGATTTACAT 77579
QY 77580 GCGATATGTTTCAAGGACTAATTTTATAGGGGACATATCATGCTGGACCTGCA 77639
Db 77580 GCGATATGTTTCAAGGACTAATTTTATAGGGGACATATCATGCTGGACCTGCA 77639
QY 77640 CGACTGCTCTCGAGCAAAATGAGACAGCTGTCCCAACGCGGAGCCAGAACCGCTCAC 77699
Db 77640 CGACTGCTCTCGAGCAAAATGAGACAGCTGTCCCAACGCGGAGCCAGAACCGCTCAC 77699
QY 77700 AACGCGAACACCTTCCGAGAGGGGCCCAATCACAAGTGGTGGCTTACCTTAAATCCG 77759
Db 77700 AACGCGAACACCTTCCGAGAGGGGCCCAATCACAAGTGGTGGCTTACCTTAAATCCG 77759
QY 77760 TAAAGATCTCGATCTGAGACCGCGGTAAATTTGAGCACAGATCTCCACTTAACCGCTC 77819
Db 77760 TAAAGATCTCGATCTGAGACCGCGGTAAATTTGAGCACAGATCTCCACTTAACCGCTC 77819
QY 77820 GCGATCTCGATCTCAGAGCGGCTCCGGTCCGGTCAACGATCAACAGTCAAGCAGATA 77879
Db 77820 GCGATCTCGATCTCAGAGCGGCTCCGGTCCGGTCAACGATCAACAGTCAAGCAGATA 77879
QY 77880 GGTCAAGATCAACCAACGAGGTGATGACCCCGTCAATGAGAACGCTGGCAGAGGG 77939
Db 77880 GGTCAAGATCAACCAACGAGGTGATGACCCCGTCAATGAGAACGCTGGCAGAGGG 77939
QY 77940 CGGTAAAGGAAAGGCCCGTTTATCCGAGAGACCAATGCTGGCCGCGGTGAGAGC 77999
Db 77940 CGGTAAAGGAAAGGCCCGTTTATCCGAGAGACCAATGCTGGCCGCGGTGAGAGC 77999
QY 78000 ATAGCGCACGACTATCGCGGAAAGCGCTTAAACGCGGACATTAAGAGCTATTA 78059
Db 78000 ATAGCGCACGACTATCGCGGAAAGCGCTTAAACGCGGACATTAAGAGCTATTA 78059
QY 78060 AAAAGTGAACCTTCATCCACATCTCTCTGTGCGCACGATTAAGAGTATTTGAGAG 78119
Db 78060 AAAAGTGAACCTTCATCCACATCTCTCTGTGCGCACGATTAAGAGTATTTGAGAG 78119
QY 78120 ACTGTGCGACGACACTGGGACAGTGTGCTTCAAGTGTGCTGCGGCGCCGACCGGT 78179
Db 78120 ACTGTGCGACGACACTGGGACAGTGTGCTTCAAGTGTGCTGCGGCGCCGACCGGT 78179

Db 78120 ACTGTGCGACGACACTGGGACAGTGTGCTTCAAGTGTGCTGCGGCGCCGACCGCT 78179
QY 78180 GCAACCCGAGAGTGTTCACGAGATGACAGCTTACCCGTATAGTCAAGTGTGGCGGCGAG 78239
Db 78180 GCAACCCGAGAGTGTTCACGAGATGACAGCTTACCCGTATAGTCAAGTGTGGCGGCGAG 78239
QY 78240 AAGCGGCTGTGGCCAAAAAGTTAGCCTGGCTAACTAACAGCTTATACAAACCTT 78299
Db 78240 AAGCGGCTGTGGCCAAAAAGTTAGCCTGGCTAACTAACAGCTTATACAAACCTT 78299
QY 78300 GCTCAAGTGTGAGCGGGGAGAAACACAGCCCACTGTTGGCGAGCGCAAAAAAC 78359
Db 78300 GCTCAAGTGTGAGCGGGGAGAAACACAGCCCACTGTTGGCGAGCGCGCAAAAAAC 78359
QY 78360 GCTAGGCTGTGGGAGCTGAGGCTCTCGCGGCTTATCGAGAAAGTCTGGCGTGGC 78419
Db 78360 GCTAGGCTGTGGGAGCTGAGGCTCTCGCGGCTTATCGAGAAAGTCTGGCGTGGC 78419
QY 78420 CCAGGTGCTGATCTCAAAACAGATCGTTGAACGACGAACTAGATATCTTAGA 78479
Db 78420 CCAGGTGCTGATCTCAAAACAGATCGTTGAACGACGAACTAGATATCTTAGA 78479
QY 78480 CAGTAGTCAGACGCTGTGACCTGGTCACTCCAAATCAAGCATTTGCATACAGT 78539
Db 78480 CAGTAGTCAGACGCTGTGACCTGGTCACTCCAAATCAAGCATTTGCATACAGT 78539
QY 78540 CTTCTTGGAGAAATCAGGGTGAAGTTAGCCTGCTGAAGCAGTAACTTACCTGTGTAT 78599
Db 78540 CTTCTTGGAGAAATCAGGGTGAAGTTAGCCTGCTGAAGCAGTAACTTACCTGTGTAT 78599
QY 78600 AAATAACCGCTGTGGGAGAGGCGGACCTGGCGGAGAGTGAAGTGAATTTTAACT 78659
Db 78600 AAATAACCGCTGTGGGAGAGGCGGACCTGGCGGAGAGTGAAGTGAATTTTAACT 78659
QY 78660 AATTAACCCCTGGGAGGAGGCGGCAACCTGGCGGAGAGTGAAGTGAATTTTAACT 78719
Db 78660 AATTAACCCCTGGGAGGAGGCGGCAACCTGGCGGAGAGTGAAGTGAATTTTAACT 78719
QY 78720 TGGCAGAGCCTGTACCTGTTTAAAGTCTTCTTCTGAGAAATTAAGACCGGAGATGAT 78779
Db 78720 TGGCAGAGCCTGTACCTGTTTAAAGTCTTCTTCTGAGAAATTAAGACCGGAGATGAT 78779
QY 78780 GGGACTCTTAATTAATTAAGTGTGAGAGCTACACCAATGCTTGAAGCGGAGTGT 78839
Db 78780 GGGACTCTTAATTAATTAAGTGTGAGAGCTACACCAATGCTTGAAGCGGAGTGT 78839
QY 78840 CATTAACACCCAGCCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 78899
Db 78840 CATTAACACCCAGCCATGATGATGATGATGATGATGATGATGATGATGATGAT 78899
QY 78900 AGTGAATTAATTAACCCATGATGATGATGATGATGATGATGATGATGATGAT 78959
Db 78900 AGTGAATTAATTAACCCATGATGATGATGATGATGATGATGATGATGATGAT 78959
QY 78960 TGCATTAACCCCATTAACCAATTAATTAATTAATTAATTAATTAATTAATTAAT 79019
Db 78960 TGCATTAACCCCATTAACCAATTAATTAATTAATTAATTAATTAATTAATTAAT 79019
QY 79020 TGCAGAGGTTCTGTCTCGGAAACAATAGAGAGTGTGCGCACTAGGCGGACGTTCT 79079
Db 79020 TGCAGAGGTTCTGTCTCGGAAACAATAGAGAGTGTGCGCACTAGGCGGACGTTCT 79079
QY 79080 ATAGCCTTGTATTAACGCGGATGTTATTTACGGAAGTGCACATGAAACCGTGGCG 79139
Db 79080 ATAGCCTTGTATTAACGCGGATGTTATTTACGGAAGTGCACATGAAACCGTGGCG 79139
QY 79140 GCGTAACAGTAAACCGGCTCCATGCGCAAGTTTACAAACATTAATTAAGGCGACGT 79199
Db 79140 GCGTAACAGTAAACCGGCTCCATGCGCAAGTTTACAAACATTAATTAAGGCGACGT 79199
QY 79200 TTAATAGCGTTTATTTGAACATACACATTTTCAAGAGTGTGCTTATTAATTAAT 79259
Db 79200 TTAATAGCGTTTATTTGAACATACACATTTTCAAGAGTGTGCTTATTAATTAAT 79259

OY		79260	CTTCATTCATTCAAAAGTGGCGGATAATATTTTCACGCTGTGGACAAACAATCATATGGGCC	79319
Dd		79260		
OY		79320	CTGTGATTGATTCCTCTCCTCTGTAATAGGACACAGGCAGACACCACCAATCTGTGCANAACGG	79379
Dd		79320		
OY		79380	ATCGGGTGCCCGGGGATACAGAAGGTGTGGTACTGTGGCTTACTTTAACAATGTATTCTATC	79438
Dd		79380		
OY		79440	GGTATCAAAAACGCGATGTCCACCCACAGATGGACGCGCTTGTTCAAGAGTGTTTGA	79499
Dd		79440		
OY		79500	GGTATTCGCCACGGAACCATTAATTAAGAAAATCCATATGACCTTCATATATCCATATCTG	79558
Dd		79500		
OY		79560	ACAACCTCACAAAAAACAATGCGCTCCTCAGGGGGTGAACGGCTTCACAAAGTGTCTCAA	79619
Dd		79560		
OY		79620	CATTAATAATCGTTCATCATATATAGGCGCGGGGGCAACACMACTGAAGCGGCCGGGAGC	79679
Dd		79620	CATTAATAATCGTTCATCATATATAGGCGCGGGGGCAACACMACTGAAGCGGCCGGGAGC	79679
OY		79680	CATCGACAACGTGGTGTTCATTTTTTATCCGTTGGTCTGTGTGATTAACGAACGCCCATCCC	79738
Dd		79680		
OY		79740	AGATGGGCTAAATCTGTCTTGAAGGACCCCATATATATTAATTAACGTATATGCAATAAA	79799
Dd		79740	AGATGGGCTAAATCTGTCTTGAAGGACCCCATATATATTAATTAACGTATATGCAATAAA	79799
OY		79800	TCCCCACGGGCTGTCAACAGATGGCGCCAACACGCAAGAAAGACCGCTCGATGCAGATAG	79855
Dd		79800	TCCCCACGGGCTGTCAACAGATGGCGCCAACACGCAAGAAAGACCGCTCGATGCAGATAG	79855
OY		79860	CGGCAAGGGCGGTTCCTCCGGGGCAACGCAACCGGGCCGCCCTT	79900
Dd		79860	CGGCAAGGGCGGTTCCTCCGGGGCAACGCAACCGGGCCGCCCTT	79900
RESULT 2				
AF210726				
LOCUS		Macaca mulatta rhadinovirus 26-95 long unique region L-DNA,		
DEFINITION		complete sequence.		
ACCESSION		AF210726		
VERSION		AF210726.1 GI:7329990		
KEYWORDS				
SOURCE				
ORGANISM		Macaca mulatta rhadinovirus 26-95		
REFERENCE		Viruses; dsDNA viruses, no RNA stage; Herpesviridae;		
AUTHORS		Gammaherpesvirinae; Rhadinovirus.		
		1 (bases 1 to 130733)		
		Alexander,L., Denekamp,L., Knapp,A., Auerbach,M.R., Damania,B. and		
		DeRoosiers,R.C.		
TITLE		The primary sequence of rhesus monkey rhadinovirus isolate 26-95:		
JOURNAL		sequence similarities to Kaposi's sarcoma-associated herpesvirus		
MEDLINE		and rhesus monkey rhadinovirus isolate I/577		
PUBMED		J. Virol. 74 (7), 3388-3398 (2000)		
REFERENCE		2 (bases 1 to 130733)		
AUTHORS		Alexander,L., Denekamp,L.M., Knapp,A., Auerbach,M., Czajak,S.,		
		Damania,B. and DeRoosiers,R.C.		
TITLE		Direct Submission		
JOURNAL		Submitted (02-DEC-1999) Microbiology, New England Regional Primate		
		Research Center, One Pinehill Dr., Southborough, MA 01772, USA		

FEATURES	SOURCE
Location/Qualifiers	1. .130733
/organism="Macaca mulatta rhadinovirus 26-95"	
/mol_type="genomic DNA"	
/isolate="Macaca mulatta rhadinovirus isolate 26-95"	
/db_xref="taxon:119193"	
513. .1784	
/gene="R1"	
513. .1784	
/gene="R1"	
/codon_start=1	
/product="ORF01"	
/protein_id="AAFS9980.1"	
/db_xref="GI:7329991"	
/translation="MFVLYLFLMLLPVSVLLPAKILSPTEPCSPHPHGGVTLITCRCT STADDSSTOMFRNNITLMRSNFTIGRLVSYTLPNATISDRACQTKTTRNNITDRS SSRLTLDRCSSSTGTYTANNTRVLRCTSGGVNTLRNVFHLNGAVTNGTNRNTHFV LTETVGGTFCASATIGNEKEYSDTINVEFTSFEPKPNNDIPNESHFKTQIIOOTASV OHPENNVYFVPVPSIGVLGTGIALSLIMCMLFTIRCNENSSSTNSYASOTSYIOPSH NORNTNCSRHTRYRNAHOESIEELNODTSEDSCCQVLLKVVAAVDGPOENT NEVEYOYDVVYVENIETOTSIEDNEEHYDGTINPNFNYSGLILEEDVDFVNELEEN OYHLILENDHNENYHNLNLEMTQYDWLE"	
complement(1852. .2418)	
/gene="ORF02"	
complement(1852. .2418)	
/gene="ORF02"	
/codon_start=1	
/product="DHPR"	
/protein_id="AAFS9981.1"	
/db_xref="GI:7329992"	
/translation="MDIAVNCIYAVDQLGKNGTNPMPYLRENEMYFOKMTSTPSV VGEENNVIMGKRTWFSIPKKRPLRVNINILSELLEPSPHGAFLRTLDDDFNFYR QKRLKEQNTVMYVIGKSVSYESVLYNCKPLKLYITRIRSFSDCVFPPSINTEYTWL SELGKDINFEENIGIKKKFOYEKENFKK"	
2595. .3782	
/gene="ORF04"	
2595. .3782	
/gene="ORF04"	
/codon_start=1	
/product="complement binding protein"	
/protein_id="AAFS9982.1"	
/db_xref="GI:7329993"	
/translation="MEWPIITLCITCYVILVDSKDGENYTCLEPPPRENWKANONE NYAAGRVELICRPGFYKLOANVVECLSGVTWTPPAECRRKCSNPEIDILNGEVIIT TDSNARKFGSNTIKYKCNQGTGLLGATVRICLKYDSNLVDMQPAATCEIECKKQAP DIEGKRYVPOEENYLETITFTCNKDFSLGNTTTCMTNGWISSPVCOCITCSA PIDNHTGLVSSRVYKHGOSVITGCGDGLFNHKKCTCEYSLAMPPLPCVAINTP DPPSEYSPGTEKQEMPTPEPNPSHSESTTTTPTPTQNHKSTSPKAPNPETHKRP TTPAGISKQTTTNRPSKPSQNPPIAPPSKKKRHVVLVPSVASSLVLYALAYCC FLK"	
4213. .7611	
/gene="ORF06"	
4213. .7611	
/gene="ORF06"	
/codon_start=1	
/product="sDBP"	
/protein_id="AAFS9983.1"	
/db_xref="GI:7329994"	
/translation="MASKGNAGOPLEDNOCSSRAVIGAGVYVAYSKODPEFAASLIGL NRPGSVFSPLIYGLTVEHEEPLFYAKAAKADDTTLLAVKYVFPREYVFINASL FRPQDGTGLNELCEEARALFEGYPLTEPGPPHSIMPLDEPOLPDDMEFLGVVRE GFKRLMRGCLYPAVRPOTOOYQIAGRQAFYPLATDELPAPHGMRPFRYKQVSAVL YDSLFTSIADLRKDYTAIHATEKOPMDHKITAKIVOKORSTTLPTTDOSSHM IVDSVVAELALSTGCMFLBECPOACCELLNDVSWIFDGCDSPEARVVALRWSAEQAVV HVAQALFAANSVLYLTRVOKAPRGQGDVNVNVSFLQGLGFLNBAATIKENGSEAF KGYSNALDSSSFTPYHLAYAAASRPHLLKALCYMOLFQHHKSTMOADNMHYVST AANSEMTCLGNTPATCLMTLRYLRDREKATLTPQRDPYVVTGAGDENDELIGL NFASEFRBEDGNADDEHPKTYTWOLOCTVTEKXISAGITEDDHNHYNLTINOSFLR VFKTIDSDVGEYWKPYNSMKNNFNREHYKSHHILQFCANVYAPCAVNLNLY KSLMTITDIDLCYCMITIEDONPAMGILPSSWLMKHFOTLMTNFKACGLDGVLTGGE LKLIYHRMFCDFEDTDAGSSGLMAPEKMOVRIIAAMNVYKSIKIKRILITSNAGSE AVOGEFAPGTGTRDTYVAGPYMKLHRALEPPDKRTAALYLMHKISOTNTPYVLK DVDPDELAELVSYKTNLSAEEFNINLVADVDSLMSYARIKNGALIRACGOIQFYAT	

```
TLHCLPVLQITDAEEFPHVIGSAAITAPVLAIEIRGTAITVOTTAQPAATGRL
RHYVTPVAVNKTITVGNNGNNVFCGNGLTFAGRVDENLWPESSPFKGTGVSAMLR
RHVMTPIILRLIKRAAGQITSTFEASVRSVQALLEDKNPMLKSVILILIRLIG
KGCODLSEEDVOYLYDYCMLEDEVILFTLDNTAOGSGVPTIEDAGALLIEDRODADLO
EYVSDDIATASQCPPEEOLPTPSAGALLAGKKRKINALLSIDL"
7636..9696
/gene="ORF07"
7636..9696
/gene="ORF07"
/codon_start=1
/product="transport protein"
/protein_id="AAF59984.1"
/db_xref="GI:7329995"
/translation="MARELALYLAQLSALANDLSVITADPPSIDGARLIKTKTIOEN
LARDLPLIREGNSVETSSLSLEVEHLKNIIDKLGELERSLQRYSSREHEETLRLR
PECHHSTVTFQYGGGLDVNMCILINDELLCKRIGSVFYICIGANELSGIDRYLFE
LSTLRGISIPHPIDLYVTISPCVCLREIETLAVNOGSSLLAVLADRHCHGLKVAE
PHGLEFETLSGLGKTKRSDAIOGVSSADOLBESSLAIDODHNFKRRSASIME
LSNLIYMANAGTQLOTGTENECGOMARLLTHRADHEHRLITPKLSNHFYDCRRPD
PIESLFCGGFLNSIDDTINALSRDCSVTFQOANTTNARKONELETRLSILKRGSA
GSOKEATPSEPTTVAATAADSVIKDOYRREOYMKVARDGFKKLTCELOTQGAVL
ANALCMRWGVAAGEASELVNHFLLRRFVALPWEARCDQILFENSKYIKNSLS
OILSREHEIITLQFGLITGELTQSDLEPGPAAVLAACEAAGMLPHHMLYSEM
IMPOIOPKMDIOTENFRFYOLEBDLNAVOKSACGCTIRELVSVALYNRTMKTIRF
SLAREKLSISNDVAKGLTSGILTYEODAPVLISQNTGMIKDLIALLYHHLQSDG
HDDN"
9683..12172
/gene="ORF08"
9683..12172
/gene="ORF08"
/codon_start=1
/product="ORF08"
/protein_id="AAF59985.1"
/db_xref="GI:7329996"
/translation="MMITNRRLRLANVLIATGAVGENVTPFKATTTAKPTPG
STPTPENPRAEAFKFRVCSATGELFRNLKTEKGTEDKTEOEGILWFKKNIV
PHIEKVRKRVATSVTVYRGWTEFAVKGKQVIRPVOYEINHMDTYOCPSMRVN
VNGIYNTYDRDTNQTQVYFIQDIBGLTINIOYRESOPVLKTPPGPGIYRVRTTNC
EIVDMIASABEYSITFYALGDTVEVSPCHNDSTCSAETKENGELGRALNTTIVD
FATRKPTTEIRFADSGEIVTSKAEDEKSAVCAVLTKEPRALQITHEASVYFVAN
DYATKTPLESEVANETGTYSCLDEKVIDKLTNDITKIKSDIEHTVNSAQYITEGFL
LLMQLPLTSLIDEEMRGLNGTIPAPATTSTVSRRVRSNTMEQATNIAAQLQFAY
DKLRASIKNVELELSRAMCREGVADTYVETLSKINPSVMAITGIRVSAFQVDAI
SVTDCVAVDOASVSIHKSRLSTPGMCVSRPPTREINLTSTLFCQCGRRNEITLD
NOVEKCTCEHYFIASVNTYTYKDYVYKKTINSEITLGTFFIALNLSFENIDPFI
IELYSRAEKLKSGSVFLEIMFREYNTYTKRLAGREDIDNTGLTINLNRLLADEIIV
ADLGVGRTVAVNASVITLFGSIVSGFINFKSPGGMMLVIVAVYLIVFALNRR
TNAIQAPITRMIPYDIDKMOFSGKVDQEOIKNIIAGMHQLOOEERRRLDEQORSAPS
LERRASDGLKRRFRGYKPLENEAOEYEMSK"
12290..15334
/gene="ORF09"
12290..15334
/gene="ORF09"
/codon_start=1
/product="polymerase"
/protein_id="AAF59986.1"
/db_xref="GI:7329997"
/translation="MDFNPYLYGPRGPRPHSHRGTDAPAPAGAAVOPPPDYCRLLIPA
CLRTPGAGGMIIPVITPPTTYFENGARDVLLANERSMWTADRKPVPAPDDQSGITF
HAYDVETTYAADRCAEVSRQDIIISGSAVTLKLGTEDEGTSCVAVFROOVYFA
KVPAGINTHTILOALKNYAGAACGSTRNRYRLIKTYADRAHPMEITLSSSML
STLSRLIYACCGCEVPESNVDAVRVLDHGTITBWRVICTCARITPELARDATTALEFD
CSMEDLSVQDRSDMPYRIYAFDIETCEGGEFPATDGAVIDISCVFTYLRGAP
NPNTLFSVGTCDIPIDVLDIEPEHYDMLVSFAMIDFEVDFTLGNISFEDLYL
ITRASQVYNLRNLETYKIKTGSIEFPEYRGGGGMFSVSKITAGVNIIDMYOVCR
EKLISDYKLDYVLAOCIGCKEEDYSYDIPLEFRSGGGRKAVSYCVMSVLMDL
LKMEIHIYESIAKLAKLTOARVYLTDDQOIRVESCILEAARERFITPVPPESOGG
YOGATVNPPIGFEYDEYLVYDPSALYPSITQAHNLCSTYIHGNDLHLPLPTDDY
ETVYLSGSPVHFVKKHRESLLGRLLVWLKRRIRITLLAACDPSLTKTLLDKQOLA
IKVCNAVYGTGVAAGLLPCINIAETVTLGRRTMLEMKSVLEALTEDETRIGREK
VTARHGAIRVYVGTDLSTFIACDYSAEVASFCDLLAARTADLPFPKILEKEKT
FKCLLTLTKRRTIGVILNDKMWKGVLDIRTKACKFVOERCAIILDIVLHPVEYAAA
RLCRRPHAYVEBGLPAGFTIKIYEVNLASVLDLRNSVYPIEQLFTFELSAPVCYDK
```

```
TTNULHNAVYQKLASRCEELPOYHRIPIVFPADAGSKLSDAEHPDYVRKHQIYVAV
DLYFDKLVHGANITLQCLFNGNADTVALLNFWLPKLES"
15429..16679
/gene="ORF10"
15429..16679
/gene="ORF10"
/codon_start=1
/product="ORF10"
/protein_id="AAF59987.1"
/db_xref="GI:7329998"
/translation="MLVNELSVVLGDMVEYTFHGRFSEVNLRLQTFKHGGYARVRL
PSLIDILHOFARFGLVTRIKELPEPSCVVALIAPLDGSGADARVAPGFLDSSRP
LTVWNASGRHRIIRCCLFLKRIIDLEBRATYYFEGNGARBSGTKPTPCATESLPGGP
LKVSGEASQTSPHSVAFEPYANVSACSLILQVRFPSDDAAHDANI SPKIVTFNS
SGVNYCKASVHTLSPSRCKTQAMQELIYAPGNABIVLGQSGPVLPRTGKRVLGVA
DAEKTIOGSSAEVVOULFOGAAARGLAFVLGVGAPLEPLFVTPPALLSGCTTHL
RLFNENGPPTTKRDTLVAAAPCVVRLSSADPARDLVASPDGALSLINAFITPVG
PGGVASACHVSLRNGVHERNNH"
16688..17917
/gene="ORF11"
16688..17917
/gene="ORF11"
/codon_start=1
/product="ORF11"
/protein_id="AAF59988.1"
/db_xref="GI:7329999"
/translation="WGTVPVRFREFGEMOTSSLVNDGTPRYSLSLWAAITHDGYTLVNR
SELCTERSPCGLACPSIGRLVGRFRPEFAFASVATGDRGTFFVYAGHRNPLDIIY
PAVERRADRELVLVHAHPQTEIVSRXGLKFAVIAIVVRPQVFLHFPDRVPIALTD

Query Match      57.0%; Score 22809; DB 1; Length 130733;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 25189; Conservative 0; Mismatches 26; Indels 10; Gaps 8;

gene
CDS
39900 AACACTATCAGACCCGGCTCTACACGGAACGGGCTTAAGAAGCCTGTTAAGTCAGACA 39959
|||||
37908 AAACACTATCAGACCCGGCTCTACACGGAACGGGCTTAAGAAGCCTGTTAAGTCAGACA 37967
39960 TGGTGTCCATGTTCAAAAGCTACCTTATGATTAAGTCTGTTTCTCGACAAATCAGACA 40019
|||||
37968 TGGTGTCCATGTTCAAAAGCTACCTTATGATTAAGTCTGTTTCTCGACAAATCAGACA 38027
40020 TGGCGCTAAGGGAAGGACGTACGTCGTGCTCTCCGACATGGGCGGGGGGGGT 40079
|||||
38028 TGGCGCTAAGGGAAGGACGTACGTCGTGCTCTCCGACATGGGCGGGGGGGGT 38087
40080 GTACAGAAACGGTTTTTAAAGGGAAGATACGTATCTGTCTGCATCGGAGAGCCCAATTG 40139
|||||
38088 GTACAGAAACGGTTTTTAAAGGGAAGATACGTATCTGTCTGCATCGGAGAGCCCAATTG 38147
40140 CCGGAGTCAATGACACACACGGAACGTAATCGGAACCTGTTAAACATGCTAGTCAAG 40199
|||||
38148 CCGGAGTCAATGACACACACGGAACGTAATCGGAACCTGTTAAACATGCTAGTCAAG 38207
40200 TTGACGGGGGCATGTCGGGTCCGGGCTCTTACGCCAATTAGCTGTACGGGGCGAAATTC 40259
|||||
38208 TTGACGGGGGCATGTCGGGTCCGGGCTCTTACGCCAATTAGCTGTACGGGGCGAAATTC 38267
40260 TCGTAAACCGCCGTGACGTACGTCGCGTCATCGCAAGCTTTGACACGTTCAATGAACGCA 40319
|||||
38268 TCGTAAACCGCCGTGACGTACGTCGCGTCATCGCAAGCTTTGACACGTTCAATGAACGCA 38327
40320 TAGTGGACCGTCCCAACGCGGACCCACGCTGCAGATGATCGGAGCGGCGGCGAGC 40379
|||||
38328 TAGTGGACCGTCCCAACGCGGACCCACGCTGCAGATGATCGGAGCGGCGGCGAGC 38387
40380 GGCACGACTCCCTCGCCAAACACCGATCGGGCGGCGTATTCAGATTGGAAGTAAAC 40439
|||||
38388 GGCACGACTCCCTCGCCAAACACCGATCGGGCGGCGTATTCAGATTGGAAGTAAAC 38447
40440 TGGTGGCTTTGGAAGTTTACAGCAATGTACACGAACCAACGAGTTTCCCTCCGTTAA 40499
|||||
38448 TGGTGGCTTTGGAAGTTTACAGCAATGTACACGAACCAACGAGTTTCCCTCCGTTAA 38507
```

OY	40500	ACAGGGCTATGACACTATACTTATTTTTCCTCCACTTGGGTTGCACATGCCGCTCTCACT	40559
Dp	38508	ACAGGGCTATGACACTATACTTATTTTTCCTCCACTTGGGTTGCACATGCCGCTCTCACT	38567
OY	40560	ATTCCAGCTGGGGCACAAATTAAAGGGGGTGGAGCACCCAGCGGACAAATCCGTCGAAAGCT	40619
Dp	38568	ATTCCAGCTGGGGCACAAATTAAAGGGGGTGGAGCACCCAGCGGACAAATCCGTCGAAAGCT	38627
OY	40620	GGATTTGTTAAATTAATAAACAGTACTCTGTAAGTTTCAATTATGCATAAACCGCGCTCAAGTCCA	40679
Dp	38628	GGATTTGTTAAATTAATAAACAGTACTCTGTAAGTTTCAATTATGCATAAACCGCGCTCAAGTCCA	38687
OY	40680	TCTGTCAATCCCGCGCATGACACAAACCCGATGCCGTGTGGGACAGCTTTGGGTACAGCGCTTTC	40739
Dp	38688	TCTGTCAATCCCGCGCATGACACAAACCCGATGCCGTGTGGGACAGCTTTGGGTACAGCGCTTTC	38747
OY	40740	CAGATCCCGGACACAGTTTCACAGGTACGAGCAAAAGATCTGAGACACCCCGGACATGAACC	40799
Dp	38748	CAGATCCCGGACACAGTTTCACAGGTACGAGCAAAAGATCTGAGACACCCCGGACATGAACC	38807
OY	40800	TATACGGGCTGTGTGTACACTATTACAGGGCAAAAAGTGGCACAGTTCCGATGTGC	40859
Dp	38808	TATACGGGCTGTGTGTACACTATTACAGGGCAAAAAGTGGCACAGTTCCGATGTGC	38867
OY	40860	CCCTTAAAGGGGAGAGTATGACAGATGATGTGTGTGACCAACCTGSCACGAGAGAGC -TT	40918
Dp	38868	CCCTTAAAGGGGAGAGTATGACAGATGATGTGTGTGACCAACCTGSCACGAGAGAGC -TT	38926
OY	40919	CGTTTGGAGGTTGACCCGATGTTTGAATTTTTCGTTTCATCAGACGCTGTGTGCGCAAGCC	40978
Dp	38927	CGTTTGGAGGTTGACCCGATGTTTGAATTTTTCGTTTCATCAGACGCTGTGTGCGCAAGCC	38986
OY	40979	GCGTATAGGGCGACCCACAGACTATGTGTGGGTAAATTTCCACAAACCCCTGGCGCCCAAC	41038
Dp	38987	GCGTATAGGGCGACCCACAGACTATGTGTGGGTAAATTTCCACAAACCCCTGGCGCCCAAC	39046
OY	41039	GAGTTTCAAAAACAGACAGAGCGCTGCAGTTTGAACAGAGCGGGCGCTGTGCTACGTCGTC	41098
Dp	39047	GAGTTTCAAAAACAGACAGAGCGCTGCAGTTTGAACAGAGCGGGCGCTGTGCTACAGTCGTC	39106
OY	41099	GACCACTCAACAGATGCAAAATATTCAGAAATACGGCGCTTGGACAGCTGTACCCACTATCTC	41158
Dp	39107	GACCACTCAACAGATGCAAAATATTCAGAAATATTCAGAAATATTCAGAAATATTCAGAAATATTC	39166
OY	41159	TGTTATGTCAATGCAATGCGCTCATCTTCACGAGACAGAGACAAATTTTGTATTAATCTCCT	41218
Dp	39167	TGTTATGTCAATGCAATGCGCTCATCTTCACGAGACAGAGACAAATTTTGTATTAATCTCCT	39226
OY	41219	TTAATTTGATTTAAACATTTGAACCTTACTGGAAACATGCCGGAACCTGGCGTTTATTAAAC	41278
Dp	39227	TTAATTTGATTTAAACATTTGAACCTTACTGGAAACATGCCGGAACCTGGCGTTTATTAAAC	39286
OY	41279	AGCTTCCCTTATGCTGGGATTTATCTCGCTTCAACCTGGGCAAGGTATTTTCTAAAGAC	41338
Dp	39287	AGCTTCCCTTATGCTGGGATTTATCTCGCTTCAACCTGGGCAAGGTATTTTCTAAAGAC	39346
OY	41339	GTTGACCCCATTAACGAAAGTTTGGGCAACTGTGTGTTTGGACAGAGCGGCTCTCG	41398
Dp	39347	GTTGACCCCATTAACGAAAGTTTGGGCAACTGTGTGTTTGGACAGAGCGGCTCTCG	39406
OY	41399	AAAAATCGGGGCCACGAGTGTGGGGGCGCAGGCCGCTCCGAGCTGATTAACTGTCTT	41458
Dp	39407	AAAAATCGGGGCCACGAGTGTGGGGGCGCAGGCCGCTCCGAGCTGATTAACTGTCTT	39466
OY	41459	CAGGACCCCAATCTTTTGGCGCCTTGGCTTAACATGAGCTTTTTCACAAACGCTCAAG	41518
Dp	39467	CAGGACCCCAATCTTTTGGCGCCTTGGCTTAACATGAGCTTTTTCACAAACGCTCTCAG	39526
OY	41519	CAGTCTTGCGGCGACCCCATGTTACTATAGGCGACAGAGGGTACGAAACGGAATAATGAC	41578
Dp	39527	CAGTCTTGCGGCGACCCCATGTTACTATAGGCGACAGAGGGTACGAAACGGAATAATGAC	39586

QY	41579	AGGGATACGTCACATGCAACGTCACAGAGAAAAATGGAGAGACTAGTCGGTACATGGTTAAC	41538
Db	39587	AGGGATACGTCACATGCAACGTCACAGAGAAAAATGGAGAGACTAGTCGGTACATGGTTAAC	39646
QY	41639	ATTTCACAGACCCAGAAAAACAACGGGAGATCATAGACGGCGGCAGTCCCTTACATCGATCGCC	41698
Db	39647	ATTTCACAGACCCAGAAAAACAACGGGAGATCATAGACGGCGGCAGTCCCTTACATCGATCGCC	39706
QY	41699	TTTTAATGAAAAACGAAACGACATAGGCTGTGCTGGAAAAAGCTTTTTTATTACGTGGTTCG	41758
Db	39707	TTTTAATGAAAAACGAAACGACATAGGCTGTGCTGGAAAAAGCTTTTTTATTACGTGGTTCG	39766
QY	41759	CCACGCTGTACCAACGCTGACGTCCTGGCGCATGGCGCTGATTTTGACACGTGGCCCTG	41818
Db	39767	CCACGCTGTACCAACGCTGACGTCCTGGCGCATGGCGCTGATTTTGACACGTGGCCCTG	39836
QY	41819	GGCCTGACGTACAAACCGCCGAGGTTTTCGTGACGTGTACACCCGACATGAGATTTTG	41878
Db	39827	GGCCTGACGTACAAACCGCCGAGGTTTTCGTGACGTGTACACCCGACATGAGATTTTG	39886
QY	41879	GACCACTGTGAGAAACGGGAGCGCTCCGCGAGATCTCGAGGCTTTCCGATATTACACCCACC	41938
Db	39887	GACCACTGTGAGAAACGGGAGCGCTCCGCGAGATCTCGAGGCTTTCCGATATTACACCCACC	39946
QY	41939	GTTTCACATGATTTGCAACTCTTTTGCACGTCGTTTCTACCTGCCCGTTTGTACCCAGGCC	41998
Db	39947	GTTTCACATGATTTGCAACTCTTTTGCACGTCGTTTCTACCTGCCCGTTTGTACCCAGGCC	40006
QY	41999	TCCCGTGTGTGACTCAGCGGGAGACCCCGCCACCTGTTCACCACTACAGACGACGGGAGA	42058
Db	40007	TCCCGTGTGTGACTCAGCGGGAGACCCCGCCACCTGTTCACCACTACAGACGACGGGAGA	40066
QY	42059	TACGTGAGCCAGACATGTCCTCGTTAACGGGTTTGGCGGCTTTCCTATTCACATTAAGTCT	42118
Db	40067	TACGTGAGCCAGACATGTCCTCGTTAACGGGTTTGGCGGCTTTCCTATTCACATTAAGTCT	40126
QY	42119	CGTGACGTTGCCGAGACCATGTTTAAACCCGCGTCCGTTCAACAAGCTGTACACGATCCC	42178
Db	40127	CGTGACGTTGCCGAGACCATGTTTAAACCCGCGTCCGTTCAACAAGCTGTACACGATCCC	40186
QY	42179	CTGCTGGCGGCGCACGCTCCACCCGCTGTGTGGCAATTACGTACGCGCTGCCGCCACG	42238
Db	40187	CTGCTGGCGGCGCACGCTCCACCCGCTGTGTGGCAATTACGTACGCGCTGCCGCCACG	40246
QY	42239	CGCGTGGCGGCGCGGTTTAACGTACGTCCCGCGGCTCATGCGCAGTACGAGGAGTGGCAC	42298
Db	40247	CGCGTGGCGGCGCGGTTTAACGTACGTCCCGCGGCTCATGCGCAGTACGAGGAGTGGCAC	40306
QY	42299	AAGTCTCCAAATGCTGGGCTTACGCTAACCTGTGCCGATGACGCCACGTCGTTGAGCAC	42358
Db	40307	AAGTCTCCAAATGCTGGGCTTACGCTAACCTGTGCCGATGACGCCACGTCGTTGAGCAC	40366
QY	42359	CTGGCGGACATGCACATGAAGCTGTCCGGCGCGGGTTCACTGTCCACGCCAAAGCACAG	42418
Db	40367	CTGGCGGACATGCACATGAAGCTGTCCGGCGCGGGTTCACTGTCCACGCCAAAGCACAG	40426
QY	42419	ATTTCACCCGGGCTTTGGAGATGACCGCGCGTCCGAACCGATGAGGTGTGGCGGAGAACTTG	42478
Db	40427	ATTTCACCCGGGCTTTGGAGATGACCGCGCGTCCGAACCGATGAGGTGTGGCGGAGAACTTG	40486
QY	42479	CTATTATTAGTCCAGAGGCGCTTGACGTCCATGTTTTTATGGGACAGCATCGGTTATAGCTCGG	42538
Db	40487	CTATTATTAGTCCAGAGGCGCTTGACGTCCATGTTTTTATGGGACAGCATCGGTTATAGCTCGG	40546
QY	42539	GAACTCAGGGCGGACGACGTCACGTTTGAAGTGAATCATGAGTTGGCATCGCTGGACATG	42598
Db	40547	GAACTCAGGGCGGACGACGTCACGTTTGAAGTGAATCATGAGTTGGCATCGCTGGACATG	40606
QY	42599	GGCGTGGGTTATTTCTTCCACATACAGCGCCCGCCAGTTGGCGGCAATTACCTCGGACATG	42658
Db	40607	GGCGTGGGTTATTTCTTCCACATACAGCGCCCGCCAGTTGGCGGCAATTACCTCGGACATG	40666
QY	42659	GGCGTTCACGTGACGATGTTTCTTCATGTTTTCCGGGGACCTGACAGGACGACGACC	42718

Db	40667	GGCGTTCCTGTCAGGACATGTTTCTATGTTTCCGGGAGCTGTAACAGACAGGACC	40726
OY	42719	CTCAACGACTACGTTAAACAAAAGCCGATGCCAAAGATTCGGTGGTCTGTGCCAGATT	42778
Db	40727	CTCAACGACTACGTTAAACAAAAGCCGATGCCAAAGATTCGGTGGTCTGTGCCAGATT	40786
OY	42779	CGTAGCCCGCTGCTTACGTTGGGGGGGTCCGCACTCGGACAACTACCGGGTCTCACG	42838
Db	40787	CGTAGCCCGCTGCTTACGTTGGGGGGGTCCGCACTCGGACAACTACCGGGTCTCACG	40846
OY	42839	CACGACAGCTGGGACAGTGTGAGATTTGTTTGACGCCGTTACTGCAGAGCTTACTCTAT	42898
Db	40847	CACGACAGCTGGGACAGTGTGAGATTTGTTTGACGCCGTTACTGCAGAGCTTACTCTAT	40906
OY	42899	TTTCAAAACCCCAACAGTCCCGGGGAGCGGACATCTGCTGATCTGTTGACGCGTAC	42958
Db	40907	TTTCAAAACCCCAACAGTCCCGGGGAGCGGACATCTGCTGATCTGTTGACGCGTAC	40966
OY	42959	AACACAGAAACCGGGAAAGCTTTGCTTTTGACACTCCATCCGGAATTCGTGCAGAA	43018
Db	40967	AACACAGAAACCGGGAAAGCTTTGCTTTTGACACTCCATCCGGAATTCGTGCAGAA	41026
OY	43019	TACCGCACTACGTTAAACCATGGGGGCTGCACAGGGGCTCCCTGGAGACGCTGTAC	43078
Db	41027	TACCGCACTACGTTAAACCATGGGGGCTGCACAGGGGCTCCCTGGAGACGCTGTAC	41086
OY	43079	AACCTCAACCTTCGCCACAGTGCAGTGTCCAGAGGATGTACAGTCCGTGTGCCAGTTTTC	43138
Db	41087	AACCTCAACCTTCGCCACAGTGCAGTGTCCAGAGGATGTACAGTCCGTGTGCCAGTTTTC	41146
OY	43139	CACAAAGACGCTATTTTGGCTTAACATTCGGGGCTTGAAACACTAGTACGGAAATACGGC	43189
Db	41147	CACAAAGACGCTATTTTGGCTTAACATTCGGGGCTTGAAACACTAGTACGGAAATACGGC	41206
OY	43199	GCCGCGCTCAAGGGAACGCGGGGACCAAGGCGAGACGACTGAGTACCGTGGTGGTCAAC	43258
Db	41207	GCCGCGCTCAAGGGAACGCGGGGACCAAGGCGAGACGACTGAGTACCGTGGTGGTCAAC	41266
OY	43259	GGAACGGAATGTGTTTCTAGAAACAACCGTGCAGTTTCTACAGAAACGTTTCCACAGCTC	43318
Db	41267	GGAACGGAATGTGTTTCTAGAAACAACCGTGCAGTTTCTACAGAAACGTTTCCACAGCTC	41326
OY	43319	GCGCCACGTCACAGGTCCTGCTGTCGACGAATATATGTGCAATATAGTCACGACGCGCT	43378
Db	41327	GCGCCACGTCACAGGTCCTGCTGTCGACGAATATATGTGCAATATAGTCACGACGCGCT	41386
OY	43379	GTCGACATGGAACATTTATGATGAGAGAGTGGCCCTATATGAAGACTATTTAAAGATC	43438
Db	41387	GTCGACATGGAACATTTATGATGAGAGAGTGGCCCTATATGAAGACTATTTAAAGATC	41446
OY	43439	GGAACAAAGTCGCGCTTATGTTAGTACGACGAGTCTGGAGCTACGAGAGTGGCCT	43488
Db	41447	GGAACAAAGTCGCGCTTATGTTAGTACGACGAGTCTGGAGCTACGAGAGTGGCCT	41506
OY	43499	CGAATAAAGCATCGTGTCTCGGTGACGTCATGATTATTCGCGACGAGATAGCAATCT	43558
Db	41507	CGAATAAAGCATCGTGTCTCGGTGACGTCATGATTATTCGCGACGAGATAGCAATCT	41566
OY	43559	TCGACTCAAAATAGATGCAATTTTGGCTCTCAAGACGCCACCGTCTCAAAATATACA	43618
Db	41567	TCGACTCAAAATAGATGCAATTTTGGCTCTCAAGACGCCACCGTCTCAAAATATACA	41626
OY	43619	GGCGCTGGGTCTGGGGAAACCTGTGCTATAGGGATTTCCGGGGGAGATTTTATTCAGGCATA	43678
Db	41627	GGCGCTGGGTCTGGGGAAACCTGTGCTATAGGGATTTCCGGGGGAGATTTTATTCAGGCATA	41686
OY	43679	TCGACTATTTGGACAAATGCACTCTCCGCGTGTGGAAAGAGTCGCTCCCAACAGTTTACG	43738
Db	41687	TCGACTATTTGGACAAATGCACTCTCCGCGTGTGGAAAGAGTCGCTCCCAACAGTTTACG	41746
OY	43739	GCTAAGCGCATTTGATCCATGACAACTTATCAATTAAGAACGCGTACCAACGCGCTT	43798

Db	41747	GCTAAGCGGCACTTATCCATGGACATTTATCAATTAATAAAGCGTACCAACCGGCTT	41806
Qy	43799	CCATTGGGATACACTACTCAGAAATTGGATTATACCAACCGGCTTTTGGCGCAAGATGC	43858
Db	41807	CCATTGGGATTAAGTACTACAGAAATTGGATTATACCAACCGGCTTTTGGCGCAAGATGC	41866
Qy	43859	GACGCTCTCACTGGAGTCTAAACGGGTTTGAATGTGTGTTTCCCTCGCGTGTGCAGAAC	43918
Db	41867	GACGCTCTCACTGGAGTCTAAACGGGTTTGAATGTGTGTTTCCCTCGCGTGTGCAGAAC	41926
Qy	43919	ACTGGCTTAACAACATGCTGTAGAAGCTGCTGCTATATCAATATATACAGATGGCGGA	43978
Db	41927	ACTGGCTTAACAACATGCTGTAGAAGCTGCTGCTATATCAATATATACAGACT - GCGGA	41985
Qy	43979	GAC - GACGCCACCGAGCTCAACCTAGCCGAGGTGAAGCTGTACAGACCAATATCATCTT	44037
Db	41986	GACGAGACGCCACCGAGCTCAACCTAGCCGAGGTGAAGCTGTACAGACCAATATCATCTT	42045
Qy	44038	ACATGGGTGCGAACTACGGCCTGAGAGTGAACCCGTTGGGTGAGCTACGTATGCGGA	44097
Db	42046	ACATGGGTGCGAACTACGGCCTGAGAGTGAACCCGTTGGGTGAGCTACGTATGCGGA	42105
Qy	44098	TGCTGGAGAGCCTGTCCATTACTACCTGTGCGCTTTTGTCGCGGTAAATTCGCGCGGGTGG	44157
Db	42106	TGCTGGAGAGCCTGTCCATTACTACCTGTGCGCTTTTGTCGCGGTAAATTCGCGCGGGTGG	42165
Qy	44158	TAAAGGCTACTGACCTCATTTGGTGGCGCACAAACAACGAAATTAGTCAGATTTTGCAGG	44217
Db	42166	TAAAGGCTACTGACCTCATTTGGTGGCGCACAAACAACGAAATTAGTCAGATTTTGCAGG	42225
Qy	44218	GGGTGTGTCCACCTGAGGTACAGGCCCTGGATCTCAACAACGTAAAGCTGGCGGACGACA	44277
Db	42226	GGGTGTGTGTCCACCTGAGGTACAGGCCCTGGATCTCAACAACGTAAACCGGGCGGACGACA	42285
Qy	44278	TAAAGCGATGGGTGGCCCTCATAACTATCTAGAGTGCACATTTATTTAATCTGG	44337
Db	42286	TAAAGCGATGGGTGGCCCTCATAACTATCTAGAGTGCACATTTATTTAATCTGG	42345
Qy	44338	GCCGAGATTTACAGTTTACGCTTACGCTTCATCGGACACGAAATCCGTTCTGTGGTGTG	44397
Db	42346	GCCGAGATTTACAGTTTACGCTTACGCTTTCATCGGACACGAAATCCGTTCTGTGGTGTG	42405
Qy	44398	CATTTAACTAGAAACGGGCTCCCTGTGTCTTACATGTTCGATCCCAAAATTAATAGCG	44457
Db	42406	CATTTAACTAGAAACGGGCTCCCTGTGTCTTACATGTTCGATCCCAAAATTAATAGCG	42465
Qy	44458	TGTCCAGAGCAACGAGGTGACGGTGTGTAAATCGCGGGTGGCAACGAGACGACAGAG	44517
Db	42466	TGTCCAGAGCAACGAGGTGACGGTGTGTAAATCGCGGGTGGCAACGAGACGACAGAG	42535
Qy	44518	CGATGATTTTATACCTCTAGACCAACCACTTACCAACGAGCGCGGAGCTTGTAAAG	44577
Db	42526	CGATGATTTTATACCTCTAGACCAACCACTTACCAACGAGCGCGGAGCTTGTAAAG	42585
Qy	44578	AAGCTTTTATACCGAAACCCACAGTGACATTGTAAAGCAAAATGTTAAACGAGGCTTAC	44637
Db	42586	AAGCTTTTATACCGAAACCCACAGTGACATTGTAAAGCAAAATGTTAAACGAGGCTTAC	42645
Qy	44638	CTAATATCCAAAAAAATTTGGTCCGTTGGCGCTTGTATATATTTTATTTTGGCACTACG	44697
Db	42646	CTAATATCCAAAAAAATTTGGTCCGTTGGCGCTTGTATATATTTTATTTTGGCACTACG	42705
Qy	44698	TGTGCTTTTGGCTGTGCTCTCACTTTGGCAGATTAAACCGGTACATATGACCCACCGGCTTGG	44757
Db	42706	TGTGCTTTTGGCTGTGCTCTCACTTTGGCAGATTAAACCGGTACATATGACCCACCGGCTTGG	42765
Qy	44758	TGTTTGGCGTTTAAACCCCATGGTCCAAAACATGTCAAGAACTACGACCCGCGCTATTG	44817
Db	42766	TGTTTGGCGTTTAAACCCCATGGTCCAAAACATGTCAAGAACTACGACCCGCGCTATTG	42825
Qy	44818	TTGGCGTAGAGTTGTGGGGCAGACGCCATCTGTAAAGACTGTAGCGTCCCGCATATCAAAA	44877
Db	42826	TTGGCGTAGAGTTGTGGGGCAGACGCCATCTGTAAAGAACTGTAGCGTCCCGCATATCAAAA	42885

OY	44878	CGGAGCTTGGAAATGGTTTACCACAAACGGGGCTACGGCAATTCGTGGTCCACGGGCACACTATG	44937	OY	45958	CGTCCCGAGTTCAATGCGTAATTAACAAATTCAAACGGCTTGCTTCGCGCCCA	4601
Db	42886	CGGGGCTTGGAAATGGTTTACCACAAACGGGGCTACGGCAATTCGTGGTCCACGGGCACACTATG	42945	Db	43966	CGTTCCGAGTTCAATGCGTAATTAACAAATTCAAACGGCTTGCTTCGCGCCCA	44025
OY	44938	GGCGGCCCTGTTAAAGCGGGCCGCGCTTGTCATGAGGAATGTGTGCCGAACAGATAG	44997	OY	46018	CATGTAAATGGCGGAACGTATAAGACTGTTCTGTGTCACGTGTGTAAAAAATAAGAG	46077
Db	42946	GGCTGGCCCTGTTAAAGCGGGCCGCGCTTGTCATGAGGAATGTGTGCCGAACAGATAG	43005	Db	44026	CATGTAAATGGCGGAACGTATAAGACTGTTCTGTGTCACGTGTGTAAAAAATAAGAG	44085
OY	44998	TGCGGCAAGCGCGCTGCATTTACTTGTGTCATGGAACCGGACGGAGTGTGGATTTTAAT	45057	OY	46078	GACCGAGCAATCTCGTTTAACACGGTTGCTATGGCACTCCGGCATCTTGACTGCTTT	46137
Db	43006	TGCGGCAAGCGCGCGCTGCATTTACTTGTGTCATGGAACCGGACGGAGTGTGGATTTTAAT	43065	Db	44086	GACCGAGCAATCTCGTTTAACACGGTTGCTATGGCACTCCGGCATCTTGACTGCTTT	44145
OY	45058	CGGCAATGGCGGCACACAGCTTTTGGGATCCAGAGCGTTCTGTGTCACCGATTATG	45117	OY	46138	GCCTTCACGGCGACGTTTAAACGCGGTGATCTCGGGTGAAGGATTAACATCGCTGAAT	46197
Db	43066	CGGCAATGGCGGCACACAGCTTTTGGGATCCAGAGCGTTCTGTGTCACCGATTATG	43125	Db	44146	GCCTTCACGGCGACGTTTAAACGCGGTGATCTCGGGTGAAGGATTAACATCGCTGAAT	44207
OY	45118	AAAAAAACCTTGTCGCCCACTCGTAATGTATTAACACATCAGTTTTTACAATG	45177	OY	46198	TAAACGGCGGCACATGACGCTATCTGTGTAACGGCGGTGCGGCTTAATCTTTAGAAA	46257
Db	43126	AAAAAAACCTTGTCGCCCACTCGTAATGTATTAACACATCAGTTTTTACAATG	43185	Db	44206	TAAACGGCGGCACATGACGCTATCTGTGTAACGGCGGTGCGGCTTAATCTTTAGAAA	44265
OY	45178	AATACACTGTGCCAAATATACCTGTGGTCCCGGAAATGTAAATGTCTCTTAAGTCATG	45237	OY	46258	AAATGTCCAGCGCTTAATTAATGATTTAATCACCTTGATTTAACCGCAATCACCGC	46311
Db	43186	AATACACTGTGCCAAATATACCTGTGGTCCCGGAAATGTAAATGTCTCTTAAGTCATG	43245	Db	44266	AAATGTCCAGCGCTTAATTAATGATTTAATCACCTTGATTTAACCGCAATCACCGC	44325
OY	45238	CATGAGAAACATAAAGCTATTTCCACGCACTTCATGTAGCTTGTTTTATTTGGCTGTA	45297	OY	46318	ACCGATGCGGTGTCGGAGCGCGTCTGTGTTGTGTGTACGCGCGGCTATGTAAACGTG	46377
Db	43246	CATGAGAAACATAAAGCTATTTCCACGCACTTCATGTAGCTTGTTTTATTTGGCTGTA	43305	Db	44326	ACCGATGCGGTGTCGGAGCGCGTCTGTGTTGTGTGTACGCGCGGCTATGTAAACGTG	44385
OY	45298	AGGTATTTAACAGTAAATGGAGGTTCCGCTGGTGCCTTAAGACAAAACGCTCATAGATA	45357	OY	46378	GAGACACGGCTTATATCGCCCGCTGTATCTTGTGACGTCGCTTTAACGGCACAGATC	46437
Db	43306	AGGTATTTAACAGTAAATGGAGGTTCCGCTGGTGCCTTAAGACAAAACGCTCATAGATA	43365	Db	44386	GAGACACGGCTTATATCGCCCGCTGTATCTTGTGACGTCGCTTTAACGGCACAGATC	44445
OY	45358	ACAAATTTTGTGAATGGGAAAAATAGTCTGTAAATAGTTATCCGAACAGTATGCTGCAC	45417	OY	46438	CAATTGTGACAGGAGAGTCGCTTAACAGATTTTATCATGCTTTGAGCGGACGCTGCACG	46497
Db	43366	ACAAATTTTGTGAATGGGAAAAATAGTCTGTAAATAGTTATCCGAACAGTATGCTGCAC	43425	Db	44446	CAATTGTGACAGGAGAGTCGCTTAACAGATTTTATCATGCTTTGAGCGGACGCTGCACG	44507
OY	45418	ACACGAATGGGGTTTTTAACCAACGACGGGCTTTTCAACAGTCAACGCGGAATCGGTTCAAG	45477	OY	46498	GTCCCCCAATTAGCTCCGTGGAGAAATGCGCTTCCAAAAAAGATTAGTGTGCTCCGTAC	46557
Db	43426	ACACGAATGGGGTTTTTAACCAACGACGGGCTTTTCAACAGTCAACGCGGAATCGGTTCAAG	43485	Db	44506	GTCCCCCAATTAGCTCCGTGGAGAAATGCGCTTCCAAAAAAGATTAGTGTGCTCCGTAC	44565
OY	45478	TTTTTCATTTTATCGGATTAATTAACAAACCTCCGTTATGGGCTTTTATTTTGGCTGG	45537	OY	46558	CGTTCATCAATGTAATATATAGCAGAAATATACAGCGGTACACAGGCGACCCACAGAC	46611
Db	43486	TTTTTCATTTTATCGGATTAATTAACAAACCTCCGTTATGGGCTTTTATTTTGGCTGG	43545	Db	44566	CGTTCATCAATGTAATATATAGCAGAAATATACAGCGGTACACAGGCGACCCACAGAC	44622
OY	45538	CTATGTGCGTTATCGCGTTGGTATGTACGTGATGCGGAGGCTGTGTTGAAGGGCGCG	45597	OY	46618	AGTGTCTTGGCAAGTAAATCATCTTTATGATCCGCAACATACGTAGTTACCAACGTTAAG	46677
Db	43546	CTATGTGCGTTATCGCGTTGGTATGTACGTGATGCGGAGGCTGTGTTGAAGGGCGCG	43605	Db	44626	AGTGTCTTGGCAAGTAAATCATCTTTATGATCCGCAACATACGTAGTTACCAACGTTAAG	44685
OY	45598	TTTGTGGCGGATTCGTGTCGCGACCGCGGCTCAACCCGCGTATGAGATGTTGAATGTTAGT	45657	OY	46678	CATCTTTTCGTGGCGCTCCCTCAAAATTAAGTAAAAACATAGTTGTCAGATGAGTT	46733
Db	43606	TTTGTGGCGGATTCGTGTCGCGACCGCGGCTCAACCCGCGTATGAGATGTTGAATGTTAGT	43665	Db	44686	CATCTTTTCGTGGCGCTCCCTCAAAATTAAGTAAAAACATAGTTGTCAGATGAGTT	44745
OY	45658	TGCGTCCCGCAACGAATATCAGAGAACTTTACGTACATAGCCAAAGCGCACAGC	45717	OY	46738	ACTTTGAGATTAATAATCAGTTTTGCGTCTTTGAAGCATTAACCCAGAAATCCGCGG	46797
Db	43666	TGCGTCCCGCAACGAATATCAGAGAACTTTACGTACATAGCCAAAGCGCACAGC	43725	Db	44746	ACTTTGAGATTAATAATCAGTTTTGCGTCTTTGAAGCATTAACCCAGAAATCCGCGG	44809
OY	45718	TGCTCTCTAGCTCGTTTATTTCTAGCGATTTAAAAACAATTTATCGTTGGTGGCATGTA	45777	OY	46798	GAGGCAATCTTTTAAATGAAGTTGCGCTGCTGCAATATATAGAGGTGGAAGCTGTGTC	46857
Db	43726	TGCTCTCTAGCTCGTTTATTTCTAGCGATTTAAAAACAATTTATCGTTGGTGGCATGTA	43785	Db	44806	GAGGCAATCTTTTAAATGAAGTTGCGCTGCTGCAATATATAGAGGTGGAAGCTGTGTC	44865
OY	45778	GTGGGCAATGACGGCGCGACAAACAGCTGCTCCGAATAGTTTTTTTGGTGGCGCAGTA	45837	OY	46858	CGGGATGCTCTAAGGCAAAAGAAAACAAAACGAGTTAACCGGGGTATGGAGAACGATA	46911
Db	43786	GTGGGCAATGACGGCGCGACAAACAGCTGCTCCGAATAGTTTTTTTGGTGGCGCAGTA	43845	Db	44866	CGGGATGCTCTAAGGCAAAAGAAAACAAAACGAGTTAACCGGGGTATGGAGAACGATA	44922
OY	45838	CGTGTGACCTCCGCTTTTATAGTGAATGAACAGTATAGCTTGATTGATCTATTAATA	45897	OY	46918	CGGCTTAAGCAAAATCTCGGAAGCTGACCTTTCAACAGTCAAGGCTTCTTTCACCGTC	46977
Db	43846	CGTGTGACCTCCGCTTTTATAGTGAATGAACAGTATAGCTTGAATTGATCTATTAATA	43905	Db	44926	CGGCTTAAGCAAAATTTTGAAGCTGACCTTTCAACAGTCAAGGCTTCTTTCACCGTC	44985
OY	45898	CGCTACGGGATCAACAGATAGCTTAAATAGTGTGACACACACAGTTTGGCTAGCGCTAAA	45957	OY	46978	CGATTAGAGATCTAATTTTATCTGTGAGCTGACGCTTTAAACCACTTTAGCCTATCTGAAT	47037
Db	43906	CGCTACGGGATCAACAGATAGCTTAAATAGTGTGAGACACACAGTTTGGCTAGCGCTAAA	43965	Db	44986	CGATTAGAGATCTAATTTTATCTGTGAGCTGACGCTTTAAACCACTTTAGCCTATCTGAAT	45041
				OY	47038	CAGACGACATAATTAATGGAAGGATTTGTTCTTGTGTTGACGCTGTGGGACAGATGTGC	47091

45046 CACACGACATTAATTTGAAAGGATGTTCTTCTGCTTGACCTGGGGACGAAATGTC 45105
47098 TCTCTTAATACAGCATCGTGTCAAAAGATGTCAAAATGACGCGGTCAACAGCCCAATATG 47157
45106 TCTCTTAATACAGCATCGTGTCAAAAGATGTCAAAATGACGCGGTCAACAGCCCAATATG 45165
47158 TCGATTTTCATACGCTCTTAACCTTAACAGAGTGTGGATGTGAAGCGCATATCAGCTATG 47217
45166 TCGATTTTCATACGCTCTTAACCTTAACAGAGTGTGGATGTGAAGCGCATATCAGCTATG 45225
47218 CGACGGGGGACGCAACTGCTGATCGTGTACACTCGCGGAAATCTAGTGTATTTAAC 47277
45226 CGACGGGGGACGCAACTGCTGATCGTGTACACTCGCGGAAATCTAGTGTATTTAAC 45285
47278 GGAATACTGCTTTGGATATGTGACAGAGTATGTTGCTACGGTCCCTACAGACGCG 47337
45286 GGAATACTGCTTTGGATATGTGACAGAGTATGTTGCTACGGTCCCTACAGACGCG 45345
47338 CGTACCCGACGCTTCATCGATCCGCTGTCACACGCGACGAGGAAATGTTTAAAG 47397
45346 CGTACCCGACGCTTCATCGATCCGCTGTCACACGCGACGAGGAAATGTTTAAAG 45405
47398 CGATATCTAGGACTTTGAGAGCGTGGTGAATCTGAGCATATTTCTACCGTGT 47457
45406 CGATATCTAGGACTTTGAGAGCGTGGTGAATCTGAGCATATTTCTACCGTGT 45465
47458 CAGAATGACATTAATGATGATAGTAGATTAAATAGAGCTACGTTTAAAGATG 47517
45466 CAGAATGACATTAATGATGATAGTAGATTAAATAGAGCTACGTTTAAAGATG 45525
47518 CCTCCGCTAATAGAGCGGCGAAGTGGCAGAGACCTCGCGGCGAGCATTTTACATCA 47577
45526 CCTCCGCTAATAGAGCGGCGAAGTGGCAGAGACCTCGCGGCGAGCATTTTACATCA 45585
47578 CATATTTATCTCATTTACTCCACTAAACGGTATATGATCTCTATTTAAATGTAC 47637
45586 CATATTTATCTCATTTACTCCACTAAACGGTATATGATCTCTATTTAAATGTAC 45645
47638 GAGAAATTAATAAATATAGACACATTTGTAAAAATCACTACAGCGCAATGATGCGCATGT 47697
45646 GAGAAATTAATAAATATAGACACATTTGTAAAAATCACTACAGCGCAATGATGCGCATGT 47705
47698 CTCAACCGCGGATCGCTCGCGGGTCACTGCGAGCGGCTTTTACGATACTTCCGCGA 47757
45706 CTCAACCGCGGATCGCTCGCGGGTCACTGCGAGCGGCTTTTACGATACTTCCGCGA 45765
47758 GGGTTATCTCTGCGCAACATATTAGTGGTGAACGGCAGCGGTTTTTGGACACAT 47817
45766 GGGTTATCTCTGCGCAACATATTAGTGGTGAACGGCAGCGGTTTTTGGACACAT 45825
47818 TGGTTGCTGATCTGAGAGCAGCTTAAGACTTTTACGCTGTGGGAGCGGTTATTTCAA 47877
45826 TGGTTGCTGATCTGAGAGCAGCTTAAGACTTTTACGCTGTGGGAGCGGTTATTTCAA 45885
47878 AACACGACCGCGGCGCGGGGAGCGTCCGCGCGCTGGTCCGAGCTGGCGATTAATG 47937
45886 AACACGACCGCGGCGCGGGGAGCGTCCGCGCGCTGGTCCGAGCTGGCGATTAATG 45945
47938 CTGCTCTGCTTTTACCAATGGAATTTTCAATCGTTGATGTATTTATCTCAAGGCC 47997
45946 CTGCTCTGCTTTTACCAATGGAATTTTCAATCGTTGATGTATTTATCTCAAGGCC 46005
47998 GATACGCTGACTCTGGAAGCTGCTGACCGTGAATCTTCTGTATATGTCAATTAATGGC 48057
46006 GATACGCTGACTCTGGAAGCTGCTGACCGTGAATCTTCTGTATATGTCAATTAATGGC 46065
48058 GCTTACAGAAAGCAATGCGAGGTTTAAAGATTAAGTTTCCGATGTACCGATGCCGCC 48117
46066 GCTTACAGAAAGCAATGCGAGGTTTAAAGATTAAGTTTCCGATGTACCGATGCCGCC 46125
48118 GTTGAAGTGAAGTTCATCTCTTAACCGCTTAAAGAGCGGTTGTTATCAGCGACAT 48177

46126 GTTGACGCTGAGTTTATCTCTTAACCGCTTAAAGAGCGGTTGTTATCAGCGACAT 46185
48178 GCTACGACCGCTGCTGCGGTGCAACCCCTACAGATGTTTGAACCGGACTTTACAGTCT 48237
46186 GCTACGACCGCTGCTGCGGTGCAACCCCTACAGATGTTTGAACCGGACTTTACAGTCT 46245
48238 AGGGTACGGGACGACTGCTGACACACACCGTGGCTGCAACGCCAGTAAATGTGAGC 48297
46246 AGGGTACGGGACGACTGCTGACACACACCGTGGCTGCAACGCCAGTAAATGTGAGC 46305
48298 GGAAGTAAATGCCCCGACGGCAGCAGATGCGCAAGAGGATGCGCAATGCTGTAAAG 48357
46306 GGAAGTAAATGCCCCGACGGCAGCAGATGCGCAAGAGGATGCGCAATGCTGTAAAG 46365
48358 CTTGATATCCGCGCTCCCAACAGCAAGCAATATCCAAAGAGAGTGGGCGAGCGCTCAC 48417
46366 CTTGATATCCGCGCTCCCAACAGCAAGCAATATCCAAAGAGAGTGGGCGAGCGCTCAC 46425
48418 GTTTTCTGCTGCGGCAATTAACGCTGCTGATATGATATGATAGCAAGAACTAGATCCAG 48477
46426 GTTTTCTGCTGCGGCAATTAACGCTGCTGATATGATATGATAGCAAGAACTAGATCCAG 46485
48478 TGGCAGGGGCAAGATCCGGGCGGTTGCGGCTGATGATGTCGATCCGATCCGCTACCTG 48537
46486 TGGCAGGGGCAAGATCCGGGCGGTTGCGGCTGATGATGTCGATCCGATCCGCTACCTG 46545
48538 TTAGAGGGCATTTGTTTATAGAGCCAAAGCAAGATGCGTTTGCATTTCTATAGAAAG 48597
46546 TTAGAGGGCATTTGTTTATAGAGCCAAAGCAAGATGCGTTTGCATTTCTATAGAAAG 46605
48598 ACCTGCAAGTGTGACAACTATACCATTAATTTTCCGTTTGGATTAATAGGAC 48657
46606 ACCTGCAAGTGTGACAACTATACCATTAATTTTCCGTTTGGATTAATAGGAC 46665
48658 AACGAAACAGTACGACTTAATTAAGAGAGCAATTTATAGAGCGTGGTCCGATTTAGAAC 48717
46666 AACGAAACAGTACGACTTAATTAAGAGAGCAATTTATAGAGCGTGGTCCGATTTAGAAC 46725
48718 CAGGTGTCAGAGAGAGCGGCTGGTAAAGCGCGGCTGTTTGCACAGATAGTAACAG 48777
46726 CAGGTGTCAGAGAGAGCGGCTGGTAAAGCGCGGCTGTTTGCACAGATAGTAACAG 46785
48778 TATTGGAAGATTTTGGGATTAATGAGGACATGCGGCTCATTAAGCTGGGTAACGCTATA 48837
46786 TATTGGAAGATTTTGGGATTAATGAGGACATGCGGCTCATTAAGCTGGGTAACGCTATA 46845
48838 AAACCTACCAATCGGACACCTTCAATGCGGAGCTAAACGAGAGTGGGCTCGCTGTGAC 48897
46846 AAACCTACCAATCGGACACCTTCAATGCGGAGCTAAACGAGAGTGGGCTCGCTGTGAC 46905
48898 GAGGATTAATCTGGTCAATTTAGCGGGCAGTCACTGTTTCTTACTGTCTGCGCTAAC 48957
46906 GAGGATTAATCTGGTCAATTTAGCGGGCAGTCACTGTTTCTTACTGTCTGCGCTAAC 46965
48958 CTGACCGCTGCTGCTGCTCCCGGGGGGCTTTGTTATTAAGGCCGCTACGACCTATCA 49017
46966 CTGACCGCTGCTGCTGCTCCCGGGGGGCTTTGTTATTAAGGCCGCTACGACCTATCA 47025
49018 AGCGAGATTTAATGTTTGGGCTTGCAGATATGCGACACCGACGCTGCTACATTTCTAA 49077
47026 AGCGAGATTTAATGTTTGGGCTTGCAGATATGCGACACCGACGCTGCTACATTTCTAA 47085
49078 ATCGTTTAAACAGGAATGCAATATGTTTGCACACCGGGTACGCTCCGCTTGTGCG 49137
47086 ATCGTTTAAACAGGAATGCAATATGTTTGCACACCGGGGATACGCTCCGCTTGTGCG 47145
49138 GGTATACACCGGACACCTGCGATTTCTCCGTTTGTGACCCGCGGTAACTATAGCAAAA 49197
47146 GGTATACACCGGACACCTGCGATTTCTCCGTTTGTGACCCGCGGTAACTATAGCAAAA 47205
49198 TGGGATGTCATTAATTTTAAATGTTTAAATGATGATGATGATGATGATGATGATGATGAT 49257
47206 TGGGATGTCATTAATTTTAAATGTTTAAATGTTTAAATGTTTAAATGTTTAAATGTTG 47265

Qy	49358	CCCGTGGCTTACCGTGTACATGAATGAGATATTTCTAGATTTTGTGCGACGAGATCTGT	49317
Db	47266	CCGGTGGGTACCGTGTACATGATGAGATATCTGATTTTGTGCGACGAGATCTGT	47325
Qy	49318	CGCCATTAAGGAGCGTCCGTGTAGGGCGACGTGTGTTTAATTCGTTTGGTACCTTTC	49377
Db	47326	CGCCATTAAGGAGCGTCCGTGTAGGGCGACGTGTGTTTAATTCGTTTGGTACCTTTC	47385
Qy	49378	TAAATGCGCGAGGAGCGTTCGATACCGGGCGCTTGAACCCACATCCGGAGAACCGT	49437
Db	47386	TAAATGCGCGAGGAGCGTTCGATACCGGGCGCTTGAACCCACATCCGGAGAACCGT	47445
Qy	49438	GCCCGGGCTAACAAACAGAAATTAATACACTTTCGAAACAGTGGCCAAAGAGACAGAT	49497
Db	47446	GCCCGGGCTAACAAACAGAAATTAATACACTTTCGAAACAGTGGCCAAAGAGACAGAT	47505
Qy	49498	ACCAGATGCCATTAAGGGGAAAGAGTTCACCAAAATAATCCGTTTGTGTGAGCGG	49557
Db	47506	ACCAGATGCCATTAAGGGGAAAGAGTTCACCAAAATAATCCGTTTGTGTGAGCGG	47565
Qy	49558	AGGGGCGTTTGGGACGTTCTCTCTGCTGTGATTTTAATGCTGCTCTGCTCCGACCTCGA	49617
Db	47566	AGGGGCGTTTGGGACGTTCTCTCTGCTGTGATTTTAATGCTGCTCTGCTCCGACCTCGA	47625
Qy	49618	CACAGTTCCTGCTCCCTGGCCAGAAATCGTTGGGCTTCTTACACAGTGCATTAAGACACGTG	49677
Db	47626	CACAGTTCCTGCTCCCTGGCCAGAAATCGTTGGGCTTCTTACACAGTGCATTAAGACACGTG	47685
Qy	49678	TAAATTTGTGACGGGGGCCACGTACACGTAAACCCGTATCGCGGATACACGCCACCTGA	49737
Db	47686	TAAATTTGTGACGGGGGCCACGTACACGTAAACCCGTATCGCGGATACACGCCACCTGA	47745
Qy	49738	CTGCAAGGAGCCTCACCCCTGTGCCCCCTGCTTATGCTGCGGGGGCCAGGCGCGGGC	49797
Db	47746	CTGCAAGGAGCCTCACCCCTGTGCCCCCTGCTTATGCTGCGGGGGCCAGGCGCGGGC	47805
Qy	49798	GGATGTCCGTGTTACCGGACACGTAAATCTTTTGGGCTGCTCTTGAACCCCAAGCCTC	49857
Db	47806	GGATGTCCGTGTTACCGGACACGTAAATCTTTTGGGCTGCTCTTGAACCCCAAGCCTC	47865
Qy	49858	CCCCAAAGTGACCAAGCTGCTTTTAAAAAGAAACCCACGCCGCTGACGATAGAGAGCG	49917
Db	47866	CCCCAAAGTGACCAAGCTGCTTTTAAAAAGAAACCCACGCCGCTGACGATAGAGAGCG	47925
Qy	49918	CATGTGCGGCGTCAAGGCGGAGGAGCGAGTGCACACCCACTTCGCTACCGTGGGCCCT	49977
Db	47926	CATGTGCGGCGTCAAGGCGGAGGAGCGAGTGCACACCCACTTCGCTACCGTGGGCCCT	47985
Qy	49978	CATTGCGCTCCGGAATTTAGCCAGTCGCTGATCTATACGCTGCGCAGAACTTAAAAAG	50037
Db	47986	CATTGCGCTCCGGAATTTAGCCAGTCGCTGATCTATACGCTGCGCAGAACTTAAAAAG	48045
Qy	50038	CATGTGCTTACGTTCTTATTTAGACAGCTGCGACACATCAGCGAATCTGGCCGCCGCTCG	50097
Db	48046	CATGTGCTTACGTTCTTATTTAGACAGCTGCGACACATCAGCGAATCTGGCCGCCGCTCG	48105
Qy	50098	GGGCTCGGTACAGATGGTTCGTTTCTTTATGTCAGATTCCTTGGCCGGAAC	50157
Db	48106	GGGCTCGGTACAGATGGTTCGTTTCTTTATGTCAGATTCCTTGGCCGGAAC	48165
Qy	50158	CACCTGATAGCGTGGGATGACCTCGAGAAAAAGCGATTTGGGACGTGTTTGGTGG	50217
Db	48166	CACCTGATAGCGTGGGATGACCTCGAGAAAAAGCGATTTGGGACGTGTTTGGTGG	48225
Qy	50218	GCCACGTACCCACGTGACGTTTTCACACGAGAGAGAGACGCTGATATAGGCGAC	50277
Db	48226	GCCACGTACCCACGTGACGTTTTCACACGAGAGAGAGACGCTGATATAGGCGAC	48285
Qy	50278	ACGATCATGTTTCCGCTGACGAGGGGATTAACAAAAGCGTGGCTTCTGCTTAAC	50337
Db	48286	ACGATCATGTTTCCGCTGACGAGGGGATTAACAAAAGCGTGGCTTCTGCTTAAC	48345

Qy	50338	GTCGTAAACAGCTGCTCGGTGTTTCAATTAACCAAGTGTGCTTAAACGTGGCAAT	50397
Db	48346	GTCGTAAACAGCTGCTCGGTGTTTCAATTAACCAAGTGTGCTTAAACGTGGCAAT	48405
Qy	50398	AACGTGTGTCTTTTGGGGTCTTTGATAGACGCGATTAATAAATTAACGTGCGATGAT	50457
Db	48406	AACGTGTGTCTTTTGGGGTCTTTGATAGACGCGATTAATAAATTAACGTGCGATGAT	48465
Qy	50458	AATGTGTGAAAGGGGCTCAAGGCAACAAACCCCGGACGTAACTCCATTTTAAAT	50517
Db	48466	AATGTGTGAAAGGGGCTCAAGGCAACAAACCCCGGACGTAACTCCATTTTAAAT	48525
Qy	50518	GACGACAGTGTGGCTTAAATAACCTGCGCAGTTCTGATTAAGGGGCACTTAAGAAAGCT	50577
Db	48526	GACGACAGTGTGGCTTAAATAACCTGCGCAGTTCTGATTAAGGGGCACTTAAGAAAGCT	48585
Qy	50578	TGCTGGGTCCGTGGGGCCGATTTGATTCATATGACTGTCTTGCGCTTTGCCATTTGG	50637
Db	48586	TGCTGGGTCCGTGGGGCCGATTTGATTCATATGACTGTCTTGCGCTTTGCCATTTGG	48645
Qy	50638	ACCGGACACATGTTTGTTTAAGGATGTTGAGTTCTGCGGTTAACGGGGCAACGTA	50697
Db	48646	ACCGGACACATGTTTGTTTAAGGATGTTGAGTTCTGCGGTTAACGGGGCAACGTA	48705
Qy	50698	GCGTGGCTAGAAATTCGGGGCTTCCCAACGTAGGGGCGGCGATGGGTTCTTGAACCTCG	50757
Db	48706	GCGTGGCTAGAAATTCGGGGCTTCCCAACGTAGGGGCGGCGATGGGTTCTTGAACCTCG	48765
Qy	50758	CGGTACGTTTGAAGTAAATGCTCTTAAACACAGACTATATGCAATTAACCGCGTAATACT	50817
Db	48766	CGGTACGTTTGAAGTAAATGCTCTTAAACACAGACTATATGCAATTAACCGCGTAATACT	48825
Qy	50818	CCCAAGCATGGGTGGGCAATTCGTTCCGCTTGTGCTGCGCCGATATTAATAACGGGCGGT	50877
Db	48826	CCCAAGCATGGGTGGGCAATTCGTTCCGCTTGTGCTGCGCCGATATTAATAACGGGCGGT	48885
Qy	50878	TGCCGAAACAGTTTTCGCAACACACCGTCCGTGACACGCGCAAGTTATTTGAAGAGCT	50937
Db	48886	TGCCGAAACAGTTTTCGCAACACACCGTCCGTGACACGCGCAAGTTATTTGAAGAGCT	48945
Qy	50938	TCCGATATGCTGTGTTAACACATGTTCCCTCAAGTTTGTGAAATTAAGGGGCAACCCGAA	50997
Db	48946	TCCGATATGCTGTGTTAACACATGTTCCCTCAAGTTTGTGAAATTAAGGGGCAACCCGAA	49005
Qy	50998	ACGGAACGCGCTTCGTTTAAAGGCGTGTAGTTAGCTTTAGACCTGTGACAAACCTCGG	51057
Db	49006	ACGGAACGCGCTTCGTTTAAAGGCGTGTAGTTAGCTTTAGACCTGTGTGACAAACCTCGG	49065
Qy	51058	GGACAGTTTAACTAGTTGAACACACCTCTTAATAGTTTCTTGTGATCCAAACGTTCTG	51117
Db	49066	GGACAGTTTAACTAGTTGAACACACCTCTTAATAGTTTCTTGTGATCCAAACGTTCTG	49125
Qy	51118	CCGGAATCGCGCGGTTAGAGACTGTCCGACGCGGAAGGTTTGACTTTGAACACATT	51177
Db	49126	CCGGAATCGCGCGGTTAGAGACTGTCCGACGCGGAAGGTTTGACTTTGAACACATT	49185
Qy	51178	CACCTCCCAAAAGTAAACGAGATGAGCGTGTGCTGGGGCGATTAAGGACATGTTAAC	51237
Db	49186	CACCTCCCAAAAGTAAACGAGATGAGCGTGTGCTGGGGCGATTAAGGACATGTTAAC	49245
Qy	51238	AACGACGACAGTGCCTTAACGTTAAAGGCAAGTTCTTGAAATTCACAGGCTGCTTGT	51297
Db	49246	AACGACGACAGTGCCTTAACGTTAAAGGCAAGTTCTTGAAATTCACAGGCTGCTTGT	49305
Qy	51298	TATCTGCGGTATGACACAGACGAATGGAATTTGGGCGCTCAAGTTTAAGAAAGACAAGTTG	51357
Db	49306	TATCTGCGGTATGACACAGACGAATGGAATTTGGGCGCTCAAGTTTAAGAAAGACAAGTTG	49365
Qy	51358	GTTAAATATGGCTGTAGAGAGGCTTGTCAATATCCAGACCTGGAAGGTTTGAAGCGCTG	51417
Db	49366	GTTAAATATGGCTGTAGAGAGGCTTGTCAATATCCAGACCTGGAAGGTTTGAAGCGCTG	49425
Qy	51418	GATCCTTTACGCTCATATGCGTCTGTTTACGGTTCCGGTGGTTCTGTGGGAACCA	51477

D	49426	GATCCTTACCGGCTCATATGCTTCTGTTTACGGTTCCGGTGGTTCTGTCGGGAACA	49485
Q	51478	GAGTGCCTATATGAAACCAATTTTGGTATGAAAGGACCCATCTTAACGCCACATATG	51537
D	49486	GAGTGCCATATGAAACCGCAATTTTGGTATGAAAGGACCCATCTTAACGCCACATATG	49545
Q	51538	TATGCCCCCAAAAGACGTATGACTTTTGTCCATCATGTAATTAAGTACGTTAAATTT	51597
D	49546	TATGCCCCCAAAAGACGTATGACTTTTGTCCATCATGTAATTAAGTACGTTAAATTT	49605
Q	51598	TTATACGTGAAGCCCGGTGGGGCTTGAAACTGAACCGTCCCGCGTTTCGAGCGCTCG	51657
D	49606	TTATACGTGAAGCCCGGTGGGGCTTGAAACTGAACCGTCCCGCGTTTCGAGCGCTCG	49665
Q	51658	CGGTTGGCGGAGCGCATCGCTGCTCGGGGAGCGTGAAGGGATGACGATACCTCTCC	51717
D	49666	CGGTTGGCGGAGCGCATCGCTGCTCGGGGAGCGTGAAGGGATGACGATACCTCTCC	49725
Q	51718	GCAAAAGTGCAATGTTGTGTACACCTGTACAAAGCAAAAGCATAGATTTGATTCAAGAA	51777
D	49726	GCAAAAGTGCAATGTTGTGTACACCTGTACAAAGCAAAAGCATAGATTTGATTCAAGAA	49785
Q	51778	CACGTGGGCGGAGTCATCGCATTTAGGGGAGACCGTGCAGATATATACGTCTAGCTTT	51837
D	49786	CACGTGGGCGGAGTCATCGCATTTAGGGGAGACCGTGCAGATATATACGTCTAGCTTT	49845
Q	51838	CGGGCTCAACGGTGCACAGAGTCGGGGAGATTTTGTTTAATCCCTGTACAACTTGAA	51897
D	49846	CGGGCTCAACGGTGCACAGAGTCGGGGAGATTTTGTTTAATCCCTGTACAACTTGAA	49905
Q	51898	GGGCTCGTACATGATTAAGGAACATGCGCTCGGACAGCACTAAAAAATGTTAATTA	51957
D	49906	GGGCTCGTACATGATTAAGGAACATGCGCTCGGACAGCACTAAAAAATGTTAATTA	49965
Q	51958	GTGCGAGCTGAGTCGGGAAATCAACAAAAAATGTCATCTCCCTATTTTGACAGTTGG	52017
D	49966	GTGCGAGCTGAGTCGGGAAATCAACAAAAAATGTCATCTCCCTATTTTGACAGTTGG	50025
Q	52018	GGCGGACAGTGCCTGTTTAAACGGCAGTATTAAGGAACCAAGGGAATCGTGCCTGTA	52077
D	50026	GGCGGACAGTGCCTGTTTAAACGGCAGTATTAAGGAACCAAGGGAATCGTGCCTGTA	50085
Q	52078	CAACAGCCTAAAAAGAAAGACGATCTGCGGACCGGTTGTGGAAACGCTAAGAACTGCT	52137
D	50086	CAACAGCCTAAAAAGAAAGACGATCTGCGGACCGGTTGTGGAAACGCTAAGAACTGCT	50145
Q	52138	GCGTGAACAAACGCAATTTGGATTACTAAAGGGTTTAAACGAGAAAAAATTTGAGA	52197
D	50146	GCGTGAACAAACGCAATTTGGATTACTAAAGGGTTTAAACGAGAAAAAATTTGAGA	50205
Q	52198	GTTTGAGCGTGTGGCGGACCGGTTCCGACCTCAAGAGACAGCTGTACGAGACATGGA	52257
D	50206	GTTTGAGCGTGTGGCGGACCGGTTCCGACCTCAAGAGACAGCTGTACGAGACATGGA	50265
Q	52258	GATTCGAGGTACGCTTACAAATGAATCTGTTCCCTGGAAGAAAGTCCCAAGAGCGA	52317
D	50266	GATTCGAGGTACGCTTACAAATGAATCTGTTCCCTGGAAGAAAGTCCCAAGAGCGA	50325
Q	52318	CATTATTAAGTGAATTTGAGCGCTGTGCCAGAGTGTGCCCAAAAGCCCTTGATCCCA	52377
D	50326	CATTATTAAGTGAATTTGAGCGCTGTGCCAGAGTGTGCCCAAAAGCCCTTGATCCCA	50385
Q	52378	TTTCCAGAGTTCAACATGACGTGACAGAAACAGATGCTCCCATATACCGTCAATTA	52437
D	50386	TTTCCAGAGTTCAACATGACGTGACAGAAACAGATGCTCCCATATACCGTCAATTA	50445
Q	52438	CACCTAAGACATGGCCCAACTGAAGATACCTAAACAACCTGGGGCAGTATGACACAGG	52497
D	50446	CACCTAAGACATGGCCCAACTGAAGATACCTAAACAACCTGGGGCAGTATGACACAGG	50505
Q	52498	CGACGACGTGACCGCGCTGCTGGAGCGGCTTGATAGTGTGGTGAAGGTCAATGTCTC	52557
D	50506	CGACGACGTGACCGCGCGTCTGCGACGCGGCTTGATAGTGTGGTGAAGGTCAATGTCTC	50565
Q	52558	TGCGCGGCTCGCTTAAGCATTTTGGCAGCGCGGTGAGTTTATTAACGAGTGCATTTTA	52617
D	50566	TGCGCGGCTCGCTTAAGCATTTTGGCAGCGCGGTGAGTTTATTAACGAGTGCATTTTA	50625
Q	52618	ACGATATAGACCGGCTCGCGGAGAAACATCCCTGAAACCGCGGGGTGACCGATAC	52677
D	50626	ACGATATAGACCGGCTCGCGGAGAAACATCCCTGAAACCGCGGGGTGACCGATAC	50685
Q	52678	TATGTTTCTAGAGCGGTGCGTACATGTCGGCCCTGATTTTCCCGAGTTAACAGGA	52737
D	50686	TATGTTTCTAGAGCGGTGCGTACATGTCGGCCCTGATTTTCCCGAGTTAACAGGA	50745
Q	52738	ATCTGCTAAACGGGATTCCTTAACAGTGAACCTTAACGGGTGGCGGCTTGAATCTCG	52797
D	50746	ATCTGCTAAACGGGATTCCTTAACAGTGAACCTTAACGGGTGGCGGCTTGAATCTCG	50805
Q	52798	AGCTGAGGGAAGCGTTAGTTTCTAATATATATGTCATCGTTCACTGACATCA	52857
D	50806	AGCTGAGGGAAGCGTTAGTTTCTAATATATATGTCATCGTTCACTGACATCA	50865
Q	52858	GTCACAAAAATATACGATTAAGGGGAACTGCAACTCGTACGGGAACTTAATGATCG	52917
D	50866	GTCACAAAAATATACGATTAAGGGGAACTGCAACTCGTACGGGAACTTAATGATCG	50925
Q	52918	GAGATCTAGAGTCCGCTCTTTAACACACGGGAAACCCCTTGACCGGAGTATGAGACT	52977
D	50926	GAGATCTAGAGTCCGCTCTTTAACACACGGGAAACCCCTTGACCGGAGTATGAGACT	50985
Q	52978	CCAACTCGGGTTCGTGCACACACGATACCATTTTAAGCACCGGCGAGATTTATCTGA	53037
D	50986	CCAACTCGGGTTCGTGCACACACGATACCATTTTAAGCACCGGCGAGATTTATCTGA	51045
Q	53038	AGCACATTTACGGCGCTGCTCTCTACACGGGTGCTGCTGTCGTCGCGCGGGGCGC	53097
D	51046	AGCACATTTACGGCGCGCTGCTCTCTCTACACGGGTGCTGCTGTCGTCGCGCGGGGCGC	51105
Q	53098	CGCAGGCGCATATGCTTAATACGCGCTTCCAAATCACTCACACTCGGTCTCACAATTG	53157
D	51106	CGCAGGCGCATATGCTTAATACGCGCTTCCAAATCACTCACACTCGGTCTCACAATTG	51165
Q	53158	ACATATGTCGCCGTGTTATAGTTTCTGATGTCGATGAGAAATATCTCGACGACGCG	53217
D	51166	ACATATGTCGCCGTGTTATAGTTTCTGATGTCGATGAGAAATATCTCGACGACGCG	51225
Q	53218	ACCCATTTCCCGACGAGGAGCGTTGGCGGACGCTTCCCGCAATCCGCGCACCCATGT	53277
D	51226	ACCCATTTCCCGACGAGGAGCGTTGGCGGACGCTTCCCGCAATCCGCGCACCCATGT	51285
Q	53278	TCTATTTGCGTGCATGCTGTCGCAAGAGTATGATGCGCGAATTTTTCGTGGCTGGG	53337
D	51286	TCTATTTGCGTGCATGCTGTCGCAAGAGTATGATGCGCGAATTTTTCGTGGCTGGG	51345
Q	53338	ACGTTCCACTCGATTTAGCATTTGACTCATCTGCGCACCGCACACTATTCCTCTAGAG	53397
D	51346	ACGTTCCACTCGATTTAGCATTTGACTCATCTGCGCACCGCACACTATTCCTCTAGAG	51405
Q	53398	AAGCGTACAGGGGGTTTTTGGCAACCACTGATTTATATAGGGCGCAATCAAAAGAGG	53457
D	51406	AAGCGTACAGGGGGTTTTTGGCAACCACTGATTTATATAGGGCGCAATCAAAAGAGG	51465
Q	53458	ATGCGTTAAGAAACGATCTCGCGGGCTGTATACGCAAAACTTTAACTAGTTCGCGA	53517
D	51466	ATGCGTTAAGAAACGATCTCGCGGGCTGTATACGCAAAACTTTAACTAGTTCGCGA	51525
Q	53518	AGCTGTTGGTCAAGGACTACTTTAGTCATTTGGGAAACAGCGCAATCATGATTTTTC	53577
D	51526	AGCTGTTGGTCAAGGACTACTTTAGTCATTTGGGAAACAGCGCAATCATGATTTTTC	51585
Q	53578	TCAGATGAGCCGATGTTTACAGAGATGCGCTTCTCGACATCGATGAGACGACGCGCTC	53637
D	51586	TCAGATGAGCCGATGTTTACAGAGATGCGCTTCTCGACATCGATGAGACGACGCGCTC	51645

OY	53638	CTCTCGAAATATGAGCCTTGCCCAACTTTTAAAAATGAGCGATGAGGCGTTTTTAAAGC	53697
Db	51646	CTCTCGAAATATGAGCCTTGCCCAACTTTTAAAAATGAGCGATGAGGCGTTTTTAAAGC	51705
OY	53698	GATTAACAAAAGGAATTAAGCATGCGCGGTATACGGTTCGCTATATTTTATACATATC	53757
Db	51706	GATTAACAAAAGGAATTAAGCATGCGCGGTATACGGTTCGCTATATTTTATACATATC	51765
OY	53758	GCCAGGTGGGAGATTTTATACGCAACACGACGATGATTTTACGTCACTGCGGTG	53817
Db	51766	GCCAGGTGGGAGATTTTATACGCAACACGACGATGATTTTACGTCACTGCGGTG	51825
OY	53818	TTACAGGGGAGCGCCTGACGCGCCTGTCGGAGTGTACGACGCGTCCCTAAACATGCAC	53877
Db	51826	TTACAGGGGAGCGCCTGACGCGCCTGTCGGAGTGTACGACGCGTCCCTAAACATGCAC	51885
OY	53878	CCCCACGATGACACCACTGTGTGATTTGATTAAGAACAGGTACGCCGGGCCAAACATC	53937
Db	51886	CCCCACGATGACACCACTGTGTGATTTGATTAAGAACAGGTACGCCGGGCCAAACATC	51945
OY	53938	AAATCTCTGTGGGACGCTCTGAGAGGACGGCATAAATTCGTCTCAAAAATTTTCACGTGGCC	53997
Db	51946	AAATCTCTGTGGGACGCTCTGAGAGGACGGCATAAATTCGTCTCAAAAATTTTCACGTGGCC	52005
OY	53998	ATAAACACACAGATTCGTCCAAAAAAATTTTTTAAACCCGTGGCCTATAGTCAACATCAC	54057
Db	52006	ATAAACACACAGATTCGTCCAAAAAAATTTTTTAAACCCGTGGCCTATAGTCAACATCAC	52065
OY	54058	TTTTGTACGGGGCCCCCTCGCGTTTGGACTGCGTTGCGAGGAAGTGTGTTAAAAAGTACTG	54117
Db	52066	TTTTGTACGGGGCCCCCTCGCGTTTGGACTGCGTTGCGAGGAAGTGTGTTAAAAAGTACTG	52125
OY	54118	GCAGCGTTGTGCATCCAGGCGAGGGGCACTGTGAAATPACGGAATTCAGCAGAGTCTCT	54177
Db	52126	GCAGCGTTGTGCATCCAGGCGAGGGGCACTGTGAAATPACGGAATTCAGCAGAGTCTCT	52185
OY	54178	CTCAACGGGGTTTTTGGCGTCTTCCTTGGATTTTGGATTTAACGTACGCTGACCCAAA	54237
Db	52186	CTCAACGGGGTTTTTGGCGTCTTCCTTGGATTTTGGATTTAACGTACGCTGACCCAAA	52245
OY	54238	GACGGTTTGGATTTCAACCACACTGCAAAATCTATGAATTAATATGCCGGTTTAAATGATC	54297
Db	52246	GACGGTTTGGATTTCAACCACACTGCAAAATCTATGAATTAATATGCCGGTTTAAATGATC	52305
OY	54298	ACATTTTCCAAAGTGTGAGTGTGACCCGATTTACGGTATGCTAAACTTATATACAGAG	54357
Db	52306	ACATTTTCCAAAGTGTGAGTGTGACCCGATTTACGGTATGCTAAACTTATATACAGAG	52365
OY	54358	CCGACGATGACAGACCGTTTAAAGGGTTTTTGTACTCCATATCTAAACCGCGCATCGAGTCT	54417
Db	52366	CCGACGATGACAGACCGTTTAAAGGGTTTTTGTACTCCATATCTAAACCGCGCATCGAGTCT	52425
OY	54418	GTCGGAGAGACAGGCTCCCACTGATCGACTATCTTGTGGCATATGACAAAGATGG	54477
Db	52426	GTCGGAGAGACAGGCTCCCACTGATCGACTATCTTGTGGCATATGACAAAGATGG	52485
OY	54478	GAGGTGTGTCCGGGGAAGAAAGACGCTTAACGCAAGTACACCATCTAATTTAAAGTGC	54537
Db	52486	GAGGTGTGTCCGGGGAAGAAAGACGCTTAACGCAAGTACACCATCTAATTTAAAGTGC	52545
OY	54538	ATGATTTACAACTCTACGGGCGCTTGTGATGTGTATATTTGTGCAATCCGAGGAAC	54597
Db	52546	ATGATTTACAACTCTACGGGCGCTTGTGATGTGTATATTTGTGCAATCCGAGGAAC	52605
OY	54598	GGAAGCCAAATTAATATTTAAAGCTCATGTGAGCGCCAACTATTTATAACGTCAAGCAT	54657
Db	52606	GGAAGCCAAATTAATATTTAAAGCTCATGTGAGCGCCAACTATTTATAACGTCAAGCAT	52665
OY	54658	CCGATTAATTAATCAAGTGTGCTCAGCTCTCTGTTGTACAGAGATCAATCATGCTCTCC	54717
Db	52666	CCGATTAATTAATCAAGTGTGCTCAGCTCTCTGTTGTACAGAGATCAATCATGCTCTCC	52725

QY	54718	AAGGAACCTAAAAATTTGGACACCCAGAAAAACTTTATACGCACTGGCTTTTTCAGAAA	547777
Db	52726	AAGGAACCTAAAAATTTGGGAAACCCAGAAAAACTTTATAGCGCACTGGCTTTTTCAGAAA	527855
QY	54778	CGGAGATTCAAGACCCGACGCTGCTGACATGGGGTAATTTGCCCGTGGATCCACAC	548937
Db	52786	CGGAGATTCAAGACCCGACGCTGCTGACATGGGGTAATTTGCCCGTGGATCCACAC	528455
QY	54838	GTAGAGATPACGACCCCTTTTAAATCGTAGACCCGGTATTTTCCACGCTGGCCAAACAC	548937
Db	52846	GTAGAGATPACGACCCCTTTTAAATCGTAGACCCGGTATTTTCCACGCTGGCCAAACAC	529055
QY	54898	CAACTGCTGAAGCAGCGCGACCGAATTCCTGGCGGCTAGTGTCTGTAGAGCATTTCCGAG	549537
Db	52906	CAACTGCTGAAGCAGCGCGACCGAATTCCTGGCGGCTAGTGTCTGTAGAGCATTTCCGAG	529655
QY	54958	CTACCATGGGGTTTATCTCTGCTGTGGCAAGGCCCAACCAACCGATAGATGTGAAG	550177
Db	52966	CTACCATGGGGTTTATCTCTGCTGTGGCAAGGCCCAACCAACCGATAGATGTGAAG	530255
QY	55018	GGGAGCCCATPAGATGTATCCAAAGAATTCGATCCTATATTAGAGAGAAGAAGCATTTGTCT	550777
Db	53026	GGGAGCCCATPAGATGTATCCAAAGAATTCGATCCTATATTAGAGAGAAGAAGCATTTGTCT	530855
QY	55078	TGTTTACGGCAGATGGAGCTGCCCCGCGGCGCTGTACAAACCCAAACCAAGCCATCCA	551377
Db	53086	TGTTTACGGCAGATGGAGCTGCCCCGCGGCGCTGTACAAACCCAAACCAAGCCATCCA	531455
QY	55138	AACATAAAAACAATAATTTGTCAAGATTTTGTTTAAGCATTCGTATCTTTTATTCGAGTGGG	551977
Db	53146	AACATAAAAACAATAATTTGTCAAGATTTTGTTTAAGCATTCGTATCTTTTATTCGAGTGGG	532055
QY	55198	GTGATGGTGTGGGGTTGGGAAGGAATGGGATTTGAGAGGAGATGAATGCTAGAAATCA	552577
Db	53206	GTGATGGTGTGGGGTTGGGAAGGAATGGGATTTGAGAGGAGATGAATGCTAGAAATCA	532655
QY	55258	TATGTATTTTGGATATATCATCTCTGATATGCTACAGCTTCTTCTGTTTCATATTAACGC	553177
Db	53266	TATGTATTTTGGATATATCATCTCTGATATGCTACAGCTTCTTCTGTTTCATATTAACGC	533255
QY	55318	GTTCAATTTCCGGGGAGTACTTAACCTTTTGTGCGTCTCTCTTGAAGGCCCTTGAAGAGGGG	553777
Db	53326	GTTCAATTTCCGGGGAGTACTTAACCTTTTGTGCGTCTCTCTTGAAGGCCCTTGAAGAGGGG	533855
QY	55378	TGCGTATTTCCGGGCACTTTTGGCACAATTTTCCAAATCGTTCGTATATCTTAAAGATGAT	554377
Db	53386	TGCGTATTTCCGGGCACTTTTGGCACAATTTTCCAAATCGTTCGTATATCTTAAAGATGAT	534455
QY	55438	GGCTAAGATGCAAGTGTATCGGAATCATAGAGATGTTACAGGCTATGACTTTGTGACGGCT	554977
Db	53446	GGCTAAGATGCAAGTGTATCGGAATCATAGAGATGTTACAGGCTATGACTTTGTGACGGCT	535055
QY	55498	GGCAGATATGAATACCTTGTCTGTATCCAACGAGGGGAAGAAGAGATCAGGTAACTGAC	555577
Db	53506	GGCAGATATGAATACCTTGTCTGTATCCAACGAGGGGAAGAAGAGATCAGGTAACTGAC	535655
QY	55558	AAAAACGCCAAGTATGATCCGATCCGATCTGGCTTATAGTACTTACTAGAAATAGTTCGTGT	556177
Db	53566	AAAAACGCCAAGTATGATCCGATCCGATCTGGCTTATAGTACTTACTAGAAATAGTTCGTGT	536255
QY	55618	GTTGATATPACCAAGCTATTTGAAGGACAAAAACAAGTTTATTTGAACCAAGAACAATATTC	556777
Db	53626	GTTGATATPACCAAGCTATTTGAAGGACAAAAACAAGTTTATTTGAACCAAGAACAATATTC	536855
QY	55678	GGAAACGAGCATATAGAAACTGTTTCCAAATAGCATTCATTTGTTCCAGGAGAGATATCTAA	557377
Db	53686	GGAAACGAGCATATAGAAACTGTTTCCAAATAGCATTCATTTGTTCCAGGAGAGATATCTAA	537455
QY	55738	CATGCCATGGCTATTTAAGGACAGATATTAAGATTTGGCGCCAAATGCTTTCCGTAAGCGAA	557977
Db	53746	CATGCCATGGCTATTTAAGGACAGATATTAAGATTTGGCGCCAAATGCTTTCCGTAAGCGAA	538055
QY	55798	CAGGGTGTATAGCAAGCTATTTCTCAGGAATCTGCTGTCTTAAGACGCGTAGAGACCAGGT	558577

|||||
Db 53806 CAGGGGTCTAGAACTATTCAGAGAACTGCTCTCTAAAGACCGTAGACACAGGT 53865
55858 GGGCGAATTCAGACGATATCATAGCTGAGAGTGCCTGAAACGATAGGCAAAATGTATAC 55917
|||||
Db 53866 GGGCGAATTCAGACGATATCATAGCTGAGAGTGCCTGAAACGATAGGCAAAATGTATAC 55925
55918 GTATACAAAGAGGCTTAAAGATATATGTTGATACGACAGAACGTGAATTAATACGTGAT 55977
|||||
Db 53926 GTATACAAAGAGGCTTAAAGATATATGTTGATACGACAGAACGTGAATTAATACGTGAT 53985
55978 GGTCCACAGCTCAAAATATGACATATAAACTACAGTGGAGACCTATAGACGATGCA 56037
|||||
Db 53986 GGTCCACAGCTCAAAATATGACATATAAACTACAGTGGAGACCTATAGACGATGCA 54045
56038 TGTCTGAGAGCTGCTGATTTGTTGCTGCGTGCACAGCGCTTGCGCTTGAATATGCGCAGAT 56097
54046 TGTCTGAGAGCTGCTGATTTGTTGCTGCGTGCACAGCGCTTGCGCTTGAATATGCGCAGAT 54105
56098 GGGCCACGATAGTAAACAGACGATATCCGTCACCAAAACGCCACGACATGTAGAC 56157
|||||
Db 54106 GGGCCACGATAGTAAACAGACGATATCCGTCACCAAAACGCCACGACATGTAGAC 54165
56158 AAACATTTCTGCTGCTTCCAAAACAAAGTCGCGCAGATGTTTATGACGAATCTTGAC 56217
|||||
Db 54166 AAACATTTCTGCTGCTTCCAAAACAAAGTCGCGCAGATGTTTATGACGAATCTTGAC 54225
56218 CGTTAGGTTTAAAGCGCTGTAGTTGACCAACGTTTAAAGTAGACAGGAATCCAACTCC 56277
54226 CGTTAGGTTTAAAGCGCTGTAGTTGACCAACGTTTAAAGTAGACAGGAATCCAACTCC 54285
56278 CGGGAATGTGGGGTGTACGTGACATCCGCTGACATTAATTAACATTAAGTCCAAAGATAC 56337
54286 CGGGAATGTGGGGTGTACGTGACATCCGCTGACATTAATTAACATTAAGTCCAAAGATAC 54345
56338 CAGTATTTTACCATGACGATTAAGATTAACGAGTGCCTCGGAAATTTTCTAGTTCA 56397
54346 CAGTATTTTACCATGACGATTAAGATTAACGAGTGCCTCGGAAATTTTCTAGTTCA 54405
56398 AAGATCTGCTGCGGGTGCCTCGGCAAACTAGACGATTAATCAGCAAGTGCCTTACAT 56457
54406 AAGATCTGCTGCGGGTGCCTCGGCAAACTAGACGATTAATCAGCAAGTGCCTTACAT 54465
56458 GTTACGATTTAAATATGCTGCTGCTTAAATATCATCTGCTGCAAGGAGTTAGGC 56517
54466 GTTACGATTTAAATATGCTGCTGCTTAAATATCATCTGCTGCAAGGAGTTAGGC 54525
56518 ACGGACCATGAACGCCCGGAGGTGGACATCAGGGACATGTTTGGACATATGCTGC 56577
54526 ACGGACCATGAACGCCCGGAGGTGGACATCAGGGACATGTTTGGACATATGCTGC 54585
56578 ATAGCACGACGACGCGGAAATTAATATCTGCGAGTTCATTTACTTGTATGTCAC 56637
54586 ATAGCACGACGACGCGGAAATTAATATCTGCGAGTTCATTTACTTGTATGTCAC 54645
56638 AATGGGAATTCAGGAGATGCGCATATCTATTTGTCACGAAACATTAAGCAATACG 56697
54646 AATGGGAATTCAGGAGATGCGCATATCTATTTGTCACGAAACATTAAGCAATACG 54705
56698 ACTGGGAAATATACCGGCGATAAACCGTCACGACCGTCATTAATATGACAGCGGCGTA 56757
54706 ACTGGGAAATATACCGGCGATAAACCGTCACGACCGTCATTAATATGACAGCGGCGTA 54765
56758 ATTATATGACAGTGGAACTCGTACTGTTTACGGAATCCATCATTTCAATTTGTAAGTC 56817
54766 ATTATATGACAGTGGAACTCGTACTGTTTACGGAATCCATCATTTCAATTTGTAAGTC 54825
56818 GCCAGCCGCGTGGTTAAAGTAAAGGTACGACGACCGAATATGTAATATGTTGGCTGCG 56877
54826 GCCAGCCGCGTGGTTAAAGTAAAGGTACGACGACCGAATATGTAATATGTTGGCTGCG 54885
56878 AACGAGCGTTGATATCTGTTGCTGCTGCGGTACCTGAGACCTATCTTCAATTTGGATA 56937
|||||

Db 54886 AACGAGCGTTGATATCTGTTGCTGCTGCGGTACCTGAGACCTATCTTCAATTTGGATA 54945
56938 CCACATATGACCTTTAGTTGATTTGATTGTTGTTGCCCAACCCGCGAATTTGGTCTCAG 56997
54946 CCACATATGACCTTTAGTTGATTTGATTGTTGTTGCCCAACCCGCGAATTTGGTCTCAG 55005
56998 AGATGTTTCTCAGTGTATGTTTCCACATTTGAGTTTACCTTTAAACACAGGCGGGT 57057
55006 AGATGTTTCTCAGTGTATGTTTCCACATTTGAGTTTACCTTTAAACACAGGCGGGT 55065
57058 TATACTATGAGGATGAGTGGCCAGCATGCGGAAAGGCGGAAAGTGGCGCATGG 57117
55066 TATACTATGAGGATGAGTGGCCAGCATGCGGAAAGGCGGAAAGTGGCGCATGG 55125
57118 GTATTCGTATATCTTTAAATGGAATCTGTAATTAACAGTTGCCGCGGAGAAATGAC 57177
55126 GTATTCGTATATCTTTAAATGGAATCTGTAATTAACAGTTGCCGCGGAGAAATGAC 55185
57178 CCTTGAGTATCGGACCGCAACATTTTACGTTTCTGCGGTGGAGACGAGGCGTATGTGA 57237
55186 CCTTGAGTATCGGACCGCAACATTTTACGTTTCTGCGGTGGAGACGAGGCGTATGTGA 55245
57238 ACGGGCCCTGGCGCAATTTTATGAGCGCTGCACAAATAGTTGTTGCGCGACCGGAAAG 57297
55246 ACGGGCCCTGGCGCAATTTTATGAGCGCTGCACAAATAGTTGTTGCGCGACCGGAAAG 55305
57298 GCGTAGCGCCAAAGCTTAAAGTATGTCGCGGGGCACTCCGAGGAGAACCCCTTCC 57357
55306 GCGTAGCGCCAAAGCTTAAAGTATGTCGCGGGGCACTCCGAGGAGAACCCCTTCC 55365
57358 CCGCCATCTTTCGCGGTTTCCACACCTCCGCTGCTGTTTGAACCGCGCAAGGCTCG 57417
55366 CCGCCATCTTTCGCGGTTTCCACACCTCCGCTGCTGTTTGAACCGCGCAAGGCTCG 55425
57418 ACGTAACCGCGGTCGAAGAACTCCAAAAGCAAAATTCGAGTACACTGGCCCGCTTAA 57477
55426 ACGTAACCGCGGTCGAAGAACTCCAAAAGCAAAATTCGAGTACACTGGCCCGCTTAA 55485
57478 AAGATCAATCTTAGGGGATCAGCTTCTATACCTGGAATTCCTGCTGCTGAGACGA 57537
55486 AAGATCAATCTTAGGGGATCAGCTTCTATACCTGGAATTCCTGCTGCTGAGACGA 55545
57538 CCGTACCGGTTGTTGGCGGCTTGGGTGGAGATTTAACTTGAATCTGCGAAGACA 57597
55546 CCGTACCGGTTGTTGGCGGCTTGGGTGGAGATTTAACTTGAATCTGCGAAGACA 55605
57598 CAGAAAGCGTTGCCGATAGTGCACCACTTCTATAGTAATCATTAATTTTCTATCAC 57657
55606 CAGAAAGCGTTGCCGATAGTGCACCACTTCTATAGTAATCATTAATTTTCTATCAC 55665
57658 TGTGTGCGACGACCTTAAATGCAACCGTGTGTTTAAATGAGTAAATACATAG 57717
55666 TGTGTGCGACGACCTTAAATGCAACCGTGTGTTTAAATGAGTAAATACATAG 55725
57718 CAACCATCTGTTCCACGACCTTGGCTGCTTATCAACAAAGGAATTAACACCGTTACTG 57777
55726 CAACCATCTGTTCCACGACCTTGGCTGCTTATCAACAAAGGAATTAACACCGTTACTG 55785
57778 CCACCATTTTACGTTGGCGGCGGAGCGGATACCTGCGGCGGCGCATTTGATTAACAA 57837
55786 CCACCATTTTACGTTGGCGGCGGAGCGGATACCTGCGGCGGCGCATTTGATTAACAA 55845
57838 CAGTATTCATCAAGGCTCCCGACGCTCAGGACGCTGAAGTGTGCTGCGCATCACTAA 57897
55846 CAGTATTCATCAAGGCTCCCGACGCTCAGGACGCTGAAGTGTGCTGCGCATCACTAA 55905
57898 ATAGTTGCCGTAGGAAACATGTTACGAAGGTTAAATTAACAGTTCAATTTCTTCA 57957
55906 ATAGTTGCCGTAGGAAACATGTTACGAAGGTTAAATTAACAGTTCAATTTCTTCA 55965
57958 GGAACAGCAAAAGGTCGACCCGCTTGAAGCGCATTTGGGACTTCCGTCAGAGAAAC 58017
55966 GGAACAGCAAAAGGTCGACCCGCTTGAAGCGCATTTGGGACTTCCGTCAGAGAAAC 56025

OY	58018	TTCCACCGCGCTGACTGGCTCAAGTGTAGAGTCTGCTCCGGCTCGGTGTTTTAAAAAT	58077
Db	56026	TTCCCGCCCACTGACCTGAGCTCAAGTGTAGAGTCTCTCCGGCTCGGTGTTTTAAAAAT	56085
OY	58078	ACCAAGCCGGGGTTTTGTATGCCGACTCGCAGAGACCCCAACAGGGAAGCAAAAGGGA	58137
Db	56086	ACCAAGCCGGGGTTTTGTATGCCGACTCGCAGAGACCCCAACAGGGAAGCAAAAGGGA	56145
OY	58138	CTCGTGGCTGGACTGCTGTAGTAAGAGCGAGACGTGTGTCCTTAAACAATCACTAGTGTAC	58197
Db	56146	CTCGTGGCTGGACTGCTGTAGTAAGAGCGAGACGTGTGTCCTTAAACAATCACTAGTGTAC	56205
OY	58198	GATTGGGGCGCTGCGGGGATCTTCAACCAACCCCTTTTGGCAACAGCGGTGTGTAAATT	58257
Db	56206	GATTGGGGCGCTGCGGGGATCTTCAACCAACCCCTTTTGGCAACAGCGGTGTGTAAATT	56265
OY	58258	TTGGCTCTCTCCACAGCGCGCTGGGTAAATTCGGCGCCATATGCCCCCTACCGATTGA	58317
Db	56366	TTGGCTCTCTCCACAGCGCGCTGGGTAAATTCGGCGCCATATGCCCCCTACCGATTGA	56325
OY	58318	CTGTGTTACGCCCTCAACAGTGTTCGTGACAAAGACGTGGACCAATTCGTGTAGCAAGA	58377
Db	56326	CTGTGTTACGCCCTCAACAGTGTTCGTGACAAAGACGTGGACCAATTCGTGTAGCAAGA	56385
OY	58378	ATGGCCGTTCACGGGTGACGTGATTATTTATGATCTACATCAAGAGGACATATGTGTTTT	58437
Db	56386	ATGGCCGTTCACGGGTGACGTGATTATTTATGATCTACATCAAGAGGACATATGTGTTTT	56445
OY	58438	TATGCTGTGTCCACACGGGAGGTTACGAGATCAACGGGACAAATATACGCAATTTGA	58497
Db	56446	TATGCTGTGTCCACACGGGAGGTTACGAGATCAACGGGACAAATATACGCAATTTGA	56505
OY	58498	GAACTTTGAAAGGACTATGTTTATTTTAAAAACAAGCTGCTGTGGGATCTGTGTAG	58557
Db	56506	GAACTTTGAAAGGACTATGTTTATTTTAAAAACAAGCTGCTGTGGGATCTGTGTAG	56565
OY	58558	GCTGTGTTATTTGAAATATTTTAAATACCGATGCGTTATAGAGTGTCTGTAAAAATGT	58617
Db	56566	GCTGTGTTATTTGAAATATTTTAAATACCGATGCGTTATAGAGTGTCTGTAAAAATGT	56625
OY	58618	GCCGCATTTAAATATGTATTAAAGTCACGGGTGCGCTGTCTCCAAAGTCGTCTGT	58677
Db	56626	GCCGCATTTAAATATGTATTAAAGTCACGGGTGCGCTGTCTCTCCAAAGTCGTCTGT	56685
OY	58738	GTCACACAGCTTATGAGATTGTGAACCGCACTAGGGCGGAGACGCCAAATCCTTGGGG	58797
Db	56746	GTCACACAGCTTATGAGATTGTGAACCGCACTAGGGCGGAGACGCCAAATCCTTGGGG	56805
OY	58798	TGGGTTTAACGTCGGGATGTCGGCCCAAGGTCGACGCTATACATCGATCCCATCAATAC	58857
Db	56806	TGGGTTTAACGTCGGGATGTCGGCCCAAGGTCGACGCTATACATCGATCCCATCAATAC	56865
OY	58858	AAACGCGGAATTCATTACACGTATACCTCTCTGTAGTAGTACCTGTGCCCCGCTCAAGCGCGA	58917
Db	56866	AAACGCGGAATTCATTACACGTATACCTCTCTGTAGTAGTACCTGTGCCCCGCTCAAGCGCGA	56925
OY	58918	CAGGATTAATGATAGGGGGGGCTTATCTGATGTTTCCAGCATRGAAGAATGACAGCAG	58977
Db	56926	CAGGATTAATGATAGGGGGGGCTTATCTGATGTTTCCAGCATRGAAGAATGACAGCAG	56985
OY	58978	TTCTGTTACGCTCGCGCTGCGCGGCTTAAACACACTCAGCGGCTCAAAAAACGTCGCG	59037
Db	56986	TTCTGTTACGCTCGCGCTGCGCGGCTTAAACACACTCAGCGGCTCAAAAAACGTCGCG	57045
OY	59038	ATATATGTCCAGTGTGCGATCATGCTCTGTTTGACACAGCACGCAAGACAAACCC	59097
Db	57046	ATATATGTCCAGTGTGCGATCATGCTCTGTTTGACACAGCACGCAAGACAAACCC	57105

QY	59098	AGTAAACGTTGCCGACATGAAAGCCTGGTGGCCAGCTGCAGCGCTAAATTCAGAAACGTTTAG	59157
Db	57106	AGTAAAGCTTGGCCGACATGAAAGCCTGGTGGCCAGCTGCAGCGCTAAATTCAGAAACGTTTAG	57165
QY	59158	TGCGTCCGAAACACACAGCTTAGCGCGATTGGAAGCATTGCAAAATGCTATTATTTTATTAG	59217
Db	57166	TGCGTCCGAAACACACAGCTTAGCGCGATTGGAAGCATTGCAAAATGCTATTATTTTATTAG	57225
QY	59218	TACTTCCACATCATGTCGCCGAAAACATTGGATTAAATATATAGGGCCCTCTGAGAGCATTC	59277
Db	57226	TACTTCCACATCATGTCGGGGAAAGAACTGGATTAAATATATAGGGCCCTCTGAGAGCATTC	57285
QY	59278	TGTTTCAGGCATTACGCCCTCAGATGGTGTCTCTCCCAATTAGACGCTTCAGTATTTTG	59337
Db	57286	TGTTTCAGGCATTACGCCCTCAGATGGTGTCTCTCCCAATTAGACGCTTCAGTATTTTG	57345
QY	59338	GTCATAGGGTTCCAGCGTGGCTAATTGTTCCGAATATTTGCGGCTATGCTATTATAT	59397
Db	57346	GTCATAGGGTTCCAGCGTGGCTAATTGTTCCGAATATTTGCGGCTATGCTATTATAT	57405
QY	59398	ACACAGACAGCGTCTGTCCACATACAGCTGTCGTCGAATATCGTGTAACTTAAGAAA	59457
Db	57406	ACACAGACAGCGTCTGTCCACATACAGCTGTCGTCGAATATCGTGTAACTTAAGAAA	57465
QY	59458	TGAGAGAGTGATTTATGAGTCCATGTGAGTCAGTTTGGCGATTATATGACGTAAACGGGC	59517
Db	57466	TGAGAGAGTGATTTATGAGTCCATGTGAGTCAGTTTGGCGATTATATGACGTAAACGGGC	57525
QY	59518	CTAGACAAATGGAACCGGTGCTCCGCGAGTAGAGCGAATGCTGCTTGGCTGCCCTGATTTGT	59577
Db	57526	CTAGACAAATGGAACCGGTGCTCCGCGAGTAGAGCGAATGCTGCTGCTGCCCTGATTTGT	57585
QY	59578	CGACACAGGGGTGAGGTTGTAGGTTTGAACATTTTCCCTCCACAGAGCTAGTTAGCT	59637
Db	57586	CGACACAGGGGTGAGGTTGTAGGTTTGAACATTTTCCCTCCACAGAGCTAGTTAGCT	57645
QY	59638	CTTTGAGCATCTCCATAAACGAGAGGACGATTATTTGAAAAAAGCTTTTACTAGCGAGC	59697
Db	57646	CTTTGAGCATCTCCATAAACGAGAGGACGATTATTTGAAAAAAGCTTTTACTAGCGAGC	57705
QY	59698	TGCGTTTAGGATGTGACATTGCGATAGGTTATAGTTGGGTGGCGGACAGCGGATTAAG	59755
Db	57706	TGCGTTTAGGATGTGACATTGCGATAGGTTATAGTTGGGTGGCGGACAGCGGATTAAG	57765
QY	59758	CCTCGCAACGTTATCTGAGTAGTATTAATATATCGTGTGGGCGTCCCTCCCTCGGTA	59817
Db	57766	CCTCGCAACGTTATCTGAGTAGTATTAATATATCGTGTGGGCGTCCCTCCCTCGGTA	57825
QY	59818	AACGTGTGAAGCACTGCGTTTCAATGCAATGCAATCTTCTTTACGTAGTGCCTCGTCTT	59877
Db	57826	AACGTGTGAAGCACTGCGTTTCAATGCAATGCAATCTTCTTTACGTAGTGCCTCGTCTT	57885
QY	59878	TCTCAAGGTTAAGAAATGTATCGAACCTGCTGTGATCTGGTTCGTGCAGGCAATTTGAACA	59937
Db	57886	TCTCAAGGTTAAGAAATGTATCGAACCTGCTGTGATCTGGTTCGTGCAGGCAATTTGAACA	57945
QY	59938	CGGATTATTGAAACCTGTTTCCGGAGACCGTGGGTCGACTTTCGTAACGGTCCCAAAA	59997
Db	57946	CGGATTATTGAAACCTGTTTCCGGAGACCGTGGGTCGACTTTCGTAACGGTCCCAAAA	58005
QY	59998	GCTTGTATTGTGTCCACATGTTTGTGAGAGACGCTGTGTGACGAATCCTCAACAGCTGTG	60057
Db	58006	GCTTGTATTGTGTCCACATGTTTGTGAGAGACGCTGTGTGACGAATCCTCAACAGCTGTG	58065
QY	60058	TTATGCCGCTACAGTTTGTCTCCGCGAGCTTTATCAGCAAGTTTAGAGCTCCCTCT	60117
Db	58066	TTATGCCGCTACAGTTTGTCTCCGCGAGCTTTATCAGCAAGTTTAGAGCTCCCTCT	58125
QY	60118	TGGGTGGGTTTGTGAGAGATATGCTTAAGGAGAGCAATATGCTTTATATACATGCT	60177
Db	58126	TGGGTGGGTTTGTGAGAGATATGCTTAAGGAGAGCAATATGCTTTATATACATGCT	58185
QY	60178	TGCACGTGCTACCGACACGCGTTTATGAGCGCGGATTATTAGTAACGTCAATCAATTGG	60237

58186 TGCACGTGCTACCGACACCGCCTTTTAGAGCGCGGCTATTCTACTGACATACCTTGG 58245
60238 CGTGCTCCGCGGTCTGTGACATGTCATATCGCGGTAATAATACCGGTACAGAGGCTAT 60297
58246 CGTGCTCCGCGGTCTGTGACATGTCATATCGCGGTAATAATACCGGTACAGAGGCTAT 58305
60298 CAAAGCGACGCGTCCATTGTAAATATAGCCCGTAAACACTTCACTGTTATATCTT 60357
58306 CAAAGCGACGCGTCCATTGTAAATATAGCCCGTAAACACTTCACTGTTATATCTT 58365
60358 TTGTGCTGAGTGGCCGAGATFAAGACGCTTATCTCGTTAAACCTCACAGACACTCGG 60417
58366 TTGTGCTGAGTGGCCGAGATFAAGACGCTTATCTCGTTAAACCTCACAGACACTCGG 58425
60418 CGTAGCTGGAATATFAAATAGACGTACATCGGTCATTATCGAGGTAATCTCTGTGCA 60477
58426 CGTAGCTGGAATATFAAATAGACGTACATCGGTCATTATCGAGGTAATCTCTGTGCA 58485
60478 GTTTCGACGCAATCCGCGATATCGTAGCTCTCCGAAACGTAACGTTTCTCATCTGT 60537
58486 GTTTCGACGCAATCCGCGATATCGTAGCTCTCCGAAACGTAACGTTTCTCATCTGT 58545
60538 GACAGTGTCTGTATCTGCGGATGCTGTCGCGCGGCGGCGCTGACAATATGGA 60597
58546 GACAGTGTCTGTATCTGCGGATGCTGTCGCGCGGCGGCGCTGACAATATGGA 58605
60598 CCAACCCAAAGGCGACCAACCCAGTCGATCTGTTCTGACGATAAACAGTCTGTGT 60657
58606 CCAACCCAAAGGCGACCAACCCAGTCGATCTGTTCTGACGATAAACAGTCTGTGT 58665
60658 GTAGTACCTGATTAATAGTGTTCAGTAACAGTGTGACGACTGTAGACGAGGTACGTG 60717
58666 GTAGTACCTGATTAATAGTGTTCAGTAACAGTGTGACGACTGTAGACGAGGTACGTG 58725
60718 CCCAGATTCAAACGATAGACGCTTTGTAATCCGGCTCAGAGTCTGACACCGCGCAAC 60777
58726 CCCAGATTCAAACGATAGACGCTTTGTAATCCGGCTCAGAGTCTGACACCGCGCAAC 58785
60778 GGGTCTTCAGGGTGGTCTCGAAGTTGGTCCAGTCTTTAAGACGTTGCTATGTGACAC 60837
58786 GGGTCTTCAGGGTGGTCTCGAAGTTGGTCCAGTCTTTAAGACGTTGCTATGTGACAC 58845
60838 TCCCAATGCGCTTGTACAGGTGTATACAGCGTCTTCCAAAGATCCCTGGAATTC 60897
58846 TCCCAATGCGCTTGTATGACAGGTGTATACAGCGTCTTCCAAAGATCCCTGGAATTC 58905
60898 GAAGACTGGAGTGTAGCGTTTGTACCGCGAAGCTACGCTACTTGCCCTGTAGATCTGA 60957
58906 GAAGACTGGAGTGTAGCGTTTGTACCGCGAAGCTACGCTACTTGCCCTGTAGATCTGA 58965
60958 AAAGGAGATGAGAGATTCCGTGCGATGGACCAACACGTCAACCAAAATCCGGGGTTCA 61017
58966 AAAGGAGATGAGAGATTCCGTGCGATGGACCAACACGTCAACCAAAATCCGGGGTTCA 59025
61018 TCTTGAACATGACGTCGATGCAAAAGTGAAGGGGTGTGTGATCAACGTCACGTGCTGT 61077
59026 TCTTGAACATGACGTCGATGCAAAAGTGAAGGGGTGTGTGATCAACGTCACGTGCTGT 59085
61078 CAAATATATACATCAAGCCACCGAAGTGGTTGTAGACACTGGCTTCTGATCCGGCTG 61137
59086 CAAATATATACATCAAGCCACCGAAGTGGTTGTAGACACTGGCTTCTGATCCGGCTG 59145
61138 AAGACTCGGGCGCTTCTTCCGTTTACCGTTTATCTAATTAACGGGAATGCTGTGCTG 61197
59146 AAGACTCGGGCGCTTCTTCCGTTTACCGTTTATCTAATTAACGGGAATGCTGTGCTG 59205
61198 GGAAGATGACGATGATCGGCTGTACCAAAATTTAAACTGCTGATCAGAGCGCGCA 61257
59206 GGAAGATGACGATGATCGGCTGTACCAAAATTTAAACTGCTGATCAGAGCGCGCA 59265
61258 CCACCATAGCCGACAGAACTATGCGCTGAAGACGTTGTCACAGACTCTCA 61317

59266 CCACCATAGCCGACAGAACTATGCGCTGCTTAAAGACGTTCTGCCACAGATCTCA 59325
61318 GCGCTTTGGCTTTAAGAGCCGACACATCAATATAGCCGTGAGAAAAAGCTCATACAGCG 61377
59326 GCGCTTTGGCTTTAAGAGCCGACACATCAATATAGCCGTGAGAAAAAGCTCATACAGCG 59385
61378 GAGCCGTATCCATAGAGCAAAATTCAGCAACAGAGAGCTATCGAAGTATTGGCCGGTTATAG 61437
59386 GAGCCGTATCCATAGAGCAAAATTCAGCAACAGAGAGCTATCGAAGTATTGGCCGGTTATAG 59445
61438 TGGACATATGAAAGAGTTTATGCGCAAAAAACCAATGGCATGTACGGAGTATATCA 61497
59446 TGGACATATGAAAGAGTTTATGCGCAAAAAACCAATGGCATGTACGGAGTATATCA 59505
61498 ACGCGAATTTTGAACCTCTCTGAGATACCGGACGCTGTTTATGAGCTTCCATATTA 61557
59506 ACGCGAATTTTGAACCTCTCTGAGATACCGGACGCTGTTTATGAGCTTCCATATTA 59565
61558 TTGTATGACGAGCGCGGAACCTGCTCTCTTACTACTCAACCCGTGCTCTTTT 61617
59566 TTGTATGACGAGCGCGGAACCTGCTCTCTTACTACTCAACCCGTGCTCTTTT 59625
61618 ACTGTTCTTAAACAGCTGGCTAAATACCCCTTCTTACCGCGGAGGGCGGTTCCGTGCA 61677
59626 ACTGTTCTTAAACAGCTGGCTAAATACCCCTTCTTACCGCGGAGGGCGGTTCCGTGCA 59685
61678 TAGTATGCGTGGTTCGCCAACGACAGCAACGCGTTCCAGTCACTTACCAACACGGA 61737
59686 TAGTATGCGTGGTTCGCCAACGACAGCAACGCGTTCCAGTCACTTACCAACACGGA 59745
61738 CGCAAAAGAGGAGATATGCTGTGAGAACATCTTACATTCATGATAGGGAAGAAG 61797
59746 CGCAAAAGAGGAGATATGCTGTGAGAACATCTTACATTCATGATAGGGAAGAAG 59805
61798 TCGTATCTGATACGTACACTTGGAGAGAACTGGCGCTGTTTATAAACAACAGCGCT 61857
59806 TCGTATCTGATACGTACACTTGGAGAGAACTGGCGCTGTTTATAAACAACAGCGCT 59865
61858 GCACCGATTCGAGTTTGGGACACCTTCTTAAATTTTATAGATATATCTTCCATCTCTG 61917
59866 GCACCGATTCGAGTTTGGGACACCTTCTTAAATTTTATAGATATATCTTCCATCTCTG 59925
61918 ACGAAGTCAATGATACGTACAGATATGCTGTCTTAAAGTAAATGATTAAGATCTCT 61977
59926 ACGAAGTCAATGATACGTACAGATATGCTGTCTTAAAGTAAATGATTAAGATCTCT 59985
61978 TAGAATACATGCTGGAGACCGCACTTTTGTCAATATGCGAGTAAAGGCGTATCTAA 62037
59986 TAGAATACATGCTGGAGACCGCACTTTTGTCAATATGCGAGTAAAGGCGTATCTAA 62045
62038 CAAACCTACACATGCTTACAGCTTAGGGGCGGATACAGGACAGAAAGCTTTTACCT 62097
60046 CAAACCTACACATGCTTACAGCTTAGGGGCGGATACAGGACAGAAAGCTTTTACCT 62105
62098 GTCCCGTGGTGTGCGAGGTGTTTGAACCCGTTTGAAGATATACAGGCGGCGTCAAC 62157
60106 GTCCCGTGGTGTGCGAGGTGTTTGAACCCGTTTGAAGATATACAGGCGGCGTCAAC 62165
62158 TCACCAACCTCAACCGTGAACCGAGTGGGTGACAAAAAACCTCTTAAATTAAGTAAATTA 62217
60166 TCACCAACCTCAACCGTGAACCGAGTGGGTGACAAAAAACCTCTTAAATTAAGTAAATTA 62225
62218 CCGCATTTGTGACACAGACATGCTCATATGTCGCCACGGAATTCACATGAGCTTGAACCC 62277
60226 CCGCATTTGTGACACAGACATGCTCATATGTCGCCACGGAATTCACATGAGCTTGAACCC 62285
62278 AGGTTACGTTTATCAACAAAGTTTGTAAAAAACAGCACAGCTGCTTAAATGAAAAACAA 62337
60286 AGGTTACGTTTATCAACAAAGTTTGTAAAAAACAGCACAGCTGCTTAAATGAAAAACAA 62345
62338 AAAAAATGATATGCTGGTTTACAGGTAGCTACTTTGAGTTCAAAAGAAATCTTAGACAGCG 62397
60346 AAAAAATGATATGCTGGTTTACAGGTAGCTACTTTGAGTTCAAAAGAAATCTTAGACAGCG 62405

OY	62398	AACCTCTTCGTGGAGACGCATTCGCAAGACCGCTCCGGAATACGTATACGGTTTCTTAACA	62457
Db	60406	AACTCTTCGTGGAGACGCATTCGCAAGACCGCTCCGGAATACGTATACGGTTTCTTAACA	60465
OY	62458	CGCTACGTCAACCGCCATGTACTCGTTTCAAGCGTCAGGCGGATACGTACGACACGACA	62517
Db	60466	CGCTACGTCAACCGCCATGTACTCGTTTCAAGCGTCAGGCGGATACGTACGACACGACA	60525
OY	62518	AAATYCTGCAAGACCTTAAATTTTGCACCCCTCCCGGCCGCTCGGCACACGGGGCGTGTAG	62577
Db	60526	AAATYCTGCAAGACCTTAAATTTTGCACCCCTCCCGGCCGCTCGGCACACGGGGCGTGTAG	60585
OY	62578	ACCTTCAACGGTTTCGTGAAGAGTTAACTGGAGACGACATCTTCTACACAGTGTGCA	62637
Db	60586	ACCTTCAACGGTTTCGTGAAGAGTTAACTGGAGACGACATCTTCTACACAGTGTGCA	60645
OY	62638	GTCCCGCCGCCACCCGGGGGTATACCGCCCTCCAGGTGTTTGGTCGACAGTACTGGGCC	62697
Db	60646	GTCCCGCCGCCACCCGGGGGTATACCGCCCTCCAGGTGTTTGGTCGACAGTACTGGGCC	60705
OY	62698	TAAAGGACGTGTTCGCCCTCCAGAAATAAAGGTGGCGTGTGCTGTTTGGCGGGAGTTTG	62757
Db	60706	TAAAGGACGTGTTCGCCCTCCAGAAATAAAGGTGGCGTGTGCTGTTTGGCGGGAGTTTG	60765
OY	62758	AGAAGGAAACAGTTTTCGGCGCTTACGGTTAACTGGCTCGTAAGAGGACGAGTTGACTTGG	62817
Db	60766	AGAAGGAAACAGTTTTCGGCGCTTACGGTTAACTGGCTCGTAAGAGGACGAGTTGACTTGG	60825
OY	62818	TCTCCCTTCAGAACGTCTCAAGGGGCTGTGTGGCTGTTGCATCGACCGTTGAATCGTATA	62877
Db	60826	TCTCCCTTCAGAACGTCTCAAGGGGCTGTGTGGCTGTTGCATCGACCGTTGAATCGTATA	60885
OY	62878	AAATTTAAGGGGTACAGCTTTTAAACGGGTACGTTTGGTCGTGTCTCAGGGTTTGCCACTCA	62937
Db	60886	AAATTTAAGGGGTACAGCTTTTAAACGGGTACGTTTGGTCGTGTCTCAGGGTTTGCCACTCA	60945
OY	62938	GTGATGACCTCAGGAACAATGCCCTCCCTGGTCCGTGACGAGACATCTACCGGTTTATGCG	62997
Db	60946	GTGATGACCTCAGGAACAATGCCCTCCCTGGTCCGTGACGAGACATCTACCGGTTTATGCG	61005
OY	62998	CGTCCCTTAGAAGATTAACATTAACCAATTGACCCGAACCAATGAGACGGGAGCGTTTCTC	63057
Db	61006	CGTCCCTTAGAAGATTAACATTAACCAATTGACCCGAACCAATGAGACGGGAGCGTTTCTC	61065
OY	63058	AAGTGTCTGTGGGGGACTATGGGGTCACTCAAAATTTAGCCATGACCATCTGTAAAG	63117
Db	61066	AAGTGTCTGTGGGGGACTATGGGGTCACTCAAAATTTAGCCATGACCATCTGTAAAG	61125
OY	63118	CACAGGGAAATGTGTTGGAGCGAGTACGCGTACTATTTTGGGTGCCCAAGAAAGCTCCACA	63177
Db	61126	CACAGGGAAATGTGTTGGAGCGAGTACGCGTACTATTTTGGGTGCCCAAGAAAGCTCCACA	61185
OY	63178	CAAGCCACGTGTATGTAGCAATATTCAAAGGGCTGTTTAACCTCAAAATTTATTTGGTCATGGACA	63237
Db	61186	CAAGCCACGTGTATGTAGCAATATTCAAAGGGCTGTTTAACCTCAAAATTTATTTGGTCATGGACA	61245
OY	63238	GCAACCCCCCTTAAAAACCCTCTCTCAGAGAACCACTGCATTAACACCTCCGCCAAGCATATAG	63297
Db	61246	GCAACCCCCCTTAAAAACCCTCTCTCAGAGAACCACTGCATTAACACCTCCGCCAAGCATATAG	61305
OY	63298	TCCGCGCCCTTCACAACCCCAACCAACCCCTCATCTTAATAATAATAAAAAACAACAAA	63357
Db	61306	TCCGCGCCCTTCACAACCCCAACCAACCCCTCATCTTAATAATAATAAAAAACAACAAA	61365
OY	63358	TGGAATAACATTTGTTTATTCAGTCCAAACGAGCGACAGATAGTTGTCAATTTCCACA	63417
Db	61366	TGGAATAACATTTGTTTATTCAGTCCAAACGAGCGACAGATAGTTGTCAATTTCCACA	61425
OY	63418	CACCGGGGGGTGGCGCCCATAGTTTACGACACGAAAGCGCCGGGCGCTCTGGGGTTAGA	63477
Db	61426	CACCGGGGGGTGGCGCCCATAGTTTACGACACGAAAGCGCCGGGCGCTCTGGGGTTAGA	61485

QY	63478	AGTAGCCCCCCCCCGGTGTCAGAGTCATACGTCTCTTAAAGGCCCTGGGTGTACAAAC	63537
Db	61486	AGTAGCCCCCCCCCGGTGTCAGAGTCATACGTCTCTTAAAGGCCCTGGGTGTACAAAC	61545
QY	63538	ATTAATACAGTCGCATACACGTTTGGAGTCCCGGTGAGCGGGCGCTTTCCAGAGCGAC	63597
Db	61546	ATTAATACAGTCGCATACACGTTTGGAGTCCCGGTGAGCGGGCGCTTTCCAGAGCGAC	61605
QY	63598	ACGAACAACCGCGCTTTGACGTCGATCTGCATCGTGTGCGCTGTGGAAGATGAACACAG	63657
Db	61606	ACGAACAACCGCGCTTTGACGTCGATCTGCATCGTGTGCGCTGTGGAAGATGAACACAG	61665
QY	63658	GTCATATCAATCAGTGGCGCCCGTCCCTCATCGCGCTGATTGCTCCATGTCTCAAC	63717
Db	61666	GTCATATCAATCAGTGGCGCCCGTCCCTCATCGCGCTGATTGCTCCATGTCTCAAC	61725
QY	63718	AGACCCCTGGGTGCGCATCTGTCGTCATCTGAAATTAATTAATGATGCTTTGTGTCGACGT	63777
Db	61726	AGACCCCTGGGTGCGCATCTGTCGTCATCTGAAATTAATTAATGATGCTTTGTGTCGACAT	61785
QY	63778	TGATCCAGACAACAACAG--TCTCTTCTTCAATGGGAAGACATCCGCCCTTGCCGGGTGA	63834
Db	61786	TGATCCAGACAACAACAGTCTTCTTCTTCAATGGGAAGACATCCGCCCTTGCCGGGTGA	61845
QY	63835	TCTGATATATACACTGACCAAGCGGGCGCCGTGGCGAANAACCTCAAGCTTCTCC	63894
Db	61846	TCTGATATATATACACTGACCAAGCGGGCGCCGTGGCGAANAACCTCAAGCTTCTCC	61905
QY	63895	GCCACTTTCATCAGTGCCTGTCGATGTCATCTATAAANAATGCTGTGCTGTCGATTC	63954
Db	61906	GCCACTTTCATCAGTGCCTGTCGATGTCATCTATAAANAATGCTGTGCTGTCGATTC	61965
QY	63955	AGATGACTGGGGGTGCGGGTGTGTGGCCAGTAACACACGGACGGCGCGGACCAACAA	64014
Db	61966	AGATGACTGGGGGTGCGGGTGTGTGGCCAGTAACACACGGACGGCGCGGACCAACAA	62025
QY	64015	CGCGGTCAATGTCGCGGGCGCGCTCGGTGTGTGTGGCACTGTCTGAAGTAATGACGT	64074
Db	62026	CGCGGTCAATGTCGCGGGCGCGCTCGGTGTGTGTGGCACTGTCTGAAGTAATGACGT	62085
QY	64075	AGGTAGCGGGCGCTGTGTAAAGGATCAACGCTCCGCGGTGGGGATCTAATCTGAG	64134
Db	62086	AGGTAGCGGGCGCTGTGTAAAGGATCAACGCTCCGCGGTGGGGATCTAATCTGAG	62145
QY	64135	TGGGGAGAGACCGCGCGTCTGCTTCTTCAATCCATATCACTAGTATCGACTTTCCTCA	64194
Db	62146	TGGGGAGAGACCGCGCGTCTGCTTCTTCAATCCATATCACTAGTATCGACTTTCCTCA	62205
QY	64195	ATGAGAGTCGGTTTCGTCTGTGGCTTTTGGAGTAATGAGGAGGGAATCTTGGTCANAAC	64254
Db	62206	ATGAGAGTCGGTTTCGTCTGTGGCTTTTGGAGTAATGAGGAGGGAATCTTGGTCANAAC	62265
QY	64255	ATCTCTAGGTGCATCATATGTCATCACTGGGGGGCGTCCGTCACCGGGGGATACGGGCA	64314
Db	62266	ATCTCTAGGTGCATCATATGTCATCACTGGGGGGCGTCCGTCACCGGGGGATACGGGCA	62325
QY	64315	CCCCGTACGGGACCCGCGCAACAAAAACCTCTTGTCTCTTTTCTTCTTCTTCTTCTTCTT	64374
Db	62326	CCCCGTACGGGACCCGCGCAACAAAAACCTCTTGTCTCTTTTCTTCTTCTTCTTCTTCTT	62385
QY	64375	AATCGCAGCATCTCTGGAGTGGCGCGCGGCTTGAACGGGTGCGATTAAGACATGAC	64434
Db	62386	AATCGCAGCATCTCTGGAGTGGCGCGCGGCTTGAACGGGTGCGATTAAGACATGAC	62445
QY	64435	CATGGCGGAAACGTTCACGT--AANAAGCATGCGCTATCCCGCATCACTTAATATTCGA	64493
Db	62446	CATGGCGGAAACGTTCACGTATAAACAACGATGCTATCCCGCATCACTTAATATTCGA	62505
QY	64494	GTCACAGCGACCCCTCGATTTCTGAACATAGTATGTCATTCGCAAGTTTAAATGTTGCA	64553
Db	62506	GTCACAGCGACCCCTCGATTTCTGAACATAGTATGTCATTCGCAAGTTTAAATGTTGCA	62565
QY	64554	GCTTAGAATC--TGCGGCGAAGGAACCGGTTCCCGCTGTGGCGGTAGCCAGGAGAGAC	64612

CDS	/isolate="17577" /specific_host="Macaca mulatta" /db_xref="taxon:154334" 65..1798 /note="ORF50" /codon_start=1 /product="Immediate-early transcription factor RrtA" /protein_id="AKR28330.1" /db_xref="GI:13506779" /translation="MTDDNGVYKRLRSGVDNFGLSPELRKLKLYAVLLINEAVYK KHPRDLNKITEVEYCKIWEKCSLSPIRGLIADLNFNLFCILRSRRTGVAACN VPAEBAQGIIVRLITERALDCEKMTIASKSSVLPOLARLHVIVEMKACIGL WRLLICRRPRLIMALADSVLAVYITFLDAEKLDIRLALKLVLPFLDIRLILAPML ANKMAYDNFTITGTAEKRPRVYTGSGMCPGSSLPDSLILPECPGLIPALV DISLENLENPILISAPLSEQFTTNHPSLPSVGSITITPQGVAPQCCMDWKAAVS SIHHOATPEILAILAGTSSAAGPHILACSPAGSTRQVSGVAGVCCPACYPVAL PWPVAKRMETVAOLGNAPKYNHIGGRVAPLVNPIIDLTSPSGOSPSDIANTP ESMAKSPPEPFAETATTPAKRKOPREDYADRLKLDYGAATVNHPPFGPSMRRE OGFLDIESTDVTVAASGPKNDMDLAILDLYGLQSPALIDSPSSNDNEIPE VSPSSGHGSP"									
BASE COUNT	471	a	581	c	490	g	403	t		
ORIGIN										
Query Match	4.5%;		Score 1812;	DB 1;	Length 1945;					
Best Local Similarity	99.9%;	Pred. No. 0;	Mismatches 1;	Indels 0;	Gaps 0;					
Matches 1862;	Conservative	0;								
QY	68323	CAGGCTGTAAAAA	ACTCAGAAAGTCTCTGCGTGGACAACTTTTGGCGACTCTCCGAACCG	68382						
Db	83	CAGGCTGTAAAAA	ACTCAGAAAGTCTCTGCGTGGACAACTTTTGGCGACTCTCCGAACCG	142						
QY	68383	CTCAGGGATTAAGCTGTACCA	CGCGGTGCTTTTATAACAGACATACGTCAAAAAACAT	68444						
Db	143	CTCAGGGATTAAGCTGTACCA	CGCGGTGCTTTTATAACAGACATACGTCAAAAAACAT	202						
QY	68443	GACCCACGTACCTTAATTAAGCTGTACCAAGAAAGTCTGTGATGTATTGTAAGGAATGT	68504							
Db	203	GACCCACGTACCTTAATTAAGCTGTACCAAGAAAGTCTGTGATGTATTGTAAGGAATGT	262							
QY	68503	GCTCTCCCTGGGTCCTATCTCCGGGCTCATCTGCGGATTCGAATCTTTTAACTCTGTTCTGC	68563							
Db	263	GCTCTCCCTGGGTCCTATCTCCGGGCTCATCTGCGGATTCGAATCTTTTAACTCTGTTCTGC	322							
QY	68563	CTCTACCGGGGTTCCCGGGTTAAACCCGGGGCCGCAACCTGTAAACGCCGTCGCGCA	68622							
Db	323	CTCTACCGGGGTTCCCGGGTTAAACCCGGGGCCGCAACCTGTAAACGCCGTCGCGCA	382							
QY	68623	GAAATGGCCCAAGGCAATCGTGAGAAATTCCTACCCAGAGAGGGCCCTTTGTTGTACCGAAAG	68682							
Db	383	GAAATGGCCCAAGGCAATCGTGAGAAATTCCTACCCAGAGAGGGCCCTTTGTTGTACCGAAAG	442							
QY	68683	ATGTTTAAATAGCTGTCTGCTGCGTACAGCGGGGTCGTATTAACCGCCCAAGTGGCCAGAGTTCG	68744							
Db	443	ATGTTTAAATAGCTGTCTGCTGCGTACAGCGGGGTCGTATTAACCGCCCAAGTGGCCAGAGTTCG	502							
QY	68743	CAGCAGCTTACCGCGGAAATGAAGGCGCAAGTGTTTTGGGACGCGGCTGTCTCATATGT	68802							
Db	503	CAGCAGCTTACCGCGGAAATGAAGGCGCAAGTGTTTTGGGACGCGGCTGTCTCATATGT	562							
QY	68803	TGCAAGCGGCTATTCATATGCTATTTGCGCACTGGTCTCTGCTCACTATTAATACCTCGAT	68863							
Db	563	TGCAAGCGGCTATTCATATGCTATTTGCGCACTGGTCTCTGCTCACTATTAATACCTCGAT	622							
QY	68863	GCCGAGGAAACTGGAACCTTTAAGCTCAAAAGCACTGTGCAAACTGTTTTCACACCCATC	68922							
Db	623	GCCGAGGAAACTGGAACCTTTAAGCTCAAAAGCACTGTGCAAACTGTTTTCACACCCATC	682							
QY	68923	TTTCTTCAAAAGATCTTAGCCCTTATGACAGCTACTGGCCAAAGATGGTTCTCTGAC	68982							
Db	683	TTTCTTCAAAAGATCTTAGCCCTTATGACAGCTACTGGCCAAAGATGGTTCTCTGAC	742							
QY	68983	AATTATTTTACATCAACCGGTACGCGGCAAGAGGCGCCCTGTGCTGACTGGAAGTACT	69042							

Db	743	AATTATTTTACCATACCGGTACGGCCGAGAAAGGCGCCCTGTGTCGATGGAAGTACT	802
Qy	69043	AGCGGATGACGTGTCCGGGAGAGCAGCTTGTCCCGATTCCTTAATCCCTCCAGTATGC	69102
Db	803	AGCGGATGACGTGTCCGGGAGAGCAGCTTGTCCCGATTCCTTAATCCCTCCAGTATGC	862
Qy	69103	GAACCGGGGCTTCTCCGGGACCCCTGTGACCTCAGTAATGTCTTAGAAATCCAGAA	69162
Db	863	GAACCGGGGCTTCTCCGGGACCCCTGTGACCTCAGTAATGTCTTAGAAATCCAGAA	922
Qy	69163	ATCATCTCAGCGGCCCAACCCCTGATGCAATTTGTCAATCAAAACAGCACCCAGTCTG	69222
Db	923	ATCATCTCAGCGGCCCAACCCCTGATGCAATTTGTCAATCAAAACAGCACCCAGTCTG	982
Qy	69223	CCTCAGTCAGTCACCATTTATACGCCAACCCAGGCGCTGTGTCCCGGCCAATGTTTTATG	69282
Db	983	CCTCAGTCAGTCACCATTTATACGCCAACCCAGGCGCTGTGTCCCGGCCAATGTTTTATG	1042
Qy	69283	GACACGTGGAAAGCGGTGTACAGAGCATTCACACAGCAGCAGACGCTATTGTTGGCC	69342
Db	1043	GACACGTGGAAAGCGGTGTACAGAGCATTCACACAGCAGCAGACGCTATTGTTGGCC	1102
Qy	69343	GCGGCATTAACCGGTTGACATCTGCGGCCCCCTGGCCGCAATTCGCAATGTTCCCAATT	69402
Db	1103	GCGGCATTAACCGGTTGACATCTGCGGCCCCCTGGCCGCAATTCGCAATGTTCCCAATT	1162
Qy	69403	GCGGCACAGTCTCGGCAAGGTGGAAGGTCGCGGGCGCTGCAATTCGCGGGAACACAGATGC	69462
Db	1163	GCGGCACAGTCTCGGCAAGGTGGAAGGTCGCGGGCGCTGCAATTCGCGGGAACACAGATGC	1222
Qy	69463	GTTCCGAGAGCCCGGTTACCGCCCAATGTCCCGCCCAAGAGATGGAACCGTATGACACAG	69522
Db	1223	GTTCCGAGAGCCCGGTTACCGCCCAATGTCCCGCCCAAGAGATGGAACCGTATGACACAG	1282
Qy	69523	TTGGGAAACGCTCCCGTAAACAGTCCACATTCGAGGCGCCGATACGCTCCCATGCTT	69582
Db	1283	TTGGGAAACGCTCCCGTAAACAGTCCACATTCGAGGCGCCGATACGCTCCCATGCTT	1342
Qy	69583	AATATACCAATATATAGATTAACTGCTCCCGTCAAGGTCGCGCACAGAGTCCGCGCATATC	69642
Db	1343	AATATACCAATATATAGATTAACTGCTCCCGTCAAGGTCGCGCACAGAGTCCGCGCATATC	1402
Qy	69643	GCCAACTCCAGAGTCCCGATGCGGCGGCTCTCCGCTTCGCGGAAACCGCGCA	69702
Db	1403	GCCAACTCCAGAGTCCCGATGCGGCGGCTCTCCGCTTCGCGGAAACCGCGCA	1462
Qy	69703	ACGGTCCCGCTAGAGAAACGACGACGCGAGACGCTGAGACCAAAAGACTGAAGGC	69762
Db	1463	ACGGTCCCGCTAGAGAAACGACGACGCGAGACGCTGAGACCAAAAGACTGAAGGC	1522
Qy	69763	GACGTTGGGGCGCGCAACAGTAAACACACCTTTCCCGGAGCGTCCGGATGGCGCTT	69822
Db	1523	GACGTTGGGGCGCGCGCAACAGTAAACACACCTTTCCCGGAGCGTCCGGATGGCGCTT	1582
Qy	69823	CGCGAGCAGGCTTATTCGATTTAATCGAAAAGCTCCAGGATGTAAACCGCAAGCATCT	69882
Db	1583	CGCGAGCAGGCTTATTCGATTTAATCGAAAAGCTCCAGGATGTAAACCGCAAGCATCT	1642
Qy	69883	GGACCCAAAAGCAGCAGCATGCTAGCGGCTATCTACAGGACCTTATAGACTACAG	69942
Db	1643	GGACCCAAAAGCAGCAGCATGCTAGCGGCTATCTACAGGACCTTATAGACTACAG	1702
Qy	69943	TCGCCCGGGCGCATGATTCGCCCTCCAGCAACTCGGCAATGAGAGATATTTCCACAG	70002
Db	1703	TCGCCCGGGCGCATGATTCGCCCTCCAGCAACTCGGCAATGAGAGATATTTCCACAG	1762
Qy	70003	GTTAGTCCGCATCTAGCGGCGACAGATGCTTGAAGATGACCCCAAGACGCAAGATC	70062
Db	1763	GTTAGTCCGCATCTAGCGGCGCGACAGATGCTTGAAGATGACCCCAAGACGCAAGATC	1822
Qy	70063	ACACACCGAGACAGTCCACAGCAACCGCGGATGTCTAAACGTAATAATATCACCGGT	70122
Db	1823	ACACACCGAGACAGTCCACAGCAACCGCGGATGTCTAAACGTAATAATATCACCGGT	1882

Qy	70123	TGGAAGTCCCTGTGGCGACAAAATGAGCTTCAAACTTACCATTTTCTGTCTATT	70182
Db	1883	TGGAAGTCCCTGTGGCGACAAAATGAGCTTCAAACTTACCATTTTCTGTCTATT	1942
Qy	70183	CGG 70185	
Db	1943	CGG 1945	
RESULT 4			
AF241164			
LOCUS			
DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
MEDLINE			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
REFERENCE			

```

Db      121 GGATTTCAAAACCTGTGCTGACGCGGAGATCGCTCGGCTTATCTATACGGA 180
QY      70501 GAATTAACGGCCGCTTTTCCCAATTAATGACAAATGACAGCAATACCGGAGAGTGA 70560
Db      181 GAATTAACGGCCGCTTTTCCCAATTAATGACAAATGACAGCAATACCGGAGAGTGA 240
QY      70561 AAGCTTCGCGAGCTACGCTGCGGCGGAGGCTTTTCTGCGGAGCTTCTGTCTCAGGAGTGA 70620
Db      241 AAGCTTCGCGAGCTACGCTGCGGCGGAGGCTTTTCTGCGGAGCTTCTGTCTCAGGAGTGA 300
QY      70621 TGAATCAACACCGGAGAGGCGGCTTTTCTGCGGAGCTTCTGTCTCAGGAGTGA 70680
Db      301 TGAATCAACACCGGAGAGGCGGCTTTTCTGCGGAGCTTCTGTCTCAGGAGTGA 360
QY      70681 GCGTGCATTAATTCACGCGCGGCTGCGGAGGCTGCTGCGGAGCAAGGAGCTCAGAGG 70740
Db      361 GCGTGCATTAATTCACGCGCGGCTGCGGAGGCTGCTGCGGAGCAAGGAGCTCAGAGG 420
QY      70741 GGCACATGCCGATTCGACCGGATGAGGACAGAGAGGCTGCGGAGCAATAGACTACTCAA 70800
Db      421 GGCACATGCCGATTCGACCGGATGAGGACAGAGAGGCTGCGGAGCAATAGACTACTCAA 480
QY      70801 G 70801
Db      481 G 481

RESULT 5
AF241165      875 bp      mRNA      linear      VRL 02-APR-2001
LOCUS      Cercopithecine herpesvirus 17 glycoprotein R8.1 mRNA, complete cds.
DEFINITION      AF241165.1 GI:13506782
ACCESSION      AF241165.1 GI:13506782
VERSION
KEYWORDS
SOURCE      Cercopithecine herpesvirus 17
ORGANISM      Cercopithecine herpesvirus 17
REFERENCE      1 (bases 1 to 875)
AUTHORS      Lin,S.F., Robinson,D.R., Oh,J., Kung,H.J. and Luciw,P.A.
TITLES      Gammaherpesvirinae: Rhadinovirus.
JOURNAL      (RRV) ORPR 1
FEATURES
    source      1..875
    organism="Cercopithecine herpesvirus 17"
    mol_type="mRNA"
    isolate="17577"
    specific_host="Macaca mulatta"
    db_xref="taxon:154334"
    codon_start=1
    product="glycoprotein R8.1"
    protein_id="AAK28332.1"
    /db_xref="GI:13506783"
    translation="MGFGNIRLGMRLCFMWVAVIARSGSVCTPHLITDGRKEAVRHY
    YLECKRHSGSLDGGQTKSGTATTEANISIRPNVTSQNEEPGTARASS
    HDLPRIKQVNAURLSTPELAOPLPVVKSTPREQSPVSGPAISPSFAGTNRSP
    AIVPLAIPSPKDPRLIVRVYPLRPERMODTPSRQVATKIDRKEYHAHVRSDCYG
    RCTGPQASVDFPLPSPMHLVHPLMAMAGLIGLITAIYTIQIVAHNVTYTHCE"

BASE COUNT      218 a      255 c      228 g      174 t
ORIGIN

```

Query Match 1.1%; Score 443; DB 1; Length 875;
 Best Local Similarity 100.0%; Pred. No. 2.4e-257;
 Matches 443; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY      71437 ATGGGATTAAGGATTAATTTTTTGGATCATGAGATTGGGAACATACCTGTGGGATG 71496
Db      1 ATGGGATTAAGGATTAATTTTTTGGATCATGAGATTGGGAACATACCTGTGGGATG 60
QY      71497 GAGGTTATGCTTATGCTGCTGGGTGGGTGGATTCACAGGAGGAGCGGTGGTGGCCAA 71556
Db      61 GAGGTTATGCTTATGCTGCTGGGTGGGTGGATTCACAGGAGGAGCGGTGGTGGCCAA 120
QY      71557 CTGGACCTTACAGATGGAATAATACGAGCGGTATACAGGACTTACTCTGAAAGTGGCG 71616
Db      121 CTGGACCTTACAGATGGAATAATACGAGCGGTATACAGGACTTACTCTGAAAGTGGCG 180
QY      71617 CAACATGAAGGCTCGGGAGCCTGAGCGTCCGAGACAGCAAGGAGGTCTGGAACCA 71676
Db      181 CAACATGAAGGCTCGGGAGCCTGAGCGTCCGAGACAGCAAGGAGGTCTGGAACCA 240
QY      71677 AGCAACACCGAAGCTAATATATGATTAACCTAAGTGTGTACATCAGGTCAAAATTA 71736
Db      241 AGCAACACCGAAGCTAATATATGATTAACCTAAGTGTGTACATCAGGTCAAAATTA 300
QY      71737 AGAGCCGCTGGGACAGACACCGAGCGCAATCATCACAGACCTGCCAGATCAAGCA 71796
Db      301 AGAGCCGCTGGGACAGACACCGAGCGCAATCATCACAGACCTGCCAGATCAAGCA 360
QY      71797 GGTAAAGCTCTCTCCGATTTATCAACCCCGAATTCGCGCAACACTCCCGTACTAAATC 71856
Db      361 GGTAAAGCTCTCTCCGATTTATCAACCCCGAATTCGCGCAACACTCCCGTACTAAATC 420
QY      71857 GACTCCGCGGAGTCACAGTCAG 71879
Db      421 GACTCCGCGGAGTCACAGTCAG 443

RESULT 6
EHVU20824      184427 bp      DNA      linear      VRL 02-FEB-1996
LOCUS      Equine herpesvirus 2, complete genome.
DEFINITION      EHVU20824
ACCESSION      EHVU20824
VERSION      020824.1 GI:695172
KEYWORDS
SOURCE      Equine herpesvirus 2
ORGANISM      Equine herpesvirus 2
REFERENCE      1 (bases 1 to 184427)
AUTHORS      Telford,E.A., Watson,M.S., Aird,H.C., Perry,J. and Davison,A.J.
TITLES      The DNA sequence of equine herpesvirus 2
JOURNAL      J. Mol. Biol. 249 (3), 520-528 (1995)
MEDLINE      95302501
PUBMED      7783207
FEATURES
    source      1..184427
    organism="Equine herpesvirus 2"
    mol_type="genomic DNA"
    strain="86/67"
    db_xref="taxon:133899"
    repeat_region      1..17553
    /protein_id="AAC1378.1"
    /db_xref="GI:695173"
    /product="G protein-coupled receptor"
    /protein_id="AAC1378.1"
    /db_xref="GI:695173"
    translation="MATTGATSVNTSLATMTNTFTSLTSVTTIASLVPTNNS
    EDYDLDIDVDVEESAPCYKSDPTLRAQVVALYLVLFGLGIIIVITIRMK
    IKNTYMLLNLAISDLFLFLPLFMHRTIGHWTPEISLCKLLRGVMSLSYQV"

```

polyA_signal
10494. .10499
/note="ORF E1"
/codon_start=1
/protein_id="AAC13789.1"
/db_xref="GI:695174"
/translation="MILIGLVLSLSTASTAIOAMNPQVITGHEGRPLSVRCHYAK
NPSKTMILKTIGESAFRCGTIVPRFGPYTSCSSGGVGYTOSLHMAADGRA
CMVSGENPKDSESDYDHTVNLVLEPRRSLIGPOLTPFAGRGASRLQSOTGP
LSSQSESPSYAVAKRGYKVTYGTSSLHDECFQSGTAGLNTSAVLPPKRYGEGATQVST
LSTSLTFLTLDSPVTEGTGAQKMGCVNATKDSGEYCMGIMDPEEGESGDEDFSG
VDFEKTIVTPEGDEDADDDLYLTSEBEKK"

polyA_signal
19761. .19766
/note="ORF E2"
/note="ORF E2"
19784. .19789
/note="ORF E2"
20320. .20844
/note="ORF E3: product has N- and C- hydrophobic domains
and 6 N-linked glycosylation sites"
/codon_start=1
/protein_id="AAC13790.1"
/db_xref="GI:695175"
/translation="MATEVGFACALVYLGGVAGTPTPSKSTLIYNSONCTYPSIE
NGOSSLTNGSMFRIEYFNCSGGYELQGMPTTCTIEMPKNGTINTGPPCVKLNITPT
LMPSTSTPTPTGTCTFPDPQNTHTPHHTVCKPTRRPIINLRFYTPMAITTLVIVILL
LVVTVNCGMPMF"

CDS
21360. .25319
/note="ORF 03"
/codon_start=1
/product="legument protein"
/protein_id="AAC13791.1"
/db_xref="GI:695176"
/translation="MDSTSKRSFRKARGGATYTFVPTQHPGCGOPVYSFASFL
VNEGVFGLVDGCGAGTGATAGRAAUVADGVSAEMAFILKRVLDGHRVAGASRLP
AGLSVGLSGDDGAGGCTSLRDYAPPMQALDLEH. INQOOLRPLVLDGHRVAGASRLP
GEGEATPTIPKILAVSFPHLTMSLTIQHNHAWKQDLSFASCFPTGLGTPPLG
DGEPRDLKPARVPALAPKADALAKLPMPEPHSDVLTGYNHRAKITRNPEFL
LGYLCTALPTSPVTEIDPDVSSNGKDPYRETVYVCGISGASELDLITSEACTPEM
GNVCLHLGVNGSGEDPRALDQYLBESHMLAORCGAPLILFVWVGDSAPWGMGFA
SRPHSETATRASLIISPAFLCSVPRGGGASVFMGLDFEPQPRAGAVASHDSCGRILA
SILAVQFFINWAGRGAVLSTCGSRLDEGTMAKTAACGVMLGTYTSLLEPEAVSEL
SHFSGSNMRSILSKFLNVEAOVVLITVAVNPRNNQLIEGKTFEGGRVSLGLHL
ARAKTIVYDPRSPLYCGGPRYLCEFKHKPRVALPIDRWGTSVYRTPASRYVNS
SDAGPSAREVELIGILRHPTVGCCKNTYKRVADGCASRVAAQCGVPLDIPADVYSK
VVEVSDAPSRSMETWETQVDPDCELILHEDVSVGSALGKNSVFEPYPAGAK
MAIASVLSLAPLARIEDVTYN.SLAMPILKGAQGEVFTLLRCKRFCEDEAGVSCN
VYSCASSRRAGGCGPDEGGADIKSFVASAFVTPCAAWKLTPLDLKEARVYLFPAP
GKHAFASVQVROGOKKTYGSPVNSIGAYLGLKRALVHLRAKRLASGHDVGCGGLM
AALAMAAAGKRSIDVEYVRLDGDGPMGCTLSFPRGALVEPLSSAAAVELRSKTYI
LCYRGVYGHKTCERMFITTRGDQVLLCEDEDEYGERMRSHVSEMYGEPFNHAG
EGPYEREKAEVLATYPERFILNRPNKKHRHVAALLPGCYPLAALDRLDGLAFALVS
HLDLHVLITDEVCGLFVAGVNDTSDTSTDAISALVHSRNPQVITRPLSRKDTFSIG
VGSMAKRIPLFGDGAAPFALQSDRIICVPVASCFEESRMLNVFINOSTPAVARETLIG
SLPEPMAGTGLFGVAGAPSECIDRLVASGQAAMFVGSDAVSGPAMAYPANPETTLPV
AGICGRDORHLVILLHDITASYLQMWPYHVRSLNPLAVSPKQVFTDLHAWTAHSH"
/note="ORF E4"
/codon_start=1
/protein_id="AAC13792.1"
/db_xref="GI:695177"
/translation="MYSRREFEEEMDRVLENENAKISLTNRILKNVFAQTLDMKPREV
LTLEBALLAMLVDECKKEYLHQLLLELMQVNPVSVEAFTTASINNSLDIINQTHGGCD
NFRGLTSLASQCFLEVLQSDRCISVFASELAKFYVESONIMLAVSGLSAGLRE
RFPRLSTVFALKQWMLRFYEFK"

CDS
25639. .26190
/note="ORF E4"
/codon_start=1
/protein_id="AAC13792.1"
/db_xref="GI:695177"
/translation="MYSRREFEEEMDRVLENENAKISLTNRILKNVFAQTLDMKPREV
LTLEBALLAMLVDECKKEYLHQLLLELMQVNPVSVEAFTTASINNSLDIINQTHGGCD
NFRGLTSLASQCFLEVLQSDRCISVFASELAKFYVESONIMLAVSGLSAGLRE
RFPRLSTVFALKQWMLRFYEFK"

26436..29873
/note="ORF 06"
/codon_start=1
/product="single-stranded DNA binding protein"
/protein_id="AAC13793.1"
/db_xref="gi:695178"
translation="MNSNRMAAGPREENVGQASVGCCEGYLYLPGCTFYPEASILG
NIHAGEVEFSLPLGSLGLIVEADDFHVNNAVKRKIDLPATVSVKSAVHREIVEFVMAAC
KPIPIAGGLEGELCAKQLFGVYAEFEERBAAGARPELADGLHLEAGASHTYHAGV
TESPEFRILRGQLVVAVESQISQVREGECDARVPLGPELFAKSPCEINREYVHAGV
SVYLEAHNTYSIAOLAQRVADPGLIGALERSFPDQKLPKPYVRCFPPVTHRGAGD
CSLTIVDSVATRELAYSGLFLEVDQECTALLDKPIREGCCTPPORAEALTOPKA
KQAVYVSOULSRGNSVYLILARYOKASNRGGGGENYNSFFMGLACLAEPLQKENG
LPSPFGVAPSPALSGSNYSYLHILHAYASPSOMLARHCYLIQFADHQKSNVSNAGYNPT
YVTFEPPVPSMELCGSCGASCVNTLFRLDRPPPVAVASRDYPPVVTQASVNDPL
DIAGFNANYRDKDEESNQSEREKETFYMQVQYTLERLSEAGIEGEGEDVADLIHNG
SLKAGNECTIVGDEVARPIINSWKNNVNRRESIKLHHVQYCVGVNMQPCPVLL
NIYKCYVALVADQDCLPTCMQBOENAVGCSPREMKHMQTLMTNFKNSCIDKVL
TGTETKVNKQDQDFPDVDSNAKEPVSCQTVRISRALMAVRVKIKNRITFSNS
PQTESIQMAENVGTPKSGSCVSGPYMEFLSTYHSQLPEPAKISPLFLMHTFSKRLQ
PEFVPPVPSRYVELANYVEONSRLHGESIIDVYENFYAKRVLNNALEFRACQGO
PATEIHCTPRTIQTQVPAEYEPHALGAGVADGVEYLGAAELTVPVQCTSDNICE
YKCKPIPTLVNKKYVGVNQSIOFCCALGYFTIRGDKNLNIPAGSFKKQGST
SMRKHVMTPLSDHLRLRSYQGAAVAFIEICGYRRRQQLISGDNPHYIRVDYQLY
KSLSECKSVSESYDLEIYMGQYIIPAGDVSRLDRSLDGDGWSSEWALSVLDEEEDP
LGGELEFEKFEKVEDGLHPQDDEFALAPQAAAPQYSSSSVAGKRRKANYILGLDLI."

2997..32183
/function="role in capsid maturation/DNA packaging"
/note="ORF 07"
/codon_start=1
/protein_id="AAC13794.1"
/db_xref="gi:695179"
translation="MARLEAAVYAOVFDLAAVEALSILGYCDPSSIDKRCVANSNKYFK
LCELSLPCRLQNDRECSPLSEIQLHLOLNREALAGVLTDLISGSPVPELHDS
RLBEPCKRRHARVRPREYGAKEKTSLSLNDVYFPRKLNSVYCCPAGALEAGE
TVAFVIGRLGELFELHILGADARAAAGRAGGSESREREDDEDEEERPRQGGQA
VYSDPVLGFENFELHILGADARAAAGRAGGSESREREDDEDEEERPRQGGQA
GGCALVRLTESSLSVLAGHTIPEEDDRLAIENLWYSSADRGCGVGTARTASS
HNAKFLAEHARHMRSRMALGRGAPSGHDFPSPLESIFCGVFNISIDTILALQD
CGATEFLKSNVOTLIOQONLELYRLNLEYNAGDEGAGAAEIAADAPFLPKGAS
CDPRLKSDARYRDLTYLKKTLRGLCTRTPTCITKTHYRLSDTSLVPMKSLYASNA
RLVNHFLRRQCVGLGADLTRAGBEAFENSKYIKNALHGORLNREHLDSTVHETRL
ITGPLSLDNSEHPVDNALAYCLDAAGAMPHQKLYITEMPLIESKDMLDENSEF
VSIENGEDNLDOCKTLNTRYREAVLISILYNWPKSSLSLATELRGSCIASASGEL
GGCVLYEGEATPELPLVLDVDSKGYEKDLYTLTYHLDSGRQASV"

30114..30119
/note="ORF E3, O3, E4 and O6"
32195..34819
/note="ORF 08"
/codon_start=1
/product="glycoprotein B"
/protein_id="AAC13795.1"
/db_xref="gi:695180"
translation="WGVGGRPVVLCIMCVALLCQGVAADEVAAETTPPATRPREVY
AEENANFPLPRVCGASPTGGEIFRFLPESCEPTEKDEKIEIALITYTNVYVF
NBRKRLKMTSTTITKGSEDAITNOHRSYAVPLVEOMDHYOQFSVAVNVEGH
WNTYVLDQGMENETFLKPADGLTSSITRYOSQPEVAPVAPMLLSLTPRTYVNGE
MSARMKREPEFVSVGDTITEMSPLEKNGTEBPBKILAKRHSIOLKNVAVTYKQGL
GGADATRFPAIFGDSLMAKATTENSSTCOLILMKGSNLTQHNSSLHFTANDT
ASFSPLEDEANFNETKFCINNNNOBELQKLKLEKVEYTHRGNAKAYKTKGMLYK
OPTILIDILDEHAKLYLNTNATASPTGPTGSPPRRRSDTSVSGGNNNDNSKTES
VAASOVQAVNDLRKSINRVGELSRAMCROYVASLAWELSLKINFTSVMSIYGP
VSAKILGVGVSDCISYDOKSVFHKNMKYPCKEDLCYRPAVYGCFNGSLFSGO
LGRPREYLSIOVBYCHSCENTFOAGNOMYKKKDYIYVSTLANLDIPLTHMTILN
LSLVNIDFKVIELYSTEKRLSNVFDILEFRERYNTYONLNGRLDLDDSDIDHG
SFIOQLGIMODLGLTGKVVVAVNASVLETSFGVSIYEFKNPECGMLLVIILAG
VVVVVLTFRRSRISYSAIRMLYGVGRAOEPAGHVSVDQIINILMGHICQOQR
AAEEARREKREYKGRITLEVIRDSATVSLRRRRGGGYQLRGSDDEEDYERLRO
DGGYDVQVVGACTDVC"

34855..34860
/note="ORF 07 and 08"
35089..38115
/note="ORF 09"

polyA_signal

CDS

polyA_signal

CDS

polyA_signal

CDS

```

/codon_start=1
/product="DNA polymerase replicative subunit"
/protein_id="AAC13796.1"
/db_xref="gi:695181"
/translation="MSFTNPLVVKRTFLKKAAPSPKREYRIIIPCKKTPGACGV
HTSLDPLDVCPEDEKTEPLIYDGSRSLSASGGRGGPGAGQGHTPAALTRHVGDI
ITVYQDRCDHVPFQFQFDIIPSGTVLKILGRTSDRSVCVAFRELFYVRPGL
LDPLIOQCSRENFNSSGRRYERKTSKVELEYEAERVRVASSGFVLDLAGG
TAACEVETRVDAARFIIDNGESTFGMYCCAAPVPGGAAARSMTELEDCAG
LEFAGNADMPGVNVLISFDICLGENSGPNASRPEDMTLOISCTYMKASGEAPSV
LNTGCEIEGVEYVCCSELDILYLPFTMRDDVPTVGTGYNISNDEPVIDRAT
VYINAKETFRVRSSSTFEVHKPKRSSAGPRAYSKKVAQVPLDMQVDRKLSLS
NYKLDYVAGECVGAKEDVSKELPHLRQSGPGARIGLTCVSDALVLDLRFM
HVELSEIAKLIKPIPTRLVTDGQOIRFVSCLLDVAAGRGYILPVDRAVDAGYCAT
IDPSPGVNPLVVDFASTLPITLIQAHNLCSTWIPEDRGLCLPHLDGQYFELL
SGPVHFYKHKRAVSLATLLVWLAKRAIRRELATVSDAERTILDPQOLAIVTCN

```

CDs	old_sequence	old_sequence	old_sequence	BASE COUNT	ORIGIN	Query Match	Best Local Similarity	Matches	23:	Conservative	0:	Mismatches	0:	Indels	0:	Gaps	0:	OY	Db	RESULT 8	KSU040377/c	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	MEDLINE	PUBMED	REFERENCE	AUTHORS	TITLE	JOURNAL	MEDLINE	PUBMED	REFERENCE	AUTHORS	TITLE
633..1550	/note="putative minor capsid protein; similar to Saimiriine herpesvirus ORF 26 protein, Swiss-Prot Accession Number Q01008, and EBV protein BDLF1, Swiss-Prot Accession Number P25214"	/codon_start=1	/protein_id="AAB60564.1"	410 a	518 c	481 g	446 t	0.1%; Score 23; DB 1; Length 1855; Pred. No. 0.068;	0;	0;	0;	0;	0;	0;	0;	0;	0;	44313 AGCTCAGTCTATATTAACT 44335	1455 AGTCTCAGTCTATATTAACT 1477	KSU040377	20705 bp	DNA	linear	VRL 16-FEB-1996	040377	GI:1136805	Human herpesvirus 8 (Kaposi's sarcoma-associated herpesvirus - Human herpesvirus 8)	Human herpesvirus 8	Viruses; dsDNA viruses, no RNA stage; Herpesviridae; Gammaherpesvirinae; Rhadinovirus.	1 (bases 7571 to 9425)	Chang, Y., Cesarman, E., Pessin, M. S., Lee, F., Culpepper, J., Knowles, D. M. and Moore, P. S.	Identification of herpesvirus-like DNA sequences in AIDS-associated Kaposi's sarcoma	Science 266 (5192), 1865-1869 (1994)	7997879	2 (bases 7571 to 9425)	Moore, P. S. and Chang, Y.	Detection of herpesvirus-like DNA sequences in Kaposi's sarcoma in patients with and without HIV infection	N. Engl. J. Med. 332 (18), 1181-1185 (1995)	7700310	3 (bases 7571 to 9425)	Cesarman, E., Moore, P. S., Rao, P. H., Ingthirami, G., Knowles, D. M. and Chang, Y.	In vitro establishment and characterization of two acquired immunodeficiency syndrome-related lymphoma cell lines (BC-1 and BC-2) containing Kaposi's sarcoma-associated herpesvirus-like	

JOURNAL (KSHV) DNA sequences
MEDLINE Blood 86 (7), 2708-2714 (1995)
95399773
PUBMED 7670109
REFERENCE 4 (bases 1 to 20705)
AUTHORS Moore, P.S., Gao, S.J., Dominguez, G., Cesarman, E., Lungu, O.,
Knowles, D.M., Garber, R., Pellett, P.E., McGeech, D.J., and Chang, Y.
TITLE Primary characterization of a herpesvirus agent associated with
Kaposi's sarcoma
J Virol. 70 (1), 549-558 (1996)
JOURNAL
MEDLINE 96099469
PUBMED 8523568
REFERENCE 5 (bases 1 to 20705)
AUTHORS Moore, P.S., Chang, Y., Dominguez, G., and Pellett, P.E.
TITLE Direct Submission
JOURNAL Submitted (08-NOV-1995) Patrick S. Moore, Division of Epidemiology,
Columbia University, 630 W. 168th Street, New York, NY 10032, USA
FEATURES
SOURCE Location/Qualifiers
1. .20705
/organism="Human herpesvirus 8"
/mol_type="genomic DNA"
/db_xref="taxon:37296"
/clone="KS5"
/note="submitter-supplied organism name synonym=Human
herpesvirus 8 (HHV8); lambda FIX II genomic library clone
from an AIDS Kaposi's sarcoma lesion; Open reading frame
designation follow that of the gene homologs in
herpesvirus saimiri"
complement(3. .86)
/note="ORF35: Homolog to the herpesvirus saimiri (HVS)
ORF35, equine herpesvirus 2 (EHV2) ORF35, and Epstein-Barr
virus (EBV) BGLF3.5 gene products; Method: conceptual
translation supplied by author"
/codon_start=1
/product="gene 35 protein"
/protein_id="AAB08382.1"
/db_xref="GI:154677"
/translation="MDSTNSKREFIKSALNINRAAVSLF"
complement(67. .1050)
/note="ORF34: Homolog to the HVS ORF34, EHV ORF34, and EBV
BGLF3 gene products; Method: conceptual translation
supplied by author"
/codon_start=1
/product="gene 34 protein"
/protein_id="AAB08383.1"
/db_xref="GI:1136807"
/translation="MPALSSLVSEGDPEVYSRYKQVQLADLSENPQGRKLIETPL
NSFLVSNMPEVOPICSGRPALRPDSNLHLPRIEKLQRLVGGFGAGGEIALDPS
HVEHTEKGVFEYNHYATEWMTALTLNKDALLRBAVDGLCDPGTWKGLPDPPLLM
LLENGPASFCDCLYKOHCGYGPVLLPGHMYAPKRDLSFYVNAHKATKFLYGD
SGWAAACRPPEPARIQRYVYSOKIIDASPTYISHKCLGCHIVQONSIIAGCGTHVG
GILLSGKGYIINGVQTCRPTTGDIILIPSDIPIIMIKENGINQL"
746. .1969
/note="ORF29a: first ATG located at position 1049"
/number=1
join(1049. .1969,5221. .6363)
/note="ORF29: putative DNA packaging protein: Homolog to
the HVS ORF29, EHV2 ORF29, and EBV BGLF1 gene products.
first ATG located at position 1049; Method: conceptual
translation supplied by author"
/codon_start=1
/product="gene 29 protein"
/protein_id="AAB08384.1"
/db_xref="GI:1136808"
/translation="MLSRHRERLAANLEETAKDAGEEMELSAPEFPHGCKTARMAM
PFIVVHRINSSVLETYCTRRHPATPTSANPDVCTRPSEDNVPAKRLLESTY
LQMRVREDAAHSTADOLVEXQAGRKTHDSLAAQSVYRELDAFLVNLSSEFNGCVPG
VHMLEPQOOLVMTHEFFELVYIKAPQKTHQLECFKQFLEFPNSVLQFKOKASV
LIPRRHGTWIVAIISMLASVENINIGYVAOKHANSVFAEIIKTLKRWPPKN
LIKKEKGTIIYTRPGSSSLMCATCPNKSIGGQFPNLLYVDEANFIKKDALPAI
GFMLOKAKLIEISSVNSDSBSTFLNLRNAOKMLNYSYVCADHREDHLDALV
SCPTCLHPTIYITIDESIKTTNLFMGARDTELMEGGAASSNATLKVGDALVTO
FDMCRVDITAEVQKCLGKQLFVYIDPAVTNTEASGTGAVAVTSTQTPRSLILGM

polyA_signal
CDS
complement(1648. .1653)
/note="ORF3"
complement(2026. .2964)
/note="ORF33: Homolog to the HVS ORF33, EHV2 ORF33, and
EBV BGLF2 gene products; Method: conceptual translation
supplied by author"
/codon_start=1
/product="gene 33 protein"
/protein_id="AAB08385.1"
/db_xref="GI:1136809"
/translation="MASRRRLRNPINKECITWYVNPMSGDHIKVFNACTSIPYDPE
LYTSYALSPAYVNVSVALLHKVMGCPVANGINEMITVYVSVQCVSPVPGRCMAL
ITYGQFLBEASGLNRPYIAPPSSREHVDLRLQELVHTISOVVRKDLTNCMGLEFRN
VNPVWLGGSVWLLFLGVDYMAFCGVDGMPSLARVAALLTRCDHPDVCVCHGLGRH
VNVFRGYCSAQSPGLSNICPCIKSCGNGVTRYGNRNPLGLLFDPIQSRVYALKI
TSHPYTHVENVLGVDGDTLVPSVQGLGLTNV"
complement(2957. .4321)
/note="ORF32: Homolog to the HVS ORF32, EHV2 ORF32, and
EBV BGLF1 gene products; Method: conceptual translation
supplied by author"
/codon_start=1
/product="gene 32 protein"
/protein_id="AAB08386.1"
/db_xref="GI:1136810"
/translation="MDAHAINERYVGPCHRLAHVYLPRFLHHAITLPEEIIFFSY
TFRSRSPPSSRRLVCGKRVLPGEENQCLASSPSGLALSLPFSHDGNHPPDISLRI
SCPSNLSLTVRFLYLSLVAMGAGRNARSPYDGVSPREGAVANPLELQRLARAR
DPPALTRPLQVLGLLACSGDGRATHMLALEAGVYRGSGLDPPVSOQKPARTHR
PPVRLSEPNVADVPATWRATVNYSGAPYVCYEGEGHODMLPIPLSPPEPV
PPPGVPMDLFTNTKCDPVDVPLEACRQGYTLRQRVVAIIPROAEIADAKSH
LEACTVLRGLASEASAMIRATSPPLGHAACMMDVLCIMESRPHTLGLIELGVNCGCT
GDGMLETLKQPDVQVTVSGSLVACVITVPALEAWLVLPGFAIRAKRYAKSDELVFIR
GRYG"
complement(3014. .3019)
/note="ORF32"
complement(3015. .3020)
/note="ORF34, ORF33"
complement(4288. .4962)
/note="ORF31: Homolog to the HVS ORF31, EHV2 ORF31, and
EBV BDLF4 gene products; Method: conceptual translation
supplied by author"
/codon_start=1
/product="gene 31 protein"
/protein_id="AAB08387.1"
/db_xref="GI:1136811"
/translation="MSONRKTLPAADGPGHGVLCEGVPPRRHCEKMSVASPILCOFHV
FCLQCRQCLAYHCDGAGECVLLHTTPESVCELTGNCMLNIOGQRLGPVPRFTD
NOVDRDAHGMCLACLRDIYVLTQMTPTVYIYQELIAGDGVNTDITSAIIDETGECL
PVLEAGQGVALVCSMTLHVIVSTYISTYVNSMLFKCTKKKKIDCIARKVRTKMMRM
LSTKDT"
complement(4357. .4362)
/note="ORF31; ORF30"
complement(4869. .5102)
/note="ORF30: Homolog to the HVS ORF30, EHV2 ORF30, EBV
BDLF3.5 gene products; Method: conceptual translation
supplied by author"
/codon_start=1
/product="gene 30 protein"
/protein_id="AAB08388.1"
/db_xref="GI:1136812"
/translation="MGEVDPDGHVNVKEDFECEQFPSPQLREQVAVGRALDGLGLA
DSLCHKTERLCLDLMDLVGTBECFARVCRLDTGAK"
5221. .6363
/note="ORF29b"
/number=2
complement(5269. .5274)
/note="ORF28"
complement(5335. .5340)
/note="ORF32; ORF31; ORF30"

polyA_signal

CDS

exon

polyA_signal

TATA_signal

```

polyA_signal      6359..6364
                  /note="ORF29"
                  complement(6375..6737)
CDS               /note="ORF28; Method: conceptual translation supplied by
                  author"
                  /codon_start=1
                  /product="gene 28 protein"
                  /protein_id="AAB08389.1"
                  /db_xref="GI:1136813"
                  /translation="MSMPPVSGSHRRNGRLRPGANGQASRDWSYNALPPSHRRL
                  LLHSRVPGSGSVARHPTROGHRGVSGPSHPGAGVCTCTAGCGHSYPGALPYNIHAR
                  LRGVCYNGMGLGAYDN"
TATA_signal       complement(6824..6830)
                  /note="ORF28"
polyA_signal      complement(6982..6987)
                  /note="ORF27; ORF26"
                  complement(6983..7855)
CDS               /note="ORF27; Homolog to the HVS ORF27, EBV2 ORF27, and
                  EBV BDLF2 gene products; Method: conceptual translation
                  supplied by author"
                  /codon_start=1
                  /product="gene 27 protein"
Query Match      0.1%; Score 23; DB 1; Length 20705;
Best local Similarity 100.0%; Pred. No. 0.088; 0; Indels 0; Gaps 0;
Matches 23; Conservative 0; Mismatches 0;

QY 44313 AGCTCAGTCTATATTTAATCT 44335
      |||||||
Db 7971 AGCTCAGTCTATATTTAATCT 7949

RESULT 9
LOCUS            AY170317      59673 bp      DNA      linear      VRL 24-APR-2003
DEFINITION      Porcine lymphotropic herpesvirus 2 isolate 568 long unique region,
ACCESSION      AY170317 AF494077
VERSION        AY170317.1 GI:27452844
SOURCE         Porcine lymphotropic herpesvirus 2
ORGANISM       Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
               Gammaherpesvirinae.
REFERENCE      1 (bases 1 to 59673)
AUTHORS       Chmielewicz,B., Goltz,M., Franz,T., Bauer,C., Brema,S.,
               Ellerbork,H., Beckmann,S., Rziha,H.-J., Lahrmann,K.-H., Romero,C.
               and Ehlers,B.
TITLE          A novel porcine gammaherpesvirus
JOURNAL        Virology 308 (2), 317-329 (2003)
MEDLINE        22594013
PUBMED        12706081
REFERENCE      2 (bases 1 to 59673)
AUTHORS       Chmielewicz,B., Goltz,M., Rziha,J., Romero,C., Franz,T. and
               Ehlers,B.
TITLE          Direct Submission
JOURNAL        Submitted (22-MAR-2002) P24 Xenotransplantation, Robert
               Koch-Institut, Nordufer 20, Berlin 13353, Germany
REFERENCE      3 (bases 1 to 59673)
AUTHORS       Chmielewicz,B., Goltz,M., Franz,T., Bauer,C., Brema,S.,
               Ellerbork,H., Beckmann,S., Rziha,H.-J., Lahrmann,K.-H., Romero,C.
               and Ehlers,B.
TITLE          Direct Submission
JOURNAL        Submitted (30-OCT-2002) P24 / Xenotransplantation, Robert
               Koch-Institut, Nordufer 20, Berlin 13353, Germany
COMMENT        On Apr 11, 2003 this version replaced gi:29468328.
FEATURES        Location/Qualifiers
Source           1..59673
                 /organism="Porcine lymphotropic herpesvirus 2"
                 /mol_type="genomic DNA"
                 /isolate="568"
                 /db_xref="taxon:91741"
                 <1..>59673

misc_feature

```

```

CDS               /note="long unique region: LUR"
                  359..4489
                  /note="ORF 3"
                  /codon_start=1
                  /product="tegument protein/v-FGAM-synthase"
                  /protein_id="AAO12349.1"
                  /db_xref="GI:27452845"
                  /translation="MGSQGVFLYSEPTSLTPQESTILENLHNGDKLPDPFREVEED
                  APMVITNNLLDTPVAHRYKIKLRAVRNIIGSSSHETVPPRRDGNKRYEMGPN
                  AVNDVPTTLLDDDKINIVSTSLFNSPKYFSIDRIEVRILILNGELSNLAPFIELEN
                  ILCNKTEVQPIQLEKYEPEHREYRFDDFSGSGPDEIOFMFGDGRGTGIIQODSIHT
                  SDLPVIGENPDGRKREKFGKCEADHWFSALAPDGIIRPDSTGSGSRREAVESAG
                  LAPVANNIDHGNQSLVLRNLTKLPTALPISAHNGILYHTPPQONLDGETVOYED
                  TIVQKFTGCGTSASFVSAGVPTCLGFRSNIKEDVPISGTSVCGPDRREFVST
                  HDTLKVERSGSLVLFQAGDYKILMKNHGHLRHMSGRVYLLNLNLMLTREFD
                  TQIYIGIFGNKNMNCILNHLKSOAGDNGCIEIEHGNLPLETORALKRSPNMEHN
                  NTIESMLNIVSRVYITIRINDOYTSRLMKRAFCPIPLFLGLKTSVHDIVS
                  GMEHDVPTNITFRKMLKKGSDEBRFPWEAPKGIAGSVLVIGDYSILLTILOH
                  PIVGCKKYIVFHMDCGNHINAOOGVGFDPVSDXCQLINLPVPOQSYWTEIH
                  DHVIDFEDYNENGDGIPRNVPFQSWETGLAIOVPDNRKITSEPNWIGTSALGEQ
                  NVIAQIDAKAGVAMSTTEALNLCUSPMALHEVITMTGMPVLRNVADKDAISF
                  AADFCVKGVSFEVDSCQKOVNTERGSASRCITACASCPMLPARKITPALGMGSH
                  LHFSLTNSITSGISYETITDKNFVGOSLILPSQRLKLVLEIKKEGYIISGDH
                  ISDGMFACIAWAVIAGAKOVKITLPDQTKVEPLISQSPGIIIEVSPHSTVYVSA
                  ESTGVLCRYIGSVINGMSGLERITVGGSTKSHRESIKQIOTNMEYLSNKNLIPRNGE
                  ENDDSVYGNFMILPIDKFTYISALPDEHOVTVILPBCNRPDALLNLRSGHNP
                  IISTGQKTELPQDMLSDPTTVGVITGTPNIIIESGMNASQFVLNKHIGHDLN
                  NIVKRGRFSLAIGPMACOLDFDSRIISKQOEGSVPKIVKNASGYESRWLNFHLP
                  DTKAVALLHDKGCVLPCMAOGTNGLGADPVPFMEERCOIASLFHQROVDSAT
                  KYLPNDSGEYSAGCSDEGRHLAILYDCLPAFHSOMQYVNTSVENFSPMMKMY
                  RLRLSVANRNCADVQSRNDDDPQHRFNAAOFPNDLRGAIIPAAGEVPMFLP"
                  4643..5179
                  /note="ORF E4/BALF1; similar to EBV-2 ORF E4 and EBV ORF
                  BALF1"
                  /codon_start=1
                  /product="hypothetical v-bc12"
                  /protein_id="AAO12350.1"
                  /db_xref="GI:27452846"
                  /translation="MSVNSCKEPEPSKQIREFRELSSSDIINILMAVNPOLDHE
                  LTVSESLTMLVKQCIKENFTVLVVKLIGLPNHNAAEOKIOMLQDLVLSINDQDS
                  FEKICATIAMASMYIMFLENKPEYVSLVAHILGFSYLLRHAPMWSYLOGFSTGARKK
                  YGLMSTRKLYLKNKN"
                  5271..8699
                  /note="MDBP; ORF 6"
                  /codon_start=1
                  /product="major DNA binding protein"
                  /protein_id="AAO12351.1"
                  /db_xref="GI:27452847"
                  /translation="MYIQFARNSHASGKMSKAOOLPGEEDNIIASKSPIGCGVYI
                  YKHFPCIDEVALLDGNTBHSKVSPLPILCGITVEDGAPPTNKAHOKIDNPTVYSRL
                  TSFHRQVFEHNADMFPTLFRPGDLKTCQDRKLEGGSEFTKNQORINRPSDLCPQ
                  MGSDCVNAVAVITTEGFKORLYGKLVASHIQSVIINTEVEFRJPLYDELFVRDN
                  LIHFNCHELSELYVASYGLAQAFRIKNSGLSAIHQFOADRYKLPKLDIEYDS
                  SSVINGODVTMLIINCHETSLSTGYMCELEHAPKSLDSTSEISCTPDBRM
                  NATLRNITDOOSVHVNQLETSINSVLYIKVAKOSNNARNRVDISFNGYQHGLANILE
                  QTFSEKGAITPFGVPSSCMGDNATITPHLAYASSKNNLATICYILOPQCHKSTLH
                  PSYNTSQYVGSAAVNSVCCQCKGNPCVCINLEYRLDRPPIILASSRREYVVSQ
                  TMTNELDFLGNFAFKERKDEQHLQDLDPKTYVOLNQTITEKLEAIGIRINQED
                  ITGIGKMSIKAFLEIFKTIIDSIVTESYKILNKNININRESIKGIYHIOPCNP
                  WQSCSILFNFMRSLFVLIQDIALPICAMDANDPSGMPSEMLKHYOTLMTNF
                  KSPFLDKAVTGSSELKVHSDMFSDPEPTIISANMLCPKYQVATLGHITVPLNKK
                  FKNRLIFSGASISDOYOTAFLTKLSKQDTIYINCGPIKFLNAFHSLSPPNKLKSLY
                  MSMSFKRQIPIVNDVDFDLNMLLFAFVDSNKLFEETNLEDLIPDSFTYAKORLNT
                  ALIRACGOTOFYAGTILHIVSKIQIVDEEPMHILGETPLCDEVEDYLAIGCKRMTY
                  NTSLESASAIRPTIYVLPVIVKYGITGAPNADLFQSGNAGYVLGSGVNDLIGDT
                  SFFKQINSFMKRYMFMPIYGNLIKONSOSIIMPDEINTEKKNIGDIEQGHQHV
                  PSNVYCELIKRGCKKCDLTDLDIOFYIGOPYKFAEMKLEKSTIAEIDGAMTVMAL
                  DILESQSTGYDIEFTIEFTESPRSTIEENTTLNIPANVNRKRYISLSDISLS"
                  8702..10726
                  /note="ORF 7"
                  /codon_start=1
                  /product="transport protein"
                  /protein_id="AAO12352.1"

```


/db_xref="GI:27452848"
/translation="MTQHLAALYSQIYGVCLDVSILEYCDPSGVKCALNTKKNIED
/IDTVFDYLLONRSDSSLSLEHLLANRDLAVHILGALGDSNOYFSLEHLEC
NHERIKMHFNGSIEVKMLINDVEPFKKLSVFCIPAEKATICLONVLEHFK
LRGISPAVPCYISSTPCLECFEITMIPNCKSIQDMVLEPCPHICRLSEPRQ
GLRENELKHTGVNTLDMKECPDGAETLAKMESLACLEHNLFEETIPQAMISNL
LYNSAEETTERKHQCSQRLKILQRNKMNOYRILFKDNHFEPTCHPSJELLFCS
LYSTDVIRALCKDCSATFWEQPKFQSMFHRNLEFTRLSNLLEYNTGGDDHITS
SMNSDVIRIEGKSSNEQILLEARLREKVALHKSQDKMKLOACDASNNITKLL
TLRWGSTIRKEASLVNLHLEFROWYSDSTMTDNGNTLENSKFTKSLYANLRS
EHLDKLLPESLNGPLTSTDDEFPFIPONKLAHCLDSVANMHHKMLYMHICOL
EPKMDIKFENFTTQHTLNLIOYQEWTVRELVLVSLSYNNWERNKNSIFETD
YRHCNCTMGNGIYIEESAPLILYNNRKNIFKDYALLYTHLQWYNGR"
10683..13313
/note="gb: ORF 8"
/codon_start=1
/product="glycoprotein B"
/protein_id="AA012353.1"
/db_xref="GI:27452849"
/translation="MLFYIHVCTMAGSLKRLRLALALMCOFOVALYALSKAESAT
SPANTQAMSTELALPIGOYGVDSHGERATSENEDEEHKNITGSPTEPRVCSAS
GVGDIFRFOETHDVCPSADWVHSEGLIYKONTIIPMPFRKRYKRYSTSTVNGIY
SDSTNHTFYKSTEPWETEKMDIYOCFNSLRNTGNNLTYYDRDINNTVLOQY
DGYTPVYKRGSDPLYLEPQEWGSTRRTVAVCELDHFAKSNPPDFEVATGDT
VEMSPWSEGDHENKMKNEKLMFLSVINDKVVYONRGVPLKTRIFLDREYTLIS
MEKHLNISYCPFLMKAFYNGIOTHEGSHFVANDITASFTSKEDMDENTYAC
LNDERIKAEIKKYAKVNSTHSRYGDLQYFGDGLFLWQPLIONRLDLAKKNLET
VSKRSROVSTGTPMMEATNGAGGSESNSTAVOYAVONLRINNLILEES
KAWCROHRAIMMNELSKINPTSYMSHINRPSARIGDIVSVSNCLYVDQSYSL
HKRLRLAAMDCKFSRPVTEKFMNDSTIKRGUGNNELLTITVLETCQNTETVY
FOATDMYIKYKNEHKTVPISLITDTEFLALNFTLENDVFIYVILYRDEKRLS
VFDETMRREYNYAQRVSGLRDLDLSTRNQFPVAFSLDVAVOCTVNAVS
GVATLFESIYGVFINFKNFGGMLTIIVYGFALYFLTKKRYETAPIKIYEE
IDKREKESSEIOPISSEELERITILAMHIHQSNHETAKRDKPTILTRAQNMNR
KRGGYTNLKNADSEMNTL"
13491..16496
/note="Dpol: ORF 9"
/codon_start=1
/product="DNA polymerase"
/protein_id="AA012354.1"
/db_xref="GI:27452850"
/translation="MSFNPYLKRGNGRQREKKNLFTLIPKFFDGGEGGVYSI
STNLPTFMGDELYKVPPTKISMNOPTIPATTECLSGELCHVDILETVDKOR
CDEVPTFLQTDILPCGVLKLEGTSDRSVCVQVQNYFYAVSADSYNIHIIYO
QTMVENSROCNFNVVYKRFELDTPTAEHEVYKILSSYHMAAILSNKIROCGYLI
FEAVDAVSREITNDNCTEPTAMYSCKSAPLGQFRDYSLSLEDCAVSDLVNRDN
YMPHYKIMARDIECLGEOGPNAARDGDMITIOISCIITWTGODONVAKIILSGTCS
ITNTIYISPESELDMLYARCTMIDYVEIITGNIANPDPPTILLEANNTYINPDA
YTRKSAITFOVNPKEGNELRNTKVKLSGLVIMVCKDLSLNTKYNVAVAE
CIGEKKEDMSYKEIPALFKGNANDRARLGLCIDOSTLVMDLKFFMTHEISIAKI
ANIPMRVITDGOQIRVESCILASAKNGYGLIPMPQNGNFQYOGAVIAPLSGFYNT
PVLYVDASLYPSIIQANLCYSTLIHNEDEHKYPOLEKQDQYEFELISSGVHVKVS
ISESLNLITLTLAKRKMKRELTACADPRITLITLOQALIKTYCNAVYGVFVHS
GMPLCLAIETITNOGRAMLEKTYEVENSHEDEBRICKGSIPOSSNVPDFKFKYI
YGTDSLFINCPKTNIDQIVLFGDELQVYTERLEVPKLESKRVGCLLLTKKRY
IGTDSGKILMKGVDLVACTACTVOETCAVHLVINDNVKSAANLISKRKISKCF
EEGLPEGFIKIIDLNAAYDGLSANRPDIQIYVSTELNDFCYSKYNYPHLAVYK
IILNEBEPVOHDIRISYVINGKGLISDMEDAPAEVANNRPIASDLYFKIYHGA
NIILOCFENNAAVNLINVTTRNMP"
16767..17681
/note="ORF A5/BILF1b; similar to A1HV-1 ORF A5 and EBV ORF
BILF1"
/codon_start=1
/product="hypothetical v-GCR"
/protein_id="AA012355.1"
/db_xref="GI:27452851"
/translation="WTAMELPTSLDLKNGTQCPDYVNAAFVIGNVIOELVIA
LFLMLFVKARLPTSNLAFYLAVALISRIQDDEGWMKCVLECMLEJEM
LITSVAVGSGIDCLTLFRSGRGMAPQWLVVLLVTLCTIFAAVNFESTDA
VLSPEVNAEFGROGISVESLTKELRGVYILGLVYTLVLTWTKLISLTKOK
KAVACNLILVNLICGMVYLIFSLSLKSQANLODTGCSFATGIGALIMQUTVICIA
VEYVASHRLKRLVETVYIFPGSTSQ"
17751..19004

CDS

/note="ORF 10; conserved in other gamma-herpesviruses"
/codon_start=1
/product="unknown"
/protein_id="AA012356.1"
/db_xref="GI:27452852"
/translation="MTTISLMEFLFKSTAMDIGSTLIDGLMTKANFGRTLVNMY
DMNRPSTTHNLPFSVMHVLDELYSGLVSPDISEIQTSCALMLQCGSQOYRL
PSCVLDFTDLSITKINSRTIKARELSIALFVPIHHSVSCITATYOGDDVVDIN
PLDVTSRGKNCSERTISGLARKNDKNVOLLVRGFEPMDFMNVNDICTDHAAEVAVK
TLVERDHEKLOCSMTLFPNDKRNQVYATVADIPETVLEHFEWISGYSKAL
PIYEOOKTKPESITKIKTMYALIDSSSKYKINICGLSESSFWIAESKTWQPT
PLVITFINISDRWVTLNDQPVALLISODSVCKADSIYFDIGNNSLHMOEINIP
GDSITFTMPHIAIRRECEQCMY"
19016..20245
/note="ORF 11; conserved in other gamma-herpesviruses"
/codon_start=1
/product="hypothetical v-GCR"
/protein_id="AA012357.1"
/db_xref="GI:27452853"
/translation="MTTISLMEFLFKSTAMDIGSTLIDGLMTKANFGRTLVNMY
DMNRPSTTHNLPFSVMHVLDELYSGLVSPDISEIQTSCALMLQCGSQOYRL
PSCVLDFTDLSITKINSRTIKARELSIALFVPIHHSVSCITATYOGDDVVDIN
PLDVTSRGKNCSERTISGLARKNDKNVOLLVRGFEPMDFMNVNDICTDHAAEVAVK
TLVERDHEKLOCSMTLFPNDKRNQVYATVADIPETVLEHFEWISGYSKAL
PIYEOOKTKPESITKIKTMYALIDSSSKYKINICGLSESSFWIAESKTWQPT
PLVITFINISDRWVTLNDQPVALLISODSVCKADSIYFDIGNNSLHMOEINIP
GDSITFTMPHIAIRRECEQCMY"
19016..20245

Query Match 0.1%; Score 23; DB 1; Length 5673;
Best Local Similarity 100.0%; Pred. No. 0.098;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 46742 GAGGATATAAATCAGTTTGC 46764
Db 41628 GAGGATATAAATCAGTTTGC 41650

RESULT 10

U93872

LOCUS

U93872

DEFINITION

Kaposi's sarcoma-associated herpesvirus glycoprotein M, DNA
replication protein, glycoprotein, DNA replication protein, FLICE
inhibitory protein and v-cyclin genes, complete cds, and tegument
protein gene, partial cds.

U93872

U93872.2

GI:14627174

ACCESSION

U93872

U93872.2

GI:14627174

VERSION

U93872

U93872.2

GI:14627174

KEYWORDS

U93872

U93872.2

GI:14627174

SOURCE

U93872

U93872.2

GI:14627174

ORGANISM

U93872

U93872.2

GI:14627174

REFERENCE

U93872

U93872.2

GI:14627174

AUTHORS

U93872

U93872.2

GI:14627174

TITLE

U93872

U93872.2

GI:14627174

JOURNAL

U93872

U93872.2

GI:14627174

MEDLINE

U93872

U93872.2

GI:14627174

PUBMED

U93872

U93872.2

GI:14627174

REFERENCE

U93872

U93872.2

GI:14627174

AUTHORS

U93872

U93872.2

GI:14627174

TITLE

U93872

U93872.2

GI:14627174

JOURNAL

U93872

U93872.2

GI:14627174

MEDLINE

U93872

U93872.2

GI:14627174

PUBMED

U93872

U93872.2

GI:14627174

REFERENCE

U93872

U93872.2

GI:14627174

AUTHORS

U93872

U93872.2

GI:14627174

TITLE

U93872

U93872.2

GI:14627174

Human herpesvirus 8 (Kaposi's sarcoma-associated herpesvirus -
Human herpesvirus 8)
Human herpesvirus 8
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Rhadinovirus.
1 (bases 29032 to 30108; 117733 to 118431)
Zhong, W., Wang, H., Herndler, B., and Ganem, D.
Restricted expression of Kaposi sarcoma-associated herpesvirus
(human herpesvirus 8) genes in Kaposi sarcoma
Proc. Natl. Acad. Sci. U.S.A. 93 (13), 6641-6646 (1996)
66270595
8692871
2 (bases 17242 to 17856)
Neipel, F., Albrecht, J.C., Ensser, A., Huang, Y.Q., Li, J.J.,
Friedman, Kien, A.E., and Fleckenstein, B.
Human herpesvirus 8 encodes a homolog of Interleukin-6
J. Virol. 71 (1), 839-842 (1997)
97138401
8695427
3 (bases 123309 to 124082)
Li, M., Lee, H., Yoon, D.W., Albrecht, J.C., Fleckenstein, B., Neipel, F.,
Kaposi's sarcoma-associated herpesvirus encodes a functional cyclin
and Jung, J.U.
J. Virol. 71 (3), 1984-1991 (1997)
97184528
9032330
4 (bases 122660 to 123226)
Thome, M., Schneider, P., Hofmann, K., Fickenscher, H., Meln, E.,
Neipel, F., Melmann, C., Burns, K., Bodmer, J.L., Schrotter, M.,
Scaffidi, C., Kramer, P.H., Peter, M.E., and Tschopp, J.
Viral FLICE-inhibitory proteins (FLIPs) prevent apoptosis induced
by death receptors
Nature 386 (6624), 517-521 (1997)
97242415
9087414
5 (bases 1 to 133661)
Neipel, F., Albrecht, J.C., and Fleckenstein, B.
Cell-homologous genes in the Kaposi's sarcoma-associated

rhadinovirus human herpesvirus 8: determinants of its pathogenicity? J. Virol. 71 (6), 4187-4192 (1997)

JOURNAL MEDLINE 97296220
PUBMED 9151804

REFERENCE AUTHORS 6 (bases 1 to 133661)
TITLE Neipel, F., Albrecht, J.-C., Ensser, A., Huang, Y.-Q., Li, J.J., Friedman-Kien, A.E. and Fleckenstein, B.
JOURNAL The genome of human herpesvirus 8 cloned from Kaposi's sarcoma Unpublished
AUTHORS 7 (bases 1 to 133661)
TITLE Neipel, F., Albrecht, J.-C., Ensser, A., Huang, Y.-Q., Li, J.J., Friedman-Kien, A.E. and Fleckenstein, B.
JOURNAL Direct Submission
AUTHORS Submitted (17-MAR-1997) Virology, University of Erlangen, Schloessgarten 4, Institut für Klinische und Molekulare, Erlangen 91054, Germany
TITLE 8 (bases 1 to 133661)
JOURNAL Neipel, F., Albrecht, J.-C., Ensser, A., Huang, Y.-Q., Li, J.J., Friedman-Kien, A.E. and Fleckenstein, B.
AUTHORS Submitted (09-JUN-2001) Virology, University of Erlangen, Schloessgarten 4, Institut für Klinische und Molekulare, Erlangen 91054, Germany

REMARK Sequence update by submitter
COMMENT On Jul 9, 2001 this sequence version replaced gi:2246466.
FEATURES Location/Qualifiers
source 1..133661
/organism="Human herpesvirus 8"
/mol.type="genomic DNA"
/db_xref="taxon:37296"
/note="sequence derived from overlapping lambda phage clones isolated from two libraries of Sa9a partially digested DNA from Kaposi's sarcoma biopsies"
CDS 105..959
/note="ORF K1"
/codon_start=1
/protein_id="AAB62619.1"
/db_xref="gi:2246494"
/translation="MFLVYCSLAVCFRGLSLTSLQSSPNLCPGVISTPYTLCPSPNTSLPTSMYCNDRILRLTQOTFTVDLTICNFCVSGSGHSHLMTWYPOVLTQCGQPSNVTGCOHVTLCSTGNNVTVMHLNPRNGRETSQKTYVFTLMDTEGCAVNLGSSRLSNRLCSARCANLNPETHVTSVSTGRTFPTNRGTTLDVLMKAKNTLHIOVFLVFMTLVALIGMCGILGITIIFAHCKOKRDSNKTYPOQLQDYISLHDLCTDTQPVDMY"
CDS 1127..2779
/note="ORF 04, complement control protein homolog"
/codon_start=1
/protein_id="AAB62602.1"
/db_xref="gi:2246477"
/translation="MALTROTLMWTMTTNTWVIGDNKSCSKTLIGYRLKSRGDIAVGEVTELCRSGYTYTARNITATCLOGGTWSEPTATCKKSCPNPGEIONGVPIFHGGODALKYGANISVYCNMEGYFLVGRREVYRCMIGASGOMASSPPCEKECHKRPETENGDFKDKDYENDAVHECNEGYTLVGPISHACAVNNTWTSNMPTECELAKGKPSVTMGYPLOGSFYTKHKOSVTPACNDGFLVRSPTINCNTVMDPPLPKVCLDIDDPNNSNGRLHPTEPKNGNFORSNTPPEPTKEDTTATATCDNCEQPKILPTSGENBITTSNTITKQLEDEKTTISQPTHTITSLTSKAKAGNTKNTNSITDLIASTPTSGD DATPSIPSVQPNNTNAPTRTLTSLHIEGSSNSTSEKATASTLSHNSHRNDGGIYTTLNKTKQLSTPNKTPNSOAKSSTPKPVEHNTKTSNPALSTLSDADVDPQPREPTLPPIERPASKNRYNEKQVIGLTAVALTGCLITLFLHLEFR"
CDS 3194..6592
/note="ORF 06, major ssDNA binding protein homolog"
/codon_start=1
/protein_id="AAB62603.1"
/db_xref="gi:2246478"
/translation="MALKGPOLIEENIGSAAPTCGYLAVLTTHNPDIAGSLILNGVPEAKVEPLILHLGLTVSEDFPLANKKIDATPTASVKLTSVREAIIVRHNTLROPIROCKGLEKLCRESRELEFGSTVEEQHKGLTMRPCKPOLPCANETPMAYITEGFERLTKGLVLPVPSQTPVHIGEHQAFKIPLYDEDLFGPSRAQELCRFYNPDISTYHLDSIFIGIQAOLRVKDVSTVIOASEROFPHDYOKIPKIQVANDPOCASRGDCGSTLMDISLVAELGMSGSLFIEGPDSEVLNWDTPLECEPTDPAIRALAEVHAEBAFLIGAOFLAANSVLYLTRVAKLPKONKRGDANNYNSFYLOHGGLYSEATLVKENGASAFKGVPSALDGSSYTLQHLAVASSFPHLLARMCYTIQFLPHHKNTNSQSYNVVDYVGT

APSKMCDLCOGCGPAPVCINTLFEYRMKDRPEPLSNVKKDDPYVTGCTAGYNDLTILGNFATREBEREPNVEDAPKTYTWOLCONTEKTLASMGISEGDALRTLVDPSPVYKFKGIDSTVEAELELKFINCMIKNNYNFRENISVHIILOPACVNVQACPFLTYLYKSLTAVIODICLTSCMYBQDNPAVGIVSEMLKMHQPMNFKACGCHDGLITGELKIVHOSMPCDLEDTDAAIGMFAPARMOVRIARALAMPYKTIKINRIIFSNSTAESIOAGMFPASORDSYVIGGAPYKPLNALHKLTLPSTKTSALYIMKICOTQNPPLPGVSGHLETLNCVYKASAOFEINVLIDLPOLTSYAKIKNSITLALGCGOQOPATLSCLEPVOVLAEEYPHVLGFGISSDEPYAKAGSVITVOSTLQAVSTNRKRLPLIITPLVNNKTYGNSGNVNVHCANLIGFSRGVDNRLRPSPVFKNNVSMLRKHVIMTPIVLDRVYKIVGINSCEFAKVRQVNDLEDNDNPLKRTLVLELVKHLKSCASLEEDVYIYLGPAVAGDEVLSLTSTGQAQAVPAGVASVIDIDDCELQFVGPBPCILGOGSGVELEFPSPGVSLTVGKKRKIASLSDLDL"
CDS 6609..8696
/note="ORF 7, processing and transport protein homolog (ICP18.5)"
/codon_start=1
/protein_id="AAB62620.1"
/db_xref="gi:2246495"
/translation="MAKELAAVYADVSAAMDCLSYADPATLDTKSLATLTGKEOSLHGTLPLRLRONAHESGSLSELEHLLENADATLTCVCTSRKLSPEEHPSLIHLDTGCKNHRSVREYFGNMALEKLSLINDVEIFEKLSVFCIGSGSALHEIGEVLRVGLKILSPVPGDLYVNLPCLEIQEVLCTPNQSTLOAMLPTACSHLIEGTPACGEVYRGLFENELKQLQTPESLPTTCQSRVRDDDEIRQSSLAVDHIIFGVTRSVLEISNLIVYSSGSHATCDGDRCSHLASLFTHEALMHRVNDLACGLIEGRPKFFDCRRPSLETLRGGGLFSSVEDTIESLODCSAPFOOVNTTALOKONHEFYRLKSLAAGQLNLGKSTESCPSKAROLVGGGAPDEELRAKROELVLOKVARDGFKLSDCIRHOGHILSQTGLRLMGSVIYNEASALQNLHNAOFTSLPMODLVDCDPRFNSKYKANSYCORLGRLEHEVILLTFEYKYLIGLPSKRLTLPSPNVTLAACFEAGMLPHOKMAYSEMIPSLIEPKDWIEPNQFYFENDINHLORAMEYITRELYLSVLTNRTWERELKILLTPQSGSPGFEPKAGLTGLYLTFFESAPVLVLDKCYMLFKDVLALYHHLQLSNHNDSV"
CDS 8680..11217
/note="ORF 08, glycoprotein B (gB) homolog"
/codon_start=1
/protein_id="AAB62592.1"
/db_xref="gi:2246467"
/translation="MTPRSRLATLTCTVTILVFOCGAHSRGRDFROTSSPPRGSSSKAPTPREBASPKSVDPYQPRVCASITGELFRNLNDQTPDPTDKXHOEILLVYKNIVPIHKVRKRYKRIATSVYRGLTSLATINKELPRPVLVEISHMSTYQCFSSMKNVNGVEMNTFEDDDVNTVFLOPVGGLDNDIORYSQPIVAEPMPQIVKRTLVNCEIVIMIRASABEYVYFVSLQDTEVSPFCINBSCSTTPNKNGLSOVVALNHTVYVTSNDSGTPTPNRLFEVEGATYLSMASRSKTYACPLAKMTLTPRSIQTDEDSFHEVANEITATFTAPLTPVANTDTQSLTSDINTLANSKAKLASTHVNQGVYFHTTGGXLYVWPMASAINLTHAOCDSNPNTPSPRASPMTTASRRKRSASTAAAGCGSTDNLTSTQLOFAIDKLADGINOVLEELSRMCEQYRDNLMRTLEKINFTSMYTAIYGRVSAKFPVGDALSTECINVDQSSVNIHRSLTNSKSDCYARPLATEFPLNSNLFTGQLGARNEIILTNNQVETCKDCEHFIPTRENLVYKDYARTINTTIDISTLNTFIALNSFIQNDIFKALIELYSSAEKRLASVFELEPMREYNYTRHLAGLREDLNTI DMNKEFVYRDLSEIYADLGGIGKTYVMAASVYTLGSLMGFINFKHPGGMMLIIVIAIILILPMLSRRTNTIAQAPYMYITPDDRARPSPGGAPTREIKINILLGMHQLQDEKQADLKKSTPSVFORFANGLRQRLRGKPLTQSLDISPETGE"
CDS 11344..14382
/note="ORF 09, DNA polymerase homolog"
/codon_start=1
/protein_id="AAB62593.1"
/db_xref="gi:2246468"
/translation="MDFNPFIDTPRGPRNTVROPPTSQSTVYPSERVCLIPACFOTPGPGVAAVDTPTEPPPYFOGPKRGVEFAEETGIMTRGQAANAMSHLIFHVDIVETVTLTADREDEPFSQTDIIPSGVYLKILGRLDASCVANNFORCYFETLAPQGVNLTVHVAQALQAGFGRASGCFSTPEPRKILRAYDQOAVQVKITLSSPMHTLSDRITTCGCEVESPNDAIRRFVLDGSEFTPGWEGENNAIPRTQADSWTELEPDCSWE DKTPTPERTMPPTIILSFIDIECKGEKFPNATQDEDMITQISCYLHVNGDKPYTRMLLGIGTCPLPGVEVEEPSEYDMIAALSMDRDNVEFTIGYNLANPDLPLIARATQVYDEKLODFTKIKTSVFEVHOPRGSGDGNFMFSQKVSIGVNPIDMYQCEKELSLSDYKILDTVAKOCIGROKDDISYKIDIPLEKRSQDGAKGVNCDVSYVMDLLRFOTHEISEIKLAKIPTRVLDQGOQIRANVSCLEAATAGYILPVPKGAVASQYQATVISPSPGAYDPDILVYDPAVSIYSIIQANVCSLTLPDSDLHLPHLSBDEYFVLSGPPVHFYKHKRESLLAKLITVWLAKKEIKRTLASCDPDAKTLTDDQQAIVYTCMAVYGTGVAAGLPLCLNLAETVTLQGRMSEQSQFAISPERAPKLLRRPIDVSPDAEFVYIDGTSILFCMGFNNDSDSAEELASTTTVTLFSPRTKLAEKIFKCLLLTKTKRYVCLSDDKVILMGVLDLIRTKACRFQDEKSSQVLDLILRPSYAKAKLISGQATDNNVYREGPLGKFAKIIQVILNASHACRENSVYDPDKLTFTTELSRPADYKTONLPHLTVYKCLQARQELPQIHDRIPYVVDAPGSLRSLSLAAHPREVYKHGRVAVDLY

CDS
FDKLVAHAVANIIOCLFQNNNTSATVAMLYNFLDIPVTEPTP*
14500..15756
/note="ORF 10, herpesvirus saimiri ORF 10 homolog,
conserved in other gamma-herpesviruses"
/codon_start=1
/protein_id="AA62594.1"
/db_xref="GI:2246469"
/translation="MQTEATFLLDMEITVSNCRFTCSLLTCGPLYRSSGDPYRLRIAP

Query Match 0.1%; Score 23; DB 1; Length 133661;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 44313 AGTCTCAGTCTATATTTAACT 44335
|||||
Db 48054 AGCTCAGTCTATATTTAACT 48076

RESULT 11
KSU75698 137508 bp DNA linear VRL 03-MAY-1997
LOCUS Kaposi's sarcoma-associated herpesvirus long unique region, 80
DEFINITION putative ORF's and kaposin gene, complete cds.
ACCESSION U75698.1 GI:2065526
VERSION U75698.1
KEYWORDS
SOURCE Human herpesvirus 8 (Kaposi's sarcoma-associated herpesvirus -
Human herpesvirus 8
Human herpesvirus 8
VIRUSES: dsDNA viruses, no RNA stage: Herpesviridae;
Gammaherpesvirinae: Rhadinovirus.
REFERENCE 1 (bases 47193 to 47522: 133099 to 133729)
Chang, Y., Cesarman, E., Pessin, M. S., Lee, F., Culpepper, J.,
Knowles, D. M. and Moore, P. S.
Identification of herpesvirus-like DNA sequences in AIDS-associated
Kaposi's sarcoma
Science 266 (5192), 1865-1869 (1994)
JOURNAL MEDLINE 95090463
PUBMED 7997879
REFERENCE 2 (bases 35021 to 55726)
Moore, P. S., Gao, S. J., Dominguez, G., Cesarman, E., Lungu, O.,
Knowles, D. M., Garber, R., Pellett, P. E., McGeoch, D. J. and Chang, Y.
Primary characterization of a herpesvirus agent associated with
Kaposi's sarcoma
Proc. Natl. Acad. Sci. U.S.A. 93 (13), 6641-6646 (1996)
JOURNAL MEDLINE 96099469
PUBMED 8523568
REFERENCE 3 (bases 28661 to 29741; 117919 to 118101)
Zhong, W., Wang, H., Herndler, B. and Ganem, D.
Restricted expression of Kaposi sarcoma-associated herpesvirus
(human herpesvirus 8) genes in Kaposi sarcoma
Proc. Natl. Acad. Sci. U.S.A. 93 (13), 6641-6646 (1996)
JOURNAL MEDLINE 96270595
PUBMED 862871
REFERENCE 4 (bases 122794 to 123567; 123809 to 127297; 129372 to 130400;
130551 to 134441)
Cesarman, E., Nador, R. G., Bai, F., Bohenzky, R. A., Russo, J. J.,
Moore, P. S., Chang, Y. and Knowles, D. M.
Kaposi's sarcoma-associated herpesvirus contains G protein-coupled
receptor and cyclin D homologs which are expressed in Kaposi's
sarcoma and malignant lymphoma
J. Virol. 70 (11), 8218-8223 (1996)
JOURNAL MEDLINE 97048116
PUBMED 8892957
REFERENCE 5 (bases 1 to 137508)
Moore, P. S., Boshoff, C., Weiss, R. A. and Chang, Y.
Molecular mimicry of human cytokine and cytokine response pathway
genes by KSHV
Science 274 (5293), 1739-1744 (1996)
JOURNAL MEDLINE 97094384
PUBMED 8939871
REFERENCE 6 (bases 1 to 137508)
Russo, J. J., Bohenzky, R. A., Chien, M.-C., Chen, J., Yan, M.,

TITLE
JOURNAL MEDLINE 97121480
PUBMED 8962146
REFERENCE 7 (bases 1 to 137508)
Russo, J. J., Bohenzky, R. A., Chien, M.-C., Chen, J., Yan, M.,
Maddalena, D., Parry, J. P., Peruzzi, D., Edelman, I. S., Chang, Y. and
Moore, P. S.
Direct Submission
Submitted (17-OCT-1996) Dept of Pathology/Genome Center/Division of
Epidemiology, Columbia University, 650 West 168th Street, New York,
NY 10032, USA
8 (bases 1 to 137508)
Russo, J. J., Bohenzky, R. A., Chien, M.-C., Chen, J., Yan, M.,
Maddalena, D., Parry, J. P., Peruzzi, D., Edelman, I. S., Chang, Y. and
Moore, P. S.
Direct Submission
Submitted (02-MAY-1997) Dept of Pathology/Genome Center/Division of
Epidemiology, Columbia University, 650 West 168th Street, New York,
NY 10032, USA
Sequence update by submitter
On May 3, 1997 this sequence version replaced gi:1718251.
REMARK COMMENT
FEATURES
source
1..137508
location/Qualifiers
1..137508
/organism="Human herpesvirus 8"
/mol_type="genomic DNA"
/db_xref="taxon:37296"
/cell_line="BC-1; virally infected primary effusion
lymphoma derived cell line"
/note="sequence derived from overlapping lambda phage and
cosmid clones isolated from libraries: A prototype
sequence for the terminal repeat (TR) unit is deposited
under GenBank Accession Number U75699. The left junction
variant TR sequence unit immediately preceding base pair 1
of the LUR is deposited under GenBank Accession Number
U75700. The remaining LUR sequence extending from this
sequence to the right TR unit is not available due to
difficulties in cloning and sequencing of this region"
1..137508
/note="long unique region LUR"
105..974
/note="ORF K1"
/codon_start=1
/protein_id="AAC57082.1"
/db_xref="GI:1718252"
/translation="MFLYVCSLAVCEGRLSLSSPNLCPGVISTPYTLCLNSA
SLPISWCNNRLRLTERVILDTIACNEFCVQSGHROSITWTRQVYLQICAO
PSNVTCGOHVTLCTSGNNVWMLHPNGENETVSOTKYNTFLMSOTEGCYCSNG
LSSRLSNRICMARCANTTPETHVSVSTGPFCTLSNSLYKIIHATRRVYVYKKA
KSTRHFEVHFVLYMNTVALIGTWCGILGTTIIFAHCKQRDSNKTVPQQLDYISLHD
LCTEDYQVDMVY"
1142..2794
/note="ORF 4: The HSV ORF 4 homolog has alternatively
spliced messages encoding membrane bound and secreted
proteins: complement binding protein VCBP homolog"
/codon_start=1
/protein_id="AAC57082.1"
/db_xref="GI:1718253"
/translation="MAFLRQTLMLTMTFTYVIGDNEKCSQKTLIGRLKMSRQDIA
VGEIVELRCRSGYTTVARNATATCLOGTSEPAATCNKRCSPNGEIONKVIFFHG
ODAKXGANSYVNCNEFTVAGREYVRCMIGASGOMASSSPCEKREKHPRKIGI
GDRPKDDIYRYNDVAHFECNEGTLYGPHSIRACAVNNNTWISNMPCTCLACKRPSVT
HGYPIDGSLVYKHKQSVTFACNDGPFVLRGSPITTCVNTWDPPLPKVLDDIDDPNN
SNGRLLPTPEKNGVNFORSNTPEPTKEDHDHATCTNDEPRLIPTSEGFN
ETTSNTITKOLEDEKTIQSNVTHITSLPMKKAGNTKNTNSTDILIASPTSD
DAPTSIPSVQTPNTNAPATRLTSLHIEEGSNTSEKATSELSHNSHKNDTGCI
YTTLNKTQLEPSTNKPNSOAKSKSTKPEVTHNKTSPATSLSDSDVDPQRPREPTL
PPIRPASKRYIEKOLVIGLTAVALTCGLITLFLHFR"
3210..6611
/note="ORF 6: ss DNA binding protein ssDBP homolog; EBV

BAHF2 homolog"
/codon_start=1
/protein_id="AAC57083.1"
/db_xref="GI:1718254"
/translation="MALKGPOULEENIGSAAPGCGYLAAYLTNHPIGEASILNG
YPAKVESLPLHLGLTVESDFPLNVAKVKKIDATASAKLNSYHEAIVFHNTHFO
PIFGKGLKICRESRELFGSTPEQOQKIDPESAPOLPCAPKIMAVYVWPGF
KEHLYGKLVPPPSQTPVPHIGBQAFKIPLDLDEFGSRAOELCFINPDISRLH
DSLFTGIAQLARKDVSTVIOASERQFVHDQKIPVLQAKQPPQASAGTDSSTLH
IDSLVAELGMSYGLSEIENGPDSCEVLNIDTWPIFNCESTPAKRALVWMAEQALH
IGAOLEFANSVLYLTFKAPLPQKRNQKIDPESAPOLPCAPKIMAVYVWPGF
GVVPSALDSSSYLQHLAYASSFPHILRMVYLOEPLHKNKINSQSYVVDYVGA
APSGMDLCOGCPACVNTLTPYRMKDRPYSNKRDRPVTGAGTYNDLEILGN
PAREFEREENGVEDAPKTYTQLOCONTETKIASGISEGDAITLVDPSEPKV
FNGIDSTVAELBLKTNMKNNTNRENKSVHHLQACVYVWAPCPVLTLYK
SLTYLQDICTSCMAYEQDNPAVGLPSEBMKMHQTMTEKCAQCPKGAITGEL
KIVHOSMPCDLDTDAIGMFAFMQVRIARAMVAKRTIKRRIENSTGAS
IOAGFMKPAOSRDSYVGGPYMKFLNALKHTLPEPSTALYLMHIGOTTNPLDG
VSGEHTLCLNYKASSOAFERINVLDPDLTSAKIKINSITIRAGGQGFVAT
LSCSPYVQLVPAEEYPHYLGPGILSSPEYRAKAGRSVTIYQSTLKAQVSTNGLR
PITVPLVANKTGSNGNTNVEHCANLGYFSGGVDRNLRPESVPRKNNVSMELKR
HYIMTPVRLKRVKRIYVINGSEFEAVRSVQVNLDEDNPLPTVVLVLEVKPRW
SSCALSIEDVYIYLGPAVLGDEVLSLSTVGOAGVPWTAEGVAVIIDDICELQ
FYGPEPCLIQOGSVEELFPPSPVSLTVKKRKIASILSDUL"
6628..8715
/note="ORF 7; transport protein homolog; EBV BRLF3
homolog"
/codon_start=1
/protein_id="AAC57084.1"
/db_xref="GI:1718255"
/translation="MAKELAAVYADVSALAMDCLISTVADPATIDTKSLITTKGROS
LHGTLLPLLRONAHCSGLSLELHFRTYMLMRMCALENLOKSTPSCMT
QHATSRVRFNFTGMALVELKSLINDVEITFKLSVYFICGSSALGEGEYRF
VAKLRISVPBGDLYVNLPCLEQLQEVLTIPNOSTQAMLPDACHSICTPAGE
PRGLFENELKQLOTPESITPTPCOSVRODDEROSLADGHLHIFGEVTRVL
EISNLIYMSGSHDATCDGDRCSHLASLFTHEADMKRRLVAGLGGRRKHEFD
CRRPSLETFCGGLSESVEDITESLONKNSAFYQVNTALOKVADGRRKISDL
AAGOLNKGCSGCSOSEARROLVGGGKREVELRDKHDELYLQVADGRRKISDL
IRHOGHILSQTLGLRMGSYTYNEASALONHLLHRAQFISLMODITVDCPIRENSK
YIKNSLYCORLGRHEVEILTFEYKLTGPFSKRHTLPSPRPVTLAQLFEAGMPLH
QKMWSEMIWPSIEPDMWIEPNQFISENDINHLQKRAEYIRELVLSVLMRT
WERELKILTPGSGPGEPRKPAGLTGLYLFETESAPLVADKKYGMIFKDLALLY
HHQLSNHNDQV"
8699..11236
/note="ORF 8; glycoprotein B gb homolog; EBV BRLF4
homolog"
/codon_start=1
/protein_id="AAC57085.1"
/db_xref="GI:1718256"
/translation="MPPSRRLATIGTVLLVCGCAGAHSGDGTQTSSTPMPSSS
KAPKPEGEASGPKSVDFQFVCSASTGELFRRLBETCDTDRKIQOEGILVYK
KNIYVHIFKVRKRIKATSVYVRLGESATINKELEPRVPLDETSHMDSYQCSFS
KRVNANGVENTFTDRDQVNTVFLQPEGLTNIQRYEQPVIYAEQWPEIYRAT
TVNCEVIDMARSAPYNYFVSLGTVASPCVCSSTPSPKNSLQVYVNLH
TVYVSDRGTSPONRIEFTGATLWASBSKTTAVCPALMKTFPESIOTTHDS
FHFVANEITATFTPLTFVANFTDYSCLTSDINTINLTKAKIASSTHAPNTVOYFH
TTGGLYVWOPKSAINTLHAQDSGNTSPSPSPSPSPSPSPSPSPSPSPSPSPSP
GSTDNLSITQLOPATDKLRDGINOVLEELSRMCRQVNDMLMWELKINTSVTA
LYGRVPSAFVGDALSVETCINVDSSVNIHSLRNSNDVQYARLVFKLNSNL
FTGOLGARNEIILTNNOVETCKDCEHYFTFNETLTVYDYVLAIFINTDSTNTE
IALNLSFQNIIDFKALEIYSSAEKRLASVDELREYNNYTRHKLDELMDLMTI
DNKKREPVRLSEIVADGGIGKTVVNNASVVTLCGSLVGTGFINFKHPLDGMGMI
IYVAILIITLMSRRNTIQAQPVKMIYDVYRRAPPSGAGTPEIKIILIGMHQLO
QEROKADDLKSTSPSVORTANGRLQRKGLPLOSIDISPEGE"
11363..14401
/note="ORF 9; DNA polymerase homolog; EBV BRLF5 homolog"
/codon_start=1
/protein_id="AAC57086.1"
/db_xref="GI:1718257"
/translation="MDFENPITDPTRGGRNTVROPPTSQSTVPSETRVCLIPACE
QTPGRGVAVVATPEPPYFQGRKGEVAGETGSLWTKRRQARNAQASHLIFVYD
IVETTYTADRCEDVPPSFOTDIPSGTVKGLTLDGASVQVNRQAPACVYTLAPQ
GVNLTHVLQALQAGFGRASGCFSTPEPVKKILRLAYDQVAVQKITTLSSPMPTLS

DRLTGCGEVEFSNVAIRFVLHDGFSFGWEGSNAPARTQARDSWTELEFDCSME

Query Match	0.18; Score 23; DB 1; Length 137508;
Best Local Similarity	100.0%; Pred. No. 0.11;
Matches	23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 44313	AGCTCAGTCTCTATTATTAATCT 44335
DB 47755	AGTCTCAGTCTCTATTATTAATCT 47777
RESULT 12	
AY037858/c	171096 bp DNA circular VRL 19-NOV-2002
LOCUS	AY037858
DEFINITION	Cercopithecine herpesvirus 15 strain LCL664, complete genome.
ACCESSION	AY037858 AF148640 AF148641 AF159308 AF227125 AF159309 AF159310
VERSION	AF227123 AF227124 U45963 U93160 U93909
KEYWORDS	AY037858.1 GI:18025465
SOURCE	Cercopithecine herpesvirus 15
ORGANISM	Cercopithecine herpesvirus 15
REFERENCE	Viruses; dsDNA viruses, no RNA stage; Herpesviridae; Gammaherpesvirinae; Lymphocryptovirus.
AUTHORS	1 (bases 1 to 171096)
TITLE	Franken, M., Deyere, O., Rosenzweig, M., Annis, B., Kieff, E. and Wang, F.
JOURNAL	Comparative analysis identifies conserved tumor necrosis factor receptor-associated factor 3 binding sites in the human and simian Epstein-Barr virus oncogene Lmp1
MEDLINE	J. Virol. 70 (11), 7819-7826 (1996)
PUBMED	97048062
AUTHORS	8892803
TITLE	2 (bases 1 to 171096)
JOURNAL	Rivallier, P., Quink, C. and Wang, F.
MEDLINE	Strong selective pressure for evolution of an Epstein-Barr virus LMP2 homologue in the rhesus lymphocryptovirus
PUBMED	J. Virol. 73 (10), 8867-8872 (1999)
AUTHORS	99412410
TITLE	10482645
JOURNAL	3 (bases 1 to 171096)
MEDLINE	Jiang, H., Cho, Y.G. and Wang, F.
PUBMED	Structural, functional, and genetic comparisons of Epstein-Barr virus nuclear antigen 3a, 3b, and 3c homologues encoded by the rhesus lymphocryptovirus
AUTHORS	J. Virol. 74 (13), 5921-5932 (2000)
TITLE	20304984
JOURNAL	4 (bases 1 to 171096)
MEDLINE	10846073
PUBMED	Rao, P., Jiang, H. and Wang, F.
AUTHORS	Cloning of the rhesus lymphocryptovirus viral capsid antigen and Epstein-Barr virus-encoded small RNA homologues and use in diagnosis of acute and persistent infections
TITLE	J. Clin. Microbiol. 38 (9), 3219-3225 (2000)
JOURNAL	20440633
MEDLINE	10970361
PUBMED	5 (bases 1 to 171096)
AUTHORS	Rivallier, P., Jiang, H., Cho, Y.G., Quink, C. and Wang, F.
TITLE	Complete nucleotide sequence of the rhesus lymphocryptovirus: genetic validation for an Epstein-Barr virus animal model
JOURNAL	J. Virol. 76 (1), 421-426 (2002)
MEDLINE	21602573
PUBMED	11739708
AUTHORS	6 (bases 1 to 171096)
TITLE	Wang, F., Franken, M. and Annis, B.
JOURNAL	Submitted (11-JAN-1996) Medicine, Brigham and Women's Hospital, 181 Longwood Avenue, Boston, MA 02115, USA
REFERENCE	7 (bases 1 to 171096)
AUTHORS	Moghaddam, A., Koch, J., Annis, B. and Wang, F.
TITLE	Direct Submision
JOURNAL	Submitted (12-MAR-1997) Medicine, Brigham and Women's Hospital, 181 Longwood Avenue, Boston, MA 02115, USA
REFERENCE	8 (bases 1 to 171096)

AUTHORS Moghaddam, A., Annis, B. and Wang, F.
TITLE Direct Submission
JOURNAL Submitted (17-MAR-1997) Medicine, Brigham and Women's Hospital, 181
Longwood Avenue, Boston, MA 02115, USA
REFERENCE 9 (bases 1 to 171096)
AUTHORS Rivallier, P., Quink, C. and Wang, F.
TITLE Direct Submission
JOURNAL Submitted (04-MAY-1999) Medicine, Brigham and Women's Hospital, 181
Longwood Avenue, Boston, MA 02115, USA
REFERENCE 10 (bases 1 to 171096)
AUTHORS Jiang, H. and Wang, F.
TITLE Direct Submission
JOURNAL Submitted (16-JUN-1999) Medicine, Brigham and Women's Hospital, 181
Longwood Avenue, Boston, MA 02115, USA
REFERENCE 11 (bases 1 to 171096)
AUTHORS Rao, P. Y., Jiang, H. and Wang, F.
TITLE Direct Submission
JOURNAL Submitted (21-JAN-2000) Medicine, Brigham and Women's Hospital, 181
Longwood Avenue, Boston, MA 02115, USA
REFERENCE 12 (bases 1 to 171096)
AUTHORS Rivallier, P., Jiang, H., Cho, Y.-G., Quink, C. and Wang, F.
TITLE Direct Submission
JOURNAL Submitted (01-JUN-2001) Medicine, Brigham and Women's Hospital, 181
Longwood Avenue, Boston, MA 02115, USA
REMARK Sequence updated by submitter
COMMENT On or before Dec 31, 2001 this sequence version replaced
gi:9651728, gi:9651730, gi:9651731, gi:5929880, gi:5929882,
gi:8745308, gi:8745310, gi:8745312, gi:3342233, gi:3342231,
gi:1477526.
FEATURES
source 1. 171096
/organism="Cercopithecine herpesvirus 15"
/mol_type="genomic DNA"
/strain="LC18664"
/db_xref="taxon:104228"
join(162521..162879,137..354,437..535,644..892,974..1054,
1134..1289,1377..1592,1673..>1779)
/product="LMP2a"
join(162521..162879,137..354,437..535,644..892,974..1054,
1134..1289,1377..1592,1673..1779)
/note="similar to Epstein-Barr virus LMP2a"
/codon_start=1
/product="LMP2a"
/protein_id="AAD56624.2"
/db_xref="gi:18025544"
/translation="MSALEMPEIGAPAPPTPYGODGSGESGSESVSSPSSSPG
OGPDYEDPPDDGNPPYDADGCGGPGYQPLRGDPNQLVARLGGGNGTLPPPY
SPQRTSLHLEIHPQRTMAQWLVVSAFLVWLAGIASCFASVSALVTITGLA
LSLLLAALVNSYAQRRAVTKTLIVGVTFEILTLTVQPRDAIVFALITGA
AVLQAVILVLMLEFLPTVRRMRKIVCVLLFLACAVLLVDAIMQSLGSMV
VALTLIAFLIWLSSPWGIGALTLAAALAGSLVGLNATMFLIMFLMT
LVILICSPQOTYLMRSWLLYALSLILASALLAGSGILOTWGDNTEFPPSFCM
LLIIVAGILFLAITTEMGTSKTYGCVFVCLSGTLTMAAGLVVYVIMIKILLSMTI
TAGCFIFLGLFELILKFCRLCCFCCLRESGDPQVATYQNNV"
join(166602..166718,137..354,437..535,644..892,974..1054,
1134..1289,1377..1592,1673..1781,5496..5930)
/product="LMP2b"
/note="similar to Epstein-Barr virus LMP2b"
join(141..354,437..535,644..892,974..1054,1134..1289,
1377..1592,1673..>1779)
/product="LMP2b"
join(141..354,437..535,644..892,974..1054,1134..1289,
1377..1592,1673..1779)
/note="similar to Epstein-Barr virus LMP2b"
/codon_start=1
/product="LMP2b"
/protein_id="AAK95410.1"
/db_xref="gi:18025466"
/translation="MAPGMLPVVSAFLVWLAGIASCFASVSALVTITGLSLT
LAALVNSYAQRRAVTKTLIVGVTFEILTLTVQPRDAIVFALITGA
AVLQAVILVLMLEFLPTVRRMRKIVCVLLFLACAVLLVDAIMQSLGSMV
VALTLIAFLIWLSSPWGIGALTLAAALAGSLVGLNATMFLIMFLMTIIL
LCSTPQTMVLMRSWLLYALSLILASALLAGSGILOTWGDNTEFPPSFCMILLIIV

AGLEFIATLIEWGTGSKTYGCVFVCLSGTLTMAAGLVVYVIMIKILLSMTIAGCF
IFLGLFIFLGLFELILKFCRLCCFCCLRESGDPQVATYQNNV"
1836..>5780
/product="BNRF1"
1836..5780
/note="similar to Epstein-Barr virus BNRF1"
/codon_start=1
/product="BNRF1"
/protein_id="AAK95411.1"
/db_xref="gi:18025467"
/translation="MAQSRVYVSAFLVWLAGIASCFASVSALVTITGLSLT
LAALVNSYAQRRAVTKTLIVGVTFEILTLTVQPRDAIVFALITGA
AVLQAVILVLMLEFLPTVRRMRKIVCVLLFLACAVLLVDAIMQSLGSMV
VALTLIAFLIWLSSPWGIGALTLAAALAGSLVGLNATMFLIMFLMTIIL
LCSTPQTMVLMRSWLLYALSLILASALLAGSGILOTWGDNTEFPPSFCMILLIIV
LGFHPMSNLTPAPCVESALQATVOTALELSGLIPAPCVSHARPQGCALIEH
LRSIVQKGGLLFLSHLEDYKGGIGDQATSRGIKQVETVFLNPNQSNVFLV
RQREKINGRGLVQLAKRACVAGCCQYVLSVPLAGLGNVNDLASPVSTAEVTD
APFEVEFSPISPEGEMKSPVSHDFEERDVPSSHSSMLSSCCLTSVSHPSVSK
HLVRRDVSQGRVALQPGVGPDLPLADVAEVASQWVRGCAPLPYTPMDMNE
KLVSARPTDEAPKYSQVITTLGBOGYVTYDPTGCTLAIVEALMNAARPLVPED
VLTLNLHADPEKVDSTAVMDLMTASVYARDLGVKLTLYGASCPETSAGCFETV
VTASARGEFSAPLITPVLRGSGSLSVYRDGKIQGSLFEQLFSQVATPARQAD
AMKIIETVQGLVKSGLVLSGHDVSDGLVLCVEMALAGRGVTVISVPAADYLPOL
PTEHGLVEVEGEMTEVMOTLRQNTIYPAVIGALGADQMDQVQSGSTVYR
LSLITSTWSTATQYEFELRGRRLNRSNHSVDSYGNELATSLPLGKRLGRIVTEP
DPRCAVAVLCAPGTRGHESLALFTNACLCORVYFRVYRETTFFDKAGLAVGVVHA
ARDAPLAGRATVALIDRSPLALDLKFLARETSLGEGVQVLAGLAVGCVVHA
TPEGVEINQVSPYLITNTNAGLSEHMLNPSVHPDKSVLRGICQVLPQWIOGS
HLGEFTNPAMPYVYQNSHQIACHFHSRHPMRAEHYPRNPSRSNIGSCSPDGR
HLALCDPSLCDFWQWEYIISAFAPYGCSPWTLMPQAHMLSLKRSHPSS"
6653..6824
/note="similar to Epstein-Barr virus EBER-1"
6967..7136
/note="similar to Epstein-Barr virus EBER-2"
<9920..>10453
/product="BCRF1"
9920..10453
/note="similar to Epstein-Barr virus BCRF1"
/codon_start=1
/product="BCRF1"
/protein_id="AAK95412.1"
/db_xref="gi:18025468"
/translation="MGLRSGTLTQCLVTLTQCLVYLYAPACKVSGNCGNLPMLRDLR
DAFSRYKTFQMKDQDLNILLKESLLEPKGTGCGALSEMQLFLBEMPOAENQD
HAKFVNSLGEVLTGLRLRLRCHRFELPCENKSNVDEYKNAFSLQERGVKASSEF
DIFIVYIAYAMIKIR"
join(11765..11771,11930..11959,15018..15078,15160..15294,
18100..18159,18241..18375,21181..21240,21322..21456,2462,
2462..24321,24403..24537,27343..27402,27484..27618,
29839..29871,29956..30060)
/product="EBNA-LP"
/note="similar to Epstein-Barr virus EBNA-LP"
join(11958..11959,15018..15078,15160..15294,18100..18159,
18241..18375,21181..21240,21322..21456,2462..24321,
24403..24537,27343..27402,27484..27618,29839..29871,
29956..30060)
/product="EBNA-LP"
/note="similar to Epstein-Barr virus EBNA-LP"
/codon_start=1
/product="EBNA-LP"
Query Match 0.1%: Score 22; DB 1; Length 171096;
Best Local Similarity 100.0%; Pred. No. 0.45;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
48982 GGGGGCTTGTATTAAAGGCC 49003

Db 108504 GGGGGCTTGTATTTAAGGCC 108483

RESULT 13
LOCUS HHV507799/c
DEFINITION Human herpesvirus 4 complete wild type genome.
ACCESSION AJ507799.1 GI:23893576
VERSION AJ507799.1
KEYWORDS complete genome.
SOURCE Human herpesvirus 4 (Epstein-Barr virus)
ORGANISM Human herpesvirinae; Lymphocryptovirus.

REFERENCE
AUTHORS Arrand, J.R., Rymo, L., Walsh, J.E., Bjorck, E., Lindahl, T. and Griffin, B.E.
TITLE Molecular cloning of the complete Epstein-Barr virus genome as a set of overlapping restriction endonuclease fragments
JOURNAL Nucleic Acids Res. 9 (13), 2999-3014 (1981)
MEDLINE 8201487
PUBMED 6269068

REFERENCE
AUTHORS Kozak, M.
TITLE Possible role of flanking nucleotides in recognition of the AUG initiator codon by eukaryotic ribosomes
JOURNAL Nucleic Acids Res. 9 (20), 5233-5262 (1981)
MEDLINE 82059504
PUBMED 7301588

REFERENCE
AUTHORS Deininger, P.L., Bankier, A., Farrell, P., Baer, R. and Barrell, B.
TITLE Sequence analysis and in vitro transcription of portions of the Epstein-Barr virus genome
J. Cell. Biochem. 19 (3), 267-274 (1982)
MEDLINE 83109311
PUBMED 6296170

REFERENCE
AUTHORS Farrell, P.J., Deininger, P.L., Bankier, A. and Barrell, B.
TITLE Homologous upstream sequences near Epstein-Barr virus promoters
Proc. Natl. Acad. Sci. U.S.A. 80 (6), 1565-1569 (1983)
MEDLINE 83169725
PUBMED 6300857

REFERENCE
AUTHORS Bankier, A.T., Deininger, P.L., Farrell, P.J. and Barrell, B.G.
TITLE Sequence analysis of the 17,166 base-pair EcoRI fragment C of B95-8 Epstein-Barr virus
Mol. Biol. Med. 1 (1), 21-45 (1983)
MEDLINE 85035713
PUBMED 6092825

REFERENCE
AUTHORS Seguin, C., Farrell, P.J. and Barrell, B.G.
TITLE DNA sequence and transcription of the BamHI fragment B region of B95-8 Epstein-Barr virus
Mol. Biol. Med. 1 (3), 369-392 (1983)
MEDLINE 85060424
PUBMED 6094953

REFERENCE
AUTHORS Jeang, K.T. and Hayward, S.D.
TITLE Organization of the Epstein-Barr virus DNA molecule. III. Location of the P3HR-1 deletion junction and characterization of the NotI repeat units that form part of the template for an abundant 12-O-tetradecanoylphorbol-13-acetate-induced mRNA transcript
J. Virol. 48 (1), 135-148 (1983)
MEDLINE 83294686
PUBMED 6310141

REFERENCE
AUTHORS Bankier, A.T., Deininger, P.L., Satchwell, S.C., Baer, R., Farrell, P.J. and Barrell, B.G.
TITLE DNA sequence analysis of the EcoRI Dhet fragment of B95-8 Epstein-Barr virus containing the terminal repeat sequences
Mol. Biol. Med. 1 (4), 425-445 (1983)
MEDLINE 85060428

PUBMED 6094955
REFERENCE
AUTHORS Farrell, P.J., Bankier, A., Seguin, C., Deininger, P. and Barrell, B.G.
TITLE Latent and lytic cycle promoters of Epstein-Barr virus
EMBO J. 2 (8), 1331-1338 (1983)
MEDLINE 20331131
PUBMED 10872327

REFERENCE
AUTHORS Jones, M.D., Foster, L., Sheedy, T. and Griffin, B.E.
TITLE The EB virus genome in Daudi Burkitt's lymphoma cells has a deletion similar to that observed in a non-transforming strain (P3HR-1) of the virus
EMBO J. 3 (4), 813-821 (1984)
MEDLINE 84207939
PUBMED 6327290

REFERENCE
AUTHORS Biggin, M., Farrell, P.J. and Barrell, B.G.
TITLE Transcription and DNA sequence of the BamHI L fragment of B95-8 Epstein-Barr virus
EMBO J. 3 (5), 1083-1090 (1984)
MEDLINE 84236104
PUBMED 6203743

REFERENCE
AUTHORS Yates, J., Warren, N., Reisman, D. and Sugden, B.
TITLE A cis-acting element from the Epstein-Barr viral genome that permits stable replication of recombinant plasmids in latently infected cells
Proc. Natl. Acad. Sci. U.S.A. 81 (12), 3806-3810 (1984)
MEDLINE 84222045
PUBMED 6328526

REFERENCE
AUTHORS Gibson, T., Stockwell, P., Ginsburg, M. and Barrell, B.
TITLE Homology between two EBV early genes and HSV ribonucleotide reductase and 38k genes
Nucleic Acids Res. 12 (12), 5087-5099 (1984)
MEDLINE 84247360
PUBMED 6330697

REFERENCE
AUTHORS Baer, R.J., Bankier, A.T., Biggin, M.D., Deininger, P.L., Farrell, P.J., Gibson, T.J., Hatfull, G.F., Hudson, G.S., Satchwell, S.C., Seguin, C., Tuffnell, P.S. and Barrell, B.G.
TITLE DNA sequence and expression of the B95-8 Epstein-Barr virus genome
Nature 310 (5974), 207-211 (1984)
MEDLINE 84270667
PUBMED 6087149

REFERENCE
AUTHORS Bodescot, M. and Perricaudet, M.
TITLE Clustered alternative splice sites in Epstein-Barr virus RNAs
Nucleic Acids Res. 15 (14), 5887 (1987)
MEDLINE 87289053
PUBMED 3039467

REFERENCE
AUTHORS Laux, G., Perricaudet, M. and Farrell, P.J.
TITLE A spliced Epstein-Barr virus gene expressed in immortalized lymphocytes is created by circularization of the linear viral genome
EMBO J. 7 (3), 769-774 (1988)
MEDLINE 88283646
PUBMED 2840285

REFERENCE
AUTHORS Parker, B.D., Bankier, A., Satchwell, S., Barrell, B. and Farrell, P.J.
TITLE Sequence and transcription of Raji Epstein-Barr virus DNA spanning the B95-8 deletion region
Virology 179 (1), 339-346 (1990)
MEDLINE 91021036
PUBMED 2171209

REFERENCE
AUTHORS Hatfull, G.F., Barrell, B.G., Quinn, J. and McGeoch, D.
TITLE Unpublished
19

REFERENCE
AUTHORS Binne, U.K., Amann, W. and Farrell, P.J.
TITLE Induction of Epstein-Barr virus late promoters on small plasmids in the EBV late lytic cycle requires ori lyt

JOURNAL Unpublished
 REFERENCE 20 (bases 1 to 171823)
 AUTHORS Farrell,P.J.
 TITLE Direct Submission
 JOURNAL Submitted (01-AUG-2002) Farrell P., Ludwig Institute for Cancer Research, Imperial College School of Medicine, St. Mary's Campus, Norfolk Place London W2 1PG

COMMENT
 Construction: This sequence was assembled from B95-8 EBV [14] and Raji EBV [18] with sequence corrections [16, 19]. The number of major internal repeat units has been reduced from 11.6 [14] to a more typical 7.6 and the B95-8 deletion sequences have been restored to give a sequence more representative of wild type EBV.
 Numbering: Like the modified B95-8 sequence [14, 16] accession number V01555, this sequence starts 1 base to the left of the EcoRI site separating EcoRI Dhet from EcoRI I (ie the first A of AGAATTC.).
 Location/Qualifiers
 1..171823
 /organism="Human herpesvirus 4"
 /mol_type="genomic DNA"
 /strain="B95-8"
 /db_xref="taxon:10376"
 join(1..139223,151555..171823)
 /organism="Human herpesvirus 4"
 /mol_type="genomic DNA"
 /strain="B95-8"
 /db_xref="taxon:10376"
 139224..151554
 /organism="Human herpesvirus 4"
 /mol_type="genomic DNA"
 /strain="Raji"
 /db_xref="taxon:10376"
 join(166103..171823,1..16882)
 /gene="LMP2"
 join(166103..166458,58..272,360..458,540..788,871..951,1026..1196,1280..1495,1574..1680)
 /gene="LMP2"
 /codon_start=1
 /product="terminal protein LMP2A"
 /protein_id="CAD53382.1"
 /db_xref="GI:23893577"
 /translation="WGSLEWVPMGAGPPSPGDDPDGYDNGNNSQYPSAGSSGNTPTP
 PNDERESNEPPPEYEDPYNGNRHSDYQPLGQDOSLYLGQHDNDGPPPPYS
 PRDSSQHIYEAGSGSNPVCLPIVPIYFELMAIAASCTASVYVATGALS
 LLLAAVSVYAAORKLTPVTVAATPEATCTWRIDPPENSILFLAAGG
 LOGIVYVIMVLITAYRRNRRLVCCGIMFLACVYVLIYDAVQLSPUGAVYVS
 MTLILAVLWSSPFGIGTIGALITLAAALALASLILGTLNLTMLMLMTLV
 VLLICSSCSPLSKILARLELVALALLASALIASGSLIQTNKSLSTEFPLN
 FCMLLIYAGLITLITLITLWEGSGNRTGVPVEMCGILTMVAGAVMTVMSNTLLSA
 WLTAGFLILIFLIGFALFVIRRCRCYCYCLTLESERPPEYRNTV"
 58..272
 /gene="LMP2"
 /number=2
 join(59..272,360..458,540..788,871..951,1026..1196,
 1280..1495,1574..1680)
 /gene="LMP2"
 /codon_start=1
 /product="terminal protein LMP2B"
 /protein_id="CAD53383.1"

Query Match 0.1%; Score 22; DB 1; Length 171823;
 Best Local Similarity 100.0%; Pred. No. 0.45;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 48982 GGGGCTTTGTTATTAAAGCC 49003
 ||||||||||||||||||||
 DB 114652 GGGGCTTTGTTATTAAAGCC 114631

RESULT 14
 EBV/c EBV 172281 bp DNA circular VRL 20-SEP-1999

DEFINITION Epstein-Barr virus (EBV) genome, strain B95-8.
 ACCESSION V01555 J02070 K01729 K01730 V01554 X00498 X00499 X00784
 VERSION V01555.1 GI:59074
 KEYWORDS DNA polymerase: EBNA: genome; ribonucleotide reductase; tandem repeat; terminal repeat.
 SOURCE Human herpesvirus 4 (Epstein-Barr virus)
 ORGANISM Human herpesvirus 4
 Viruses: dsDNA viruses, no RNA stage; Herpesviridae; Gammaherpesvirinae; Lymphocryptovirus.
 1 (bases 1 to 172281)
 Arrand,J.R., Rymo,L., Walsh,J.E., Bjorck,E., Lindahl,T. and Griffin,B.E.
 Molecular cloning of the complete Epstein-Barr virus genome as a set of overlapping restriction endonuclease fragments
 Nucleic Acids Res. 9 (13), 2999-3014 (1981)
 MEDLINE 82014887
 PUBMED 6269068
 REFERENCE 2 (bases 1 to 172281)
 Kozak,M.
 Possible role of flanking nucleotides in recognition of the AUG initiator codon by eukaryotic ribosomes
 Nucleic Acids Res. 9 (20), 5233-5262 (1981)
 MEDLINE 82059504
 PUBMED 7301588
 REFERENCE 3 (bases 1 to 172281)
 Deininger,P.L., Bankier,A., Farrell,P., Baer,R. and Barrell,B.
 Sequence analysis and in vitro transcription of portions of the Epstein-Barr virus genome
 J. Cell. Biochem. 19 (3), 267-274 (1982)
 MEDLINE 83109311
 PUBMED 6296170
 REFERENCE 4 (bases 1 to 172281)
 Farrell,P.J., Deininger,P.L., Bankier,A. and Barrell,B.
 Homologous upstream sequences near Epstein-Barr virus promoters
 Proc. Natl. Acad. Sci. U.S.A. 80 (6), 1565-1569 (1983)
 JOURNAL 83169725
 MEDLINE 6300857
 REFERENCE 5 (bases 142687 to 159853)
 Bankier,A.T., Deininger,P.L., Farrell,P.J. and Barrell,B.G.
 Sequence analysis of the 17,166 base-pair EcoRI fragment C of B95-8 Epstein-Barr virus
 Mol. Biol. Med. 1 (1), 21-45 (1983)
 MEDLINE 85035713
 PUBMED 6092825
 REFERENCE 6 (bases 112620 to 125316)
 Seguin,C., Farrell,P.J. and Barrell,B.G.
 DNA sequence and transcription of the BamHI fragment B region of B95-8 Epstein-Barr virus
 Mol. Biol. Med. 1 (3), 369-392 (1983)
 JOURNAL 85060424
 MEDLINE 6094953
 PUBMED 6094953
 REFERENCE 7 (bases 45644 to 52450)
 Jeang,K.T. and Hayward,S.D.
 Organization of the Epstein-Barr virus DNA molecule. III. Location of the P3HR-1 deletion junction and characterization of the NotI repeat units that form part of the template for an abundant 12-O-tetradecanoylphorbol-13-acetate-induced mRNA transcript
 J. Virol. 48 (1), 135-148 (1983)
 JOURNAL 83294686
 MEDLINE 6310141
 PUBMED 6310141
 REFERENCE 8 (bases 159853 to 172281)
 Bankier,A.T., Deininger,P.L., Satchwell,S.C., Baer,R., Farrell,P.J. and Barrell,B.G.
 DNA sequence analysis of the EcoRI Dhet fragment of B95-8 Epstein-Barr virus containing the terminal repeat sequences
 Mol. Biol. Med. 1 (4), 425-445 (1983)
 JOURNAL 85060428
 MEDLINE 6094955
 PUBMED 6094955
 REFERENCE 9 (bases 1 to 172281)
 Farrell,P.J., Bankier,A., Seguin,C., Deininger,P. and Barrell,B.G.
 Latent and lytic cycle promoters of Epstein-Barr virus
 EMBO J. 2 (8), 1331-1338 (1983)
 JOURNAL 20331131
 MEDLINE

PUBMED 10872327
 REFERENCE 10 (bases 45415 to 52824)
 AUTHORS Jones,M.D., Foster,L., Sneezy,T. and Griffin,B.E.
 TITLE The EB virus genome in Daudi Burkitt's lymphoma cells has a deletion similar to that observed in a non-transforming strain (P3HR-1) of the virus
 JOURNAL 84207939
 MEDLINE EMBU J. 3 (4), 813-821 (1984)
 PUBMED 6327290
 REFERENCE 11 (bases 87650 to 92703)
 AUTHORS Biggin,M., Farrell,P.J. and Barrell,B.G.
 TITLE Transcription and DNA sequence of the BamHI L fragment of B95-8 Epstein-Barr virus
 JOURNAL 84236104
 MEDLINE EMBU J. 3 (5), 1083-1090 (1984)
 PUBMED 6203743
 REFERENCE 12 (bases 7315 to 9312)
 AUTHORS Yates,J., Warren,N., Reisman,D. and Sugden,B.
 TITLE A cis-acting element from the Epstein-Barr viral genome that permits stable replication of recombinant plasmids in latently infected cells
 JOURNAL 84222045
 MEDLINE Proc. Natl. Acad. Sci. U.S.A. 81 (12), 3806-3810 (1984)
 PUBMED 6328526
 REFERENCE 13 (bases 76089 to 79808)
 AUTHORS Gibson,T., Stockwell,P., Ginsburg,M. and Barrell,B.
 TITLE Homology between two EBV early genes and HSV ribonucleotide reductase and 38K genes
 JOURNAL 84247360
 MEDLINE Nucleic Acids Res. 12 (12), 5087-5099 (1984)
 PUBMED 6330697
 REFERENCE 14 (bases 1 to 172281)
 AUTHORS Baer,R.D., Bankier,A.T., Biggin,M.D., Deininger,P.L., Farrell,P.J., Gibson,J.J., Hatfull,G.F., Hudson,G.S., Satchwell,S.C., Seguin,C., Tufnell,P.S. and Barrell,B.G.
 TITLE DNA sequence and expression of the B95-8 Epstein-Barr virus genome
 JOURNAL 84270667
 MEDLINE Nature 310 (5974), 207-211 (1984)
 PUBMED 6087149
 REFERENCE 15 (bases 1 to 172281)
 AUTHORS Bodescot,M. and Perricaudet,M.
 TITLE Clustered alternative splice sites in Epstein-Barr virus RNAs
 JOURNAL 87289053
 MEDLINE Nucleic Acids Res. 15 (14), 5887 (1987)
 PUBMED 3039467
 REFERENCE 16 (bases 1 to 172281)
 AUTHORS Laux,G., Perricaudet,M. and Farrell,P.J.
 TITLE A spliced Epstein-Barr virus gene expressed in immortalized lymphocytes is created by circularization of the linear viral genome
 JOURNAL EMBU J. 7 (3), 769-774 (1988)
 MEDLINE 88283646
 PUBMED 2840285
 REFERENCE 17 (bases 1 to 172281)
 AUTHORS Hatfull,G.F., Barrell,B.G., Quinn,J. and McGeoch,D.
 TITLE Unpublished
 JOURNAL 18 (bases 1 to 172281)
 REFERENCE 18 (bases 1 to 172281)
 AUTHORS Farrell,P.J. and Barrell,B.G.
 TITLE Direct Submission
 JOURNAL Submitted (05-JUN-1984)
 REFERENCE 19 (bases 1 to 172281)
 AUTHORS Farrell,P.J.
 TITLE Direct Submission
 JOURNAL Submitted (18-MAR-1988) Farrell P., Ludwig Institute for Cancer Research, St. Mary's Hospital Medical School, Norfolk Place London W2 1PG
 COMMENT
 CDS
 Listed under this feature are all known protein coding regions as well as all the major open reading frames in the sequence. In general the term major is taken as the longest frame in a particular region taking into account the adjacent longest frames and likely transcription signals. Note that on this basis some long overlapping frames have been excluded and on the other hand some

small frames have been included which might represent exons or genes because they occur in a logical combination with other features or because of some other experimental data. The reading frames are named according to the Bam HI fragment in which they start. eg BALF3 is the third leftward frame starting in Bam HI fragment A. BORF1 is the first rightward frame in Bam HI fragment O. If there is an obvious TATA sequence followed by an in frame Met codon that satisfies the rules of Kozak [12] in that there is a purine at -3 and/or a G at +4 then the reading frame is numbered from the A of the ATG to the base preceding the termination codon. If there is no obvious initiation codon or there is a substantial reading frame in phase before the ATG then the reading frame is numbered from the first base of the first codon.
 SITES OF POLYA signals
 This feature lists all occurrences of the sequence AATAAA which is found normally approximately 20 bases upstream of the mRNA processing/polyA addition site. The rarely used homolog AATAA is only listed when it is found in a position close to the end of a major reading frame.
 SITES OF DONOR and ACCEPT sequences
 This is not a comprehensive listing of all such sequences and only the positions of a few have been noted because they occur in potentially interesting positions. The number quoted in the table is the position of the terminal base in the intron in each case. Restriction enzyme SITES.
 Only the positions of the sites Bam HI (BAM) are listed.
 RPT
 This feature is used to define repetitive sequences.
 SITE DEL
 This feature defines deletions in B95-8 with respect to other strains such as Raji and also to deletions in other strains such as P3HR1 and DAUDI with respect to B95-8.
 SITE HPM
 Denotes sequences with twofold symmetry ie could form hairpin loops. This is not a comprehensive list - only a few occurrences noted.
 ORGRL
 Denotes the region that encompasses an origin of replication (ori p). [13].
 NUMBERING
 The DNA sequence of B95-8 EBV has been revised [19]. The original (Baer et al, 1984) base 359 has been deleted so the new sequence around that position reads TCAGTCCTT. To avoid renumbering the entire sequence, position 1 has been moved 1 base to the left of the EcoRI site separating EcoRI Dhet from EcoRI I (ie the first A of AGAATTC).
 Location/Qualifiers
 1..172281
 /organism="Human herpesvirus 4"
 /mol_type="genomic DNA"
 /strain="B95-8"
 /db_xref="taxon:10376"
 58..272
 mRNA
 Query Match 0.1%; Score 22; DB 1; Length 172281;
 Best Local Similarity 100.0%; Pred. No. 0.45;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 48982 GGGGGCTTGTATTAAAGGCC 49003
 Db 126940 GGGGGCTTGTATTAAAGGCC 126919
 RESULT 15
 HS4B958RAJ/c 184113 bp DNA linear VRL 12-APR-1996
 LOCUS HS4B958RAJ
 DEFINITION Epstein-Barr virus, artifactual joining of B95-8 complete genome and the sequences from Raji of the large deletion found in B95-8.
 ACCESSION M80517 M75989
 VERSION M80517.1 GI:330330
 KEYWORDS
 SOURCE Human herpesvirus 4 (Epstein-Barr virus)
 ORGANISM Human herpesvirus 4

REFERENCE 1 (sites)
 Baer R.J., Bankier A.T., Biggin M.D., Deininger P.L., Farrell P.J., Gibson T.J., Hatfull G.F., Hudson G.S., Satchwell S.C., Seguin C., Tufnell P.S. and Barrall B.G.
 DNA sequence and expression of the B95-8 Epstein-Barr virus genome
 Nature 310 (5974), 207-211 (1984)

JOURNAL MEDLINE 84270667
 PUBMED 6087149
 REFERENCE 2 (sites)
 Parker B.D., Bankier A., Satchwell S., Barrall B. and Farrell P.J.
 Sequence and transcription of Raji Epstein-Barr virus DNA spanning the B95-8 deletion region
 Virology 179 (1), 339-346 (1990)

JOURNAL MEDLINE 91021036
 PUBMED 2171209
 REFERENCE 3 (sites)
 Sample J., Brooks L., Sample C., Young L., Rowe M., Gregory C., Rickinson A. and Kieff E.
 Restricted Epstein-Barr virus protein expression in Burkitt lymphoma is due to a different Epstein-Barr nuclear antigen 1 transcriptional initiation site
 Proc. Natl. Acad. Sci. U.S.A. 88 (14), 6343-6347 (1991)

JOURNAL MEDLINE 91296817
 PUBMED 1648738
 REFERENCE 4 (bases 1 to 184113)
 Jenson H.B.
 GenBank Curator Program
 Unpublished (1992)

JOURNAL COMMENT
 Original source text: Human herpesvirus 4 DNA.
 The B95-8 genome (V01555) has a large deletion in the right side of the genome which has been sequenced in Raji (M35547). These sequences have been joined to form an extended and more complete, although artifactual, EBV sequence.
 For features, refer to feature tables of V01555 and M35547.
 Location/Qualifiers
 1. 184113
 /organism="Human herpesvirus 4"
 /mol_type="genomic DNA"
 /db_xref="taxon:10376"
 1..152008
 /note="B95-8 sequences (corresponds to 1-152,008 of V01555)"
 152009..152012
 /note="Overlap of B95-8 and Raji sequences at B95-8 deletion point (corresponds to 152,009-152,012 in V01555, and 1-4 in M35547)"
 153013..163839
 /note="Raji sequences (corresponds to 5-11,831 of M35547)"
 163840..163843
 /note="Overlap of B95-8 and Raji sequences at B95-8 deletion point (corresponds to 152,009-152,012 of V01555, and 11,832-11,835 of M35547)"
 163844..184113
 /note="B95-8 sequences (corresponds to 152,013-172,282 of V01555)"

BASE COUNT 36002 a 55824 c 54622 g 37665 t
 ORIGIN

Query Match 0.1%; Score 22; DB 1; Length 184113;
 Best Local Similarity 100.0%; Pred. No. 0.45;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 48982 GGGGCTTTGTTATTAAGGCC 49003
 Db 126940 GGGGCTTTGTTATTAAGGCC 126919

RESULT 16
 AF198100
 LOCUS AF198100 288539 bp DNA linear VRL 31-MAR-2000
 DEFINITION Fowlpox virus, complete genome.

ACCESSION AF198100
 VERSION AF198100.1 GI:7271507
 KEYWORDS
 SOURCE Fowlpox virus
 ORGANISM Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae; Avipoxvirus.

REFERENCE 1 (bases 1 to 288539)
 Alfonso C.L., Tujanman E.R., Lu Z., Zsak L., Kutish G.F. and Rock D.L.
 The genome of fowlpox virus
 J. Virol. 74 (8), 3815-3831 (2000)

JOURNAL MEDLINE 20193820
 PUBMED 10729156
 REFERENCE 2 (bases 1 to 288539)
 Alfonso C.L., Tujanman E.R., Lu Z., Zsak L., Kutish G.F. and Rock D.L.
 Direct Submission
 Submitted (24-OCT-1999) Microbiology, Plum Island Animal Disease Center, U.S. Dept. Agriculture, Agricultural Research Service, P.O. Box 848, Greenport, NY 11944-0848, USA
 Location/Qualifiers
 1..288539
 /organism="Fowlpox virus"
 /mol_type="genomic DNA"
 /db_xref="taxon:10261"
 /country="USA: APHIS Center for Veterinary Biologics, Ames, Iowa"
 /note="Virulent FPV; Fowlpox Challenge Virus"
 1..9520
 /note="left end"
 complement(1874..2491)
 /gene="FPV001"
 complement(1874..2491)
 /gene="FPV001"
 /note="C-type lectin gene family protein identical to FPV260 (vaccinia A40R), similar to Rattus norvegicus GB:AF021330"
 /codon_start=1
 /product="ORF FPV001"
 /protein_id="AAFA4603.1"
 /db_xref="GI:7271757"
 /translation="MKNNYPREYKREKKKFLRDNSEYRIPTGLCLSVYITSCFLA ALFAVRDCKRDSFLEDTTATITSSATYTRNLYHCRDMITSHGILSTGER VGFROG10KCEKISDMIGKEEEMKALKNTGNDHSREFWNRAASTFDVNECA YGRSVSEVPKVLTPSCSVRRYLCKRTDNTSSPYNOYE"
 3367..4035
 /gene="FPV002"
 3367..4035
 /gene="FPV002"
 /note="Identical to FPV259 Fowlpox GB:A06621"
 /codon_start=1
 /product="ORF FPV002 hypothetical protein"
 /protein_id="AAFA4597.1"
 /db_xref="GI:7271751"
 /translation="WIVETINAMLLYPLCLIRCLNSVSPATCKCVHCLLYPEVCC ECMSETLDLSLHSCCYCCVPLLIIRFWRVVILPTLKATDCIRLPCLVLRCKRT ICPLAKSMCRGCEFLRCLFPCMLRMRGRGLTVREGAFAFDSDDPARRGF WNDWCEDLCVIMSPCCYVRCIRMTDPTFKIKFYWFIAPASPRMPEPSPLSRK VESS"
 complement(4500..4871)
 /gene="FPV003"
 complement(4500..4871)
 /gene="FPV003"
 /note="Identical to FPV258 Fowlpox PIR:C31685 (vaccinia A40R), similar to Homo sapiens SW:Q07108"
 /codon_start=1
 /product="ORF FPV003 C-type lectin gene family protein"
 /protein_id="AAFA4606.1"
 /db_xref="GI:7271760"
 /translation="MKSILITAMLLMDCANSLNCRGPTSYNNKCIWVNRDKNHKK KTVSEASTGCLITPMTGLIARSLIDNEKDKKFLSKGMOGLIIRDDKKREVGKCAV TDGKTFGSPCNATYGFYCID"
 5125..5430
 /gene="FPV004"

gene
 CDS
 gene

CDS 5125..5430
/gene="FPV004"
/note="identical to FPV257 Fowlpox GB:A06621"
/codon_start=1
/product="ORF FPV004 hypothetical protein"
/protein_id="AAFA4598.1"
/db_xref="GI:7271752"
/translation="MNDITFTLFCYKNNKRYRGSGRRRGKTGILLPHPIHRYIGT
SAHQCYKTRRISFKLYAAPRVHSTTRCGRSHAHVRDKSFESFOKVPDHCIAGSGA"
/complement(5221..5589)
/gene="FPV005"
complement(5221..5589)
/gene="FPV005"
/note="identical to FPV256 Fowlpox PIR:E31685"
/codon_start=1
/product="ORF FPV005 EFC gene family protein"
/protein_id="AAFA4604.1"
/db_xref="GI:7271758"
/translation="MALNLRVRPVRDQESGIRKLAASDPLENDHTGDCGVARAIR
ANNEFCRARIACAAGDTYKITYLLEGDELITSRVGSPFADSGVTRKNCVPEFETDS
SCFTLMCTSYNTVYVWME"
5931..7187
/gene="FPV006"
5931..7187
/note="identical to FPV255 Fowlpox SW:P14361 (vaccinia
C10L), similar to SW:P03296"
/codon_start=1
/product="ORF FPV006 C4L/C10L-like gene family protein"
/protein_id="AAFA4599.1"
/db_xref="GI:7271753"
/translation="MEFSGTGNNOLAVHRTETRTSKKELVNLGSLDNDIKNI
CDSKIFPEKRTTELSTDKRSKOIVFNSLNDLLKLAHLIYDELSTVVDVSATVE
NVTLLIMEKGFARHDEPSTVFSKNICVHLLLYLEQETGETVYIDNNTSVKL
KIDHLEPKTIEHESITVESGRKVALFDVLEKKTLSASANNVGSIEYLOKTNLVDRE
NDLOCYCDMVIERTEDKEYSLGMSIDSGRCISLHNSGIVRKRKEYSGEFDLICI
YMMNEVDLWGTGDKHIIIMSTIDKKTGTSFIPIDVLYEKLAISKKEKEDKIDRF
CNSRREYICCSYSKYFFDLPTKTDLHEVINSIDYTKSVGTPTDWTTLTIEVKQITLG
NNSYELFNIVKGNALAEEDNEYGCD"
7599..7817
/gene="FPV007"
7599..7817
/gene="FPV007"
/note="identical to FPV254 Fowlpox GB:D00295"
/codon_start=1
/product="ORF FPV007 hypothetical protein"
/protein_id="AAFA4600.1"
/db_xref="GI:7271754"
/translation="MYSVFTRIYKIRKNNKTEMILAIYDRNAYIVKKTGISILLRD
NCTRTMNIITIDTSSRNQWMLRVSVL"
7681..8184
/gene="FPV008"
7681..8184
/gene="FPV008"
/note="identical to FPV253 SW:P14370 (vaccinia A40R),
similar to Gallus gallus GB:AB015628"
/codon_start=1
/product="ORF FPV008 C-type lectin gene family protein"
/protein_id="AAFA4607.1"
/db_xref="GI:7271761"
/translation="MPLIKQVSEVSCAIVLGIILCLIFTLIVVWTKWYAFY
PSKVPDEMIGNSKCYFTINETNWNDSKRLCDVMSDLIFETILNFSRIRGKG
SYWIDINONRKIPGINSLSLYEAGVNDICLLFDNISIIEMSCIFHERITCAVEDRYTH
WYTEYMR"
8048..8248
/gene="FPV009"
8048..8248
/gene="FPV009"
/note="identical to FPV252 Fowlpox GB:D00295"
/codon_start=1
/product="ORF FPV009 hypothetical protein"
/protein_id="AAFA4601.1"
/db_xref="GI:7271755"

gene
CDS
/translation="MKNKALMIFVYIITRTVLSKCLVYFTFKREYVLKAKIDPTIGIPNTC
VRFYTSFLNSLIYLVNRSV"
complement(9123..10190)
/gene="FPV010"
complement(9123..10190)
/gene="FPV010"
/note="Fowlpox SW:P14369, similar to Homo sapiens
GB:AB006423"
/codon_start=1
/product="ORF FPV010 Serpin gene family protein"
/protein_id="AAFA4354.1"
/db_xref="GI:7271508"
/translation="MGSILVRLKELVPEKDCISPRGYTTLIMINIMIGCKRETBDKI
KULLIGFQWVPIPIPKSEYVEYDQDELINKSIMLIEGPIKRDFTNSYDIFNA
KVVSFTDDTISTINKWELSTRLKIDISLADDIRLAIINLVYFKSKWKYFPDTE
LTSKHPFKYNGCTDVAIDMTQDVAFYKHDEIDRSQVMALEDEYRKYRMFIIPDS
VYIGDGVDSLNNGKNINKIISKDDVLTKEIYLPKFELEDVVDLKDILHMGCDL
FKSGELVGSIDPKTRLRIGNIRKQSVIKVDEYGTFAASVSECTTGGIKKIPYKANVP
EMFLVADVOTKIPLELGRQG"
complement(10276..11112)
/gene="FPV011"
complement(10276..11112)
/gene="FPV011"
/note="similar to Bos taurus PIR:S32367"
/codon_start=1
/product="ORF FPV011 alpha-SMAP"
/protein_id="AAFA4355.1"
/db_xref="GI:7271509"
/translation="MOKIKLVSPFEKFLNFGPIETEEAGVSHANLFAVSQIEMEC
AGKAFKFGSDMLQKNKNSIAAASFVDAAANPKKIDSEYALNCLISAEVTELGKF
YTVARCHNIAIYENDITELDKAIFEHYNASGYGEGEYNKLSDDMLLIRLSIQK
EDFDRAKLTEDOVGNRMNTLSKTESRQILYALMCTICSDVSRAKNSLDYKIDIFP
AKDRKECKFEIKLIAACETKNIETFTSAIEBYDHGNTIDEALMSMLTIRAKTEDE
VA"
complement(12038..13033)
/gene="FPV012"
complement(12038..13033)
/gene="FPV012"
/note="similar to Homo sapiens SW:001485"
/codon_start=1
/product="ORF FPV012 Ankyrin repeat gene family protein"
/protein_id="AAFA4356.1"
/db_xref="GI:7271510"
/translation="MDTEMDGVNNDGYSILYKETAKNKKAVVELLYKGVNPTNRVD
STYPLHIAKGTGNIRKIRRLRYGANVDEKNDGYTALITACITDITCNVLDDEGA
NPNVYKGIPIPLVILISYRPTILKLMDRGANCNOIINIQVYITMEYINLDE
YKIPILINLVPIYIISFKASIVNIEGEMRNIAALAKNSRLLEVALKCKSEIAEMFTR
GIGDLSFEICILEDIKDIDHNSFPAFLDKLIEQSQNLRIYGYTNMKIIEEMRYREL
ICSAVRVNSCNLSINTWCILPLTGKNIILSKLNNDNIKKLILNDALIKVNNKTC"
complement(13708..13890)
/gene="FPV013"
complement(13708..13890)
CDS
Query Match 0.1%; Score 22; DB 1; Length 286539;
Best Local Similarity 100.0%; Pred. No. 0.47;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 47634 GTACGAGAAATAAAAAATACGA 47655
Db 41456 GTACGAGAAATAAAAAATACGA 41477
RESULT 17
LOCUS HSBHOHU 1242 bp DNA linear VRL 25-JAN-1995
DEFINITION Bovine herpesvirus 1 (clone p95) UL24 homologue gene, complete cds.
ACCESSION L39072
VERSION L39072.1 GI:633954
KEYWORDS
SOURCE Bovine herpesvirus 1
ORGANISM Bovine herpesvirus 1
Viruses: dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Varicellovirus.

REFERENCE 1 (bases 1 to 1242)
AUTHORS Whitbeck,J.C., Lawrence,W.C. and Bello,L.J.
TITLE Characterization of the bovine herpesvirus 1 homolog of the herpes simplex virus 1 UL24 open reading frame
JOURNAL virology 200 (1), 263-270 (1994)
MEDLINE 94174724
PUBMED 8128626
COMMENT Original source text: Bovine herpesvirus 1 (strain Colorado-1) DNA.
FEATURES
source location/Qualifiers
1..1242
/organism="Bovine herpesvirus 1"
/mol_type="genomic DNA"
/strain="Colorado-1"
/db_xref="taxon:10320"
/clone="p95"
92..95
/note="putative"
117..>1149
/note="putative"
117..267
/note="putative"
268..1149
/note="ORF initiated by the first ATG codon downstream of the experimentally determined 5' end of a 5.2-kb mRNA transcript synthesized in BHK-1 infected cells.; Homologue of HSV1 UL24; putative"
/codon_start=1
/protein_id="AA61544.1"
/db_xref="GI:633955"
/translation="MARDDRRLRAGTGRHFEALACDARAAGAKLPRLAQ LKGFAPVEYKOVGVSVSEFYNLDSRRDCCLRVAPAGARAVCLVELKTCF STNMNTPSKMDQRLGRLDLSARLVRLAPPPVLAFLVPSOSGMVLRVT RLPAQRTASNAARLEAIAGLAEYAFARARRSRGSRKRAEPPRRKQGPL PLATGKRAAATAATPRPADGPGPAEAGESGPRVSGSRHAGNSAGCAKADSGAACIG EISALFVAASGPRSGV"
BASE COUNT 170 a 430 c 457 g 185 t
ORIGIN
Query Match 0.1%; Score 21; DB 1; Length 1242;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 42218 GTGACGGCCTGCCGCCAG 42238
|||||
Db 742 GTGACGGCCTGCCGCCAG 762
RESULT 18
LOCUS ZYU60962 1902 bp DNA linear VRL 13-JUL-1996
DEFINITION Zucchini yellow mosaic polyprotein gene, cytoplasmic inclusion protein region, partial cds.
ACCESSION U60962.1
VERSION GI:1418245
KEYWORDS Zucchini yellow mosaic virus
SOURCE Zucchini yellow mosaic virus
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae; Potyvirus.
1 (bases 1 to 1902)
Lee,K.C., Wong,S.M., Mahan,I.P.H. and Chng,C.G.
REFERENCE
AUTHORS Direct Submission
TITLE Submitted (16-JUN-1996) School of Biological Sciences, National University of Singapore, Lower Kent Ridge Road, Singapore 119260, Singapore
FEATURES
source location/Qualifiers
1..1902
/organism="Zucchini yellow mosaic virus"
/mol_type="genomic DNA"
/strain="Singapore isolate"
/db_xref="taxon:12232"
<1..>1902
/note="cytoplasmic inclusion protein region; nucleotide binding motif, helicase function"

/codon_start=1
/product="polyprotein"
/protein_id="AB03777.1"
/db_xref="GI:1418246"
/translation="GLEIDENLEDDKRLRTIDPINTNEAOSTTTPVHEDMNRLO QNRTVPHRTGTGFELETRSTAYVANELASSSEGEFLVNGAVSGKSTSLPHLKK GKVLLEPRLPLENVSROLADGPFQNTVLRMRGLSCGSSNITVWTSGFARHYVN NPQMLEPFDVILDECHVDSATIAFNCALEKESFAGKLIKVSATPGRCDFOFA VKKTEDHLSPNFEVGAOKTGSNADWQHGNLILVAVSEVMDLSKLTREOFQSVT KUDGPRMOGKTTTETHTGSKPHFVATNTIENGVTIDECVDEGLVFAVLESEK RCVRIKRPVSTGERIORUGVRSGRGTALRIGHEKGENIPEPTAALSTRAY GLSVTHGVSTNNLGRCTYKQMCALNFELTPEFTHLRHDSMPRLHEELKQRL RSEENVLNKVALPHEQVSQWMDQSEYERIGVHCHSLRHDSMPRLHEELKQRL CIOENKNDALFGKLSAEPKSVSTLTSTDAALPRTIATIDHLAEEMKRNHFDMS SAVTGSFSLAGIADSEFRKRYMDHTAHHTAILAQARAQLLEFNNSNVNINNSDLEG IGVRKSVLQD"
BASE COUNT 580 a 373 c 448 g 501 t
ORIGIN
Query Match 0.1%; Score 21; DB 1; Length 1902;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 51263 AGCCAGTTCCTCGAATTCAC 51283
|||||
Db 165 AGCCAGTTCCTCGAATTCAC 185
RESULT 19
LOCUS AF014811 9606 bp RNA linear VRL 04-MAY-2001
DEFINITION Zucchini yellow mosaic polyprotein gene, complete cds.
ACCESSION AF014811
VERSION AF014811.2
KEYWORDS Zucchini yellow mosaic virus
SOURCE Zucchini yellow mosaic virus
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae; Potyvirus.
1 (bases 1 to 9606)
Lee,K.C. and Wong,S.M.
REFERENCE
AUTHORS Direct Submission
TITLE Submitted (17-JUL-1997) School of Biological Sciences, National University of Singapore, Lower Kent Ridge Road, Singapore 119260, Singapore
2 (bases 1 to 9606)
Lee,K.C. and Wong,S.M.
REFERENCE
AUTHORS Direct Submission
TITLE Submitted (04-MAY-2001) School of Biological Sciences, National University of Singapore, Lower Kent Ridge Road, Singapore 119260, Singapore
REMARK Sequence update by submitter
COMMENT On May 4, 2001 this sequence version replaced gi:2462848.
FEATURES
source location/Qualifiers
1..9606
/organism="Zucchini yellow mosaic virus"
/mol_type="genomic RNA"
/strain="Singapore"
/db_xref="taxon:12232"
1..143
144..9395
/codon_start=1
/product="polyprotein"
/protein_id="AA872004.2"
/db_xref="GI:13940782"
/translation="MAIMIGSISVPIISGAQATAPIGRNVIVAPGHMAICKPMR SHAYVYHASQKLSQSGRGIEVNSFNDPEDAFIRTRGMSKVKGPGRIILRP KARHVEVRIELESKEQKGFENGEDVTVTISIKVTTGKENDLAFSLRSPFYRT CKKEKRITRENTVCVDVNNILCERIKITRDKNIPETIGKRNNHTLTFKKFKSG VCGVSLAPERSQMKHYEMSGCPDYITQACRTSRKRVHVEDIDKCGSGVSTSHA LTQKYSRLPVLVTRGRDDGIVALEPVLFTSYVEHSTRONEVQFNGRKKMDKLP HSDHTCKVDHNNEGEMAVALSQALFPAVLKLSQVCRELSVSEFEDFLSRNF THESEWSTLRDGVHCDNVLKLINGAVOTONLKLSSDIMKLVONHTSTHKQIOTIDNK

[illegible]

/protein_id="AA61652.1"
 /db_xref="GI:7385024"
 /translation="MSPTGSENAVAASSTQTLARALYGDVLSWKHTPHGISLEIO
 LDVPRKILKPGMSOTRPTVTVRAVPMGSKTTLLEMLHAKADISVLVYSCRSFSP
 TLIOREKIDAGLSGFVYVITSETYIMGKRLLIOLSELRHSEASIDSVYDLIDSEVNS
 VTGQLSPTRRLSANDSLRLNRCSTIIMATVNSOFIDILSCREDENHTIV
 CTYAGVESGRTCTILDMGIDLVRVIRKSPHEDEVRTIQLGTEFDELALRLOGL
 HNICIFESSTLSFSELVAQFCALFTDSILINSTRPCLDNEMKHFRLVYTVTVVGL
 SPMAHSHMFEAYIKPMYSGPDWYVYSGRVLRLINLEVMVDGSRGCLFSP
 MLNFTIANKFMPPHTTOITNKLCCAFRORCANAFRSMTHLEFRKXHLFEBCSL
 WSLADSNITQTLASNOILVLDGMRPTIDVSPQCATIHLDRHANAASGMSRL
 RODNSCLTDFGSGFMADNITAFMEKYLMESTITEQIVAFALACIPQLPRLVNTA
 ILGACIRIPALAEFVFORIKYTHYASGMPVLDKTEFSIATITTPAPNLTTHLELR
 RCAYIANTLKMNSTEGCVQVLDITNLFNGDLSAQLIEVMRCNVTDAKIIIN
 RPWYRTGFLDGCHNOCFRIPTEKXENIALFRLIMQLFGARVTKSTQFPGSTARK
 NLKKDLETLLDSINDRSACRTYROLYNILMSHRSHFSOQRKITTAPANAHHYFPA
 HOHMLAPHAEMQLALSELSPGSMRPNCAVNFESI"
 5515..7830

CDS

/codon_start=1
 /product="ORF52"
 /protein_id="AA61653.1"
 /db_xref="GI:7385025"
 /translation="MDAQITLVRESGHICAASTYSWTSQGLTONGLSVLYLLCK
 NSGGKYPKRAEITVQOEDLCRYSRHGGSVSAFTFASICRAASAALDANPLELGA
 DWRKCLGTALATLRLVLRGKSEYSPVTFETDNTGLLTIIDPEHALNDNPTSTV
 LRANFPAIDVSAVSAACNAHQGSLAVARLTALKSNGDQOQTPDLVEYITPXYIR
 RKYKSTPPIERGGTSDLEERLVSNGRAIYVRLLPCYFDCLTDTSTVS
 LSLIATRLMYAAAFGKGVYRPIFAVLGPELNPNGEDRDYFCYVPGMTLRTLRQ
 AVESIRATENMETDGLMPVGTGAHYIAPMGQHPPLPRQDILGQIPDGTGAD
 ATYMSDGRISTVFKOPVQDQRMNAFDFAFPTIYCAEPFMRFLGKIVLARMR
 GMGCLPALVSFEGGLRHLIPSYIKALIFIANELSLCEQTALEOGFALICTYIKDGM
 GIFDLHTRWVCSQDARCSALINLAACEAVTGLLRLOLINTFPAMEPVLRYEGVT
 HATFCTTGSMLMNLQITPPDLVGPWRSQAADLERKSLGCTCAKTIKRELOENC
 IMRVLYDIMAGOVVEARVYKTYVDFEHHVDRRTPYVSLQEOINSFTKAIIPASYLENC
 GHQDKRYKPROIIMVNRNPHCPPTVYVWELLPLSCACIPIIDCAHLKRLIHTFVIT
 INHLDAHNDSPSPLFTDPLASYNLEFL"
 complement(7877..8872)

CDS

/codon_start=1
 /product="ORF53"
 /protein_id="AA61654.1"
 /db_xref="GI:7385026"
 /translation="MORIRPYWKFEOTGGAGMADGNSINIPSLCCSVTIDNLTNR
 AEGGLDVSDVIEDLRQAIREFVCEAREVGLKPRFLANSVSLRVKREHQETLVVL
 NGDSSEVCDRYMECVTQPAFRGIFSVLTAVEDRYTVGVPRLILYRMTLERPN
 NLDETTLCVILMYLEGLIGSPGASPSLIFOLSVYLRVCOIGPLEKMRRLYEGVWML
 NLTMYVVDNNPRTKRYLPHYMYFKLLNPQGTAPNIIKAIYSCGSGORDLPHGTPP
 CPGGVQVPGCLNGPLRDSXOKSVYFMNLNRTMVTPKNVOLFETKYNSPRVYK"
 complement(8697..11006)

CDS

/codon_start=1
 /product="ORF54"
 /protein_id="AA61655.1"
 /db_xref="GI:7385027"
 /translation="MAEITSLFNNSSGSEKRIASVSIQGLNGSNPNQYKRMEDT
 YWNEAPDIGCTFPEEDGMWLIHPTTQSMFLRLIGDFGYTDGQISYVSRSTEV
 IROYQATVNLNADATRYEDLAADWEMHIQCNLHAGALAEYGLCGESAVRLEAHQY
 FETMRQTLQSSLLEFLRGITGLTSGINGRVFAKVDWIAACGIYVVRKVSSEON
 GTPAPLNTYGOAAELSQMLKADATLARGAAVYTSLECCONAVAIMDYBRTRLYYV
 NBRILMAKDDVYGMKGECLVMPVMPGEGVPSPLORISGEVLACIYALREAHQVQ
 VLNTAPLRVLIGRNEEDRSHSTRANDRINGENDTPAGSASRLVLYLNKMRAY
 GDITETVRSYLEETGNHILGSGSVDTSQPGFKANOSFNGANGSGTTNVAQAKTSYV
 VNSINGLMEGVVNLFTKIEGLKVDNSDLTERLOFKGELKRLKEERVKIKPSGSHI
 TMAETRIADLNHEVIDLTGIIIGDDAYIANSFQRYTPPGDKIKRLSELMQCLVLC
 FKLRVNNNGOEISYSNASSILVAIYAFSLRATRLGFLVTOSEVHRSEELQ
 AIFRKARTESYLSQIRILYEMOVARAYIKRGPRTPSPSGLDPTDDEDRIPENKI
 NNOYMHYKKNLSIFMKGHPERILRVAKVNAADSTLLDKIRANRRDGDGRDVRANKIT
 QHRQLQNDRLQTLNSTRGVGERDRRS"
 11018..13663

CDS

/codon_start=1
 /product="ORF55"
 /protein_id="AA61656.1"
 /db_xref="GI:7385028"
 /translation="MKRSISVDSSSPKNVNPETPNCFDSDVYLNFTSMHSIOPILSR
 IRELAAITIKERVPRLCWFKOLLELOAPEPMONELPFSVYLISGNAGSGKSTCIOT

CDS

CDS

CDS

CDS

CDS

CDS

LNBAIDCIITGSTRVAANQVNAHKLSTAYASRPINTJTFHEFGFNGNIIQOLGRAYNM
 TTTPESIEDLQKRIYVYWEVLIDITRVRQMGDDGSGTSTRTTMAIERLANKPTG
 SMGCIATACGSLPAPFRSNVYIDEDEGLLGRHLTFVYVCMMLNLIYOSPOVINR
 KPVYVQSGPTDLSLESHPODMORSHVPSNELLVLYIICNOLTRQYTNISHWAF
 INKRCOEDDEPDLKLTLEBGLPPTTEHAALVDTPFVYPASVINNAPLPWRTILYSSH
 KEVASYKSLHAHLKLSKNDHFSVFALEPTVTRILVAFDERKLTGQPGUSVEWIRIA
 NSGRILNYSOSRBDMGTVARETHSNBDLIVARDITYVINTLVVTTRLRLKLTGFS
 GTFOSFAKVRDSEYKARETSEIYVRELNLIEGGLINTFYFLNKLRLHPKVSL
 AYKRLALTLELSELDKPTLAEAAVYAGACAGIDCCADASADACFCTKARESVVA
 SIPEDDPVTFTLNDENVIDLVCQVEFSYKSSNEVHAQFLMKAIYDDRIVLIAL
 FESSFTAPPSAYVDNVPNGSELLINVGGLSLALQTDITTLTLCOTRAPVPE
 ELTKKLYRRETEMLYALHVLAMLDQOHRFVSTVNAWCEFTESIDAEELAMATVD
 YGLSSKLAMTARSGSLKVALICFPADKRLNYSVVAASRYVSSRFLKMNINPLAE
 RYERSAEISHHIILALDRDPVHHVY"
 13590..14321

/codon_start=1
 /product="ORF56"
 /protein_id="AA61657.1"
 /db_xref="GI:7385029"

/translation="MKNPOKLAITFLELVYIPYVTLICIKALKYNTNAGLJFSLGFLV
 NTPMVISGPPTEFIIYRLGVRRLVHMTLPDHOQTLYAFGGRSMAVNTDADCTM
 SGMIVLOHHTVTLTLTDCSTDESSVAFTHRDPHODKPHAFAMFPMWGSDDPS
 QLSNVGCVLSVITIEDLSMCISIVYIGLVRNRPDDOTTPPTPHOTTQSRQOETNC
 PSQPAPFTSDDDVLSILNDANA"
 complement(14430..14645)

/codon_start=1
 /product="ORF57"
 /protein_id="AA61658.1"
 /db_xref="GI:7385030"

/translation="MDVREKRVFGNASVATPGEHQKFVRELLISGHNNAVLYQTYGKW
 SDCKHGRKSVYNTGEARHPCKAHQ"
 complement(14626..15291)

/codon_start=1
 /product="ORF58"
 /protein_id="AA61659.1"
 /db_xref="GI:7385031"

/translation="MPSLPPSVPTALLQWGLHHRGCSIPNFKQVASHSVQTDPT
 ENSVDANENPPIGHACIEKTKDQVYFDTLFWYSIDELGRQLTQITIRSLIMNC
 EITVACRTKTAFGSGVSRQKHVTLSSKNKPNSSKSLQWELGRLQKHAPVRLIWE
 SIRARRRVRVYTRSTDCKSRPLVVFYEETALDRVLHKNENTLITDPIINTENGCHR
 TRT"
 complement(15321..16238)

/codon_start=1
 /product="ORF59"
 /protein_id="AA61660.1"
 /db_xref="GI:7385032"

/translation="MDVSGEPTVCSNAYANEMKLSKSDIYVLAHPYTKTKRRPRP
 PLGVKLDPPFKLNNMSHHYDTEFTFVSQSDSVSEVFSFNFISPEYDILSDLKEP
 YAKGIFLEYNRLNSGELILESTGDIAMWRFQCSOIRVITIGDDYPTAGAHGLA
 FSVKRGITPPSSILKNIPALMESYPNMTPTPHGCLSEMARQVLLMTTLTVRGGTPG
 SHVILGWRVLOVRLORLCENRGTLVEMLGNCAHOKTTPQNSRCHLVLTNAHPSPLSR
 VPRNCHHFOANRYFTRKGEPEIDMSVI"
 complement(16189..16671)

/codon_start=1
 /product="ORF60"
 /protein_id="AA61661.1"
 /db_xref="GI:7385033"

/translation="MASHKMLQWIVFLKTTITTAAYCLHIDDPPLFGAPLSDVSLI
 ITEPCVSYEAMDYAAPVNSLSEALSIGVYKRCYPEVILTFKPKOMAYTRNPVY
 TLKGLTOSVEEHRSGDIRQALDLALSGVWVDSIPSSNTINPENCVGADRLFORVCO
 complement(18216..19619)

Query Match
Best Local Similarity 100.0%; Pred. No. 1; 5;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

0.1%; Score 21; DB 1; Length 34718;
complement(20342..24274)

CDS
LEHTGDRVRCITIDLTSESDACKGSKTRKVAASPOGESNTPTSGTSGSLKHLTK
SSAGKAGKGIPIKMKKS"

61676 CATAGTATGCGTGGTGGCC 61696
11854 CATAGTATGCGTGGTGGCC 11874

RESULT 21
BHTUL/c 37000 bp DNA linear VRL 14-AUG-1996
DEFINITION Bovine herpesvirus type 1 UL22-35 genes.
ACCESSION 278205
VERSION 278205.1 GI:1491620
KEYWORDS capsid protein; DNA binding protein; DNA polymerase; envelope protein; glycoprotein B; glycoprotein H; proteinase; scaffold protein; tegument protein; thymidine kinase; UL22; UL23; UL24; UL25; UL26; UL26.5; UL27; UL28; UL29; UL30; UL31; UL32; UL33; UL34; UL35; UL36.

SOURCE
ORGANISM Bovine herpesvirus 1
VIRUSES; dsDNA viruses, no RNA stage; Herpesviridae; Alphaherpesvirinae; Varicelloviruses.
1 (bases 24211 to 27636)
Whitbeck,J.C., Bello,L.J. and Lawrence,W.C.
Comparison of the bovine herpesvirus 1 gI gene and the herpes simplex virus type 1 gB gene
J. Virol. 62 (9), 3319-3327 (1988)
88300884
2841484

JOURNAL MEDLINE 2 (bases 24215 to 27793)
PUBMED 2 (bases 24215 to 27793)
REFERENCE Misra,V., Nelson,R. and Smith,M.
Autors TITLE Sequence of a bovine herpesvirus type-1 glycoprotein gene that is homologous to the herpes simplex gene for the glycoprotein gB
JOURNAL Virology 166 (2), 542-549 (1988)
MEDLINE 89020821
PUBMED 2845660

JOURNAL MEDLINE 3 (bases 33521 to 36452)
PUBMED 3 (bases 33521 to 36452)
REFERENCE Meyer,A.L., Petrovskis,E.A., Dufus,W.P., Thomsen,D.R. and
Autors TITLE Cloning and sequence of an infectious bovine rhinotracheitis virus (BHV-1) gene homologous to glycoprotein H of herpes simplex virus
Biochim. Biophys. Acta 1090 (2), 267-269 (1991)
JOURNAL MEDLINE 92031707
PUBMED 1657187

JOURNAL MEDLINE 4 (bases 32460 to 33539)
PUBMED 4 (bases 32460 to 33539)
REFERENCE Bello,L.J., Whitbeck,J.C. and Lawrence,W.C.
Autors TITLE Sequence and transcript analysis of the bovine herpesvirus 1 thymidine kinase locus
Virology 189 (2), 407-414 (1992)
JOURNAL MEDLINE 92351539
PUBMED 1322582

JOURNAL MEDLINE 5 (bases 31487 to 32728)
PUBMED 5 (bases 31487 to 32728)
REFERENCE Whitbeck,J.C., Lawrence,W.C. and Bello,L.J.
Autors TITLE Characterization of the bovine herpesvirus 1 homolog of the herpes simplex virus 1 UL24 open reading frame
Virology 200 (1), 263-270 (1994)
JOURNAL MEDLINE 94174724
PUBMED 8128626

JOURNAL MEDLINE 6 (bases 36100 to 37000)
PUBMED 6 (bases 36100 to 37000)
REFERENCE Vleck,C., Benes,V., Lu,Z., Kutish,G.F., Paces,V., Rock,D.,
Autors TITLE Leitchworth,G.J. and Schryver,M.
Nucleotide sequence analysis of a 30-kb region of the bovine herpesvirus 1 genome which exhibits a colinear gene arrangement with the UL21 to UL4 genes of herpes simplex virus
Virology 210 (1), 100-108 (1995)
JOURNAL MEDLINE 95313343
PUBMED 7793062

REFERENCE 7 (bases 27788 to 29695)
Autors Haanes,E.J., Thomsen,D.R., Martin,S., Homa,F.L. and Lowery,D.E.
TITLE The bovine herpesvirus 1 maturational proteinase and scaffold proteins can substitute for the homologous herpes simplex virus type 1 proteins in the formation of hybrid type B capsids
JOURNAL J. Virol. 69 (11), 7375-7379 (1995)
MEDLINE 96013856
PUBMED 7474173

REFERENCE 8 (bases 1 to 644)
Autors Schryver,M., Styger,D., Vogt,B., Lowery,D.E., Simard,C., Lablasiere,S., Misra,V., Vleck,C. and Paces,V.
TITLE Gene contents in a 31-kb segment at the left genome end of bovine herpesvirus-1
Vel. Microbiol. (1996) In press
JOURNAL 9 (bases 1 to 37000)
REFERENCE Schryver,M., Vleck,C., Lowery,D.E., Bello,L.J., Meyer,G., Misra,V.,
Autors TITLE Thiry,E. and Paces,V.
Gene contents in a 37-kb segment centered in the UL part of the bovine herpesvirus 1 genome
Unpublished
10 (bases 1 to 37000)
REFERENCE Schryver,M.
Autors TITLE Direct Submission
Submitted (13-AUG-1996) Martin Schryver, Institute of Virology, Faculty of Veterinary, Medicine, University of Zurich, Winterthurerstr. 266a, Zurich, CH-8057, Switzerland
Location/Qualifiers
1..37000
/organism="Bovine herpesvirus 1"
/mol.type="genomic DNA"
/strain="Cooper"
/db_xref="taxon:10320"
/clone="HindIII fragments E (partial), G, and A (partial)"
2..7
/note="Psi site located at base 30802..30807 from left genome end"
108..9851
/note="very large tegument protein"
/codon.start=1
/product="UL36"
/protein_id="CAB01605.1"
/db_xref="GI:1491621"
/db_xref="SPTREMBL:065553"
/translation="MARPARVAPRGGEARAGAGGLINGNAARVPSTVEQSGTMSGVAGARPATADVAAVAFNRQYDIAIPGSAVACLSLSFLARAGVGDAAIGADAIDALAGAMARESGARPEMCSIHLPNITDQAGSGSLCCFSSVYEGCFYTPPAEHALSTOYVAREVDVAVMQPRTSLALYVGMGVGFAGDVAVYLFDFHGSGLVGPAPFAARMPPALYVYALIRACGQESRMAGLVHFEVSAGPEPARBELRAVSAIYGASETYLDDEPVYRRVSVHPRAPANTCTITVAVGAGAGEDEPTPARPSPALIPAEVYAMPPOITAAANAARAAGKRTSIPRRRARWTPPSSREDIRAAARAARAKPPRKVRGAETAGGEDMGEENANAARPPALGANAARAHATACAAELGARAAEVTRALDAAVAAHAIADADACVAAVAVARPPRAAERDLHAHAGLEFRVLAFLVONGARTRHDAVSAPLEISGVAALPOHTPASAFITSSGMVLEJLAATYTRISEMAROPSSALGLADAKRLRVAAVAADVDRDLDAVDELGEVDGAGAGPLECGAVSARFMRASAGRIPEKRALRDRGSRPLDARVRLFEERARERARVAFETALARETILALGTYRAAERTDAVPPDDPRVAPDSAVADLAETLAGAAVYVARSAAALSELDMALAEALROYFLRGAOYSARAILADRGGERFRVSAVAAPVLRLAGSAVDLAARVARGAAPPLRSARKKELRLDLAAGATHTEDGLAAWVALHEAQAGEAAKKEIDAVLSDVAALNGRSASRASILEASAREFAMSAARAAGAAAGAAAGAGAEADAEAVLGAEDVLRDLALATGAADREARVAAARAGLEAOALARRARVLELGEERAEALYORGLDLLPLDGLFRAAGCALERLCADGACOSAECAFEIOEAPRVAGVODRMOFGFYREALENPSALAFGALAGCPAFPAVLTGTAQANGPARAFEBGBHARVANAARAARAPAAVAVAAAASALREBAELRAGGAHVPEFALDAQVYARREAOAGARRALAAALAAVBAASGALASASALKNMTAGADAAETTTAAADAADALGAEEVLRADAEVAAGGEDADGEDASEADAGDAPAGRLGPOAKLHADLRKARALARRAEVRLRAEAERBAEGAAAROEEREMEDRALREVENASATDAEELARAAAARGDPPRLROADRALESASORATRAITAVLAFNPHPAEKATIDVPPPLAOLRGIAWMDSALAPLSALFPADVGOITRLMHATGLTFPAASGGSEPRYDVTYLLSGDLAVPPLAKTVAFYTRGHAAFEEERARLIGLRADVLOAGAGRAELISRARGVNLRPASRRALAEAGVRELPSBALASALAOLEERDFHAFAGSAVEAOELSTVRRDAAARALAAARAEASATARERILGEVVAEABARDEBAGLANLKNLIRTPPPAALGPDALDRGMEPARIDALRELTAAALLAAVEAPRLDVAAYEWMLOARSIIDSHTLRIDRDRGMEPARIDALRELTAAALLLRQIESAAAAMWDGAWELFVAARRRAASREDHGCARAAALDAAGACVYGLRADHEH

YLRPAEFTGALDRALRERDGLAFHEAARADAGLQRIQATLAAVGEAAVEGLRA
 LLAADFQVAELPMAAQAARFRLDLVLRRLYEAYKLPVRAAARGAANAAR
 AAATVSHRADPATARARARALCERDLHGRVAALCTREADESIDALA
 PRATLADAGTLCYRCYRAVGDKLAVLGSOVGSMRPLDESGVAAVAANVL
 NEIYNLRLEIRARDADGACFRYRHRARMGLADVSAALAEYAGLATTLPRRHG
 VASIGALCFSLAERGLRPARAPASGPASGGALDELTPADLVAAIMKGFHMLVETR
 LDIVQKDEYCKTLDGLVLEALTSKVAANSIAPGPGARRPVLEGADDPADGALFA
 IRAADWDAGRLSPSDVLAWMHAPDAATRAVAELARIPGALTTISVLRMCIPEG
 LLAAIMTTLAVDSIGAOTQSYDAFLARLDLPSTYHARLIGSGSEDAALAAAAAAGR
 PALCFPTSSVPTLTVRQPSSEVOTVNAITVTCALLIGAVVAMEPDVSESRIL
 IMCLRTPTRGGDADAPAVSSDLNWSGRLLALDENITENMCTIROLQSLTLTA
 SKPLRSAPCLIMDLTLQALVLMARAAAPLAWLKTAEDVDLDELSTLDYEDAL
 PPAASAADPLETHIISENNVPFAAASGDPYAHPPVQHATDMLFPAARAAGGSG
 NRVANARVAANAARPPAPASAPAPALAPASAEALWGERARLTTRTGPBKMPA
 HDADAP
 ALPMRRPPAPASVAPPPPPRLPPAPPLPPAPPLPPAPPLPPAPPLPPAPPLPPAP
 LPPAPPLPPAPSTAPVAPAPPLPPATPLTAPPTAPPTAPPTAPPTAPPTAPPTAP
 EVAPAPPLPAPPTAPPTAPPTAPPLPPAPPGAMGALSATRPTRRAGAKSLPAPV
 RQDLRSPASVAPSGSELVPPSGALGSPSPSPSPSPLEVPGLPLPPSPVQA
 PVDAP
 PATAVOSGSKIPASNALVGVAPALLRGPSPCKPGAPAPAPPTGANTARKNTAVD
 PTVIGSGSALSGSAEDADFGAGVAPPGAPAPLAAPAPASLPPAPRLAPAPAS
 LPAPPIAPPIAPPIAPPIAPPIAPPIAPPIAPPIAPPIAPPIAPPIAPPIAPPIAP
 PPIAP
 SRGNLHTQDILLASAEARICELPAPKPYLGADSDATSDLSGSGPTEETEAEAGGD
 GPGODAPKARVVPANSLIKROYLRGTGTSIVLALLILEACEIARLRRLATRDVLRQAAE
 VTADIFARLLLG"

misc_feature 639..644
 /note="EcoRI site in HindIII E fragment"

repeat_region 7697..7777

repeat_region 8609..8770

repeat_region 9110..9115

misc_feature 9110..9115

repeat_region 9120..9227

repeat_region 9928..9933

polyA_signal 9928..9933

polyA_signal 9928..9933

CDS 9928..9933

CDS 9928..9933

CDS 9928..9933

CDS 9928..9933

CDS 9928..9933

CDS 9928..9933

CDS 9928..9933

CDS 9928..9933

CDS 9928..9933

CDS 9928..9933

CDS 9928..9933

CDS 9928..9933

CDS 9928..9933

CDS 9928..9933

CDS 9928..9933

CDS 9928..9933

CDS 9928..9933

CDS 9928..9933

QY 42218 GTGACCGCGTCGCCGCCAG 42238

DB 31987 GTGACCGCGTCGCCGCCAG 31967

RESULT 22

HSSEND

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

KEYWORDS

KEYWORDS

KEYWORDS

KEYWORDS

KEYWORDS

KEYWORDS

KEYWORDS

KEYWORDS

KEYWORDS

KEYWORDS

KEYWORDS

KEYWORDS

KEYWORDS

KEYWORDS

KEYWORDS

KEYWORDS

KEYWORDS

KEYWORDS

KEYWORDS

KEYWORDS

KEYWORDS

KEYWORDS

KEYWORDS

KEYWORDS

KEYWORDS

KEYWORDS

KEYWORDS

KEYWORDS

KEYWORDS

KEYWORDS

KEYWORDS

KEYWORDS

KEYWORDS

KEYWORDS

KEYWORDS

KEYWORDS

KEYWORDS

KEYWORDS

KEYWORDS

KEYWORDS

112930 bp DNA linear VRL 25-OCT-2002

complete genome.

alkaline exonuclease; complement control protein homologue;

complete genome; cyclin homologue; DHFR gene; dihydrofolate

reductase; DNA polymerase; dihydropyrimidinase; G protein-coupled receptor

homologue; glycoprotein; glycoprotein B; glycoprotein H; helicase;

HVS R transactivator; IE-G gene; integral membrane protein; major

capsid protein; major ssDNA-binding protein; mCpH gene;

ribonucleotide reductase, large subunit; ribonucleotide reductase,

small subunit; salm1r1 transformation-associated protein; scCPH

gene; STP-A11 gene; thymidine kinase; thymidylate synthase; TK

gene; transport protein; tyrosine-specific protein kinase; uracil

DNA glucosidase.

Salm1r1 herpesvirus 2

Salm1r1 herpesvirus 2

Viruses; dsDNA viruses, no RNA stage; Herpesviridae;

Gammaherpesvirinae; Rhadinovirus.

1 (bases 1 to 112930)

Albrecht, J.C., Nicholas, J., Biller, D., Cameron, K.R., Biesinger, B.,

Newman, C., Wiltmann, S., Craxton, M.A., Coleman, H., Fleckenstein, B.

and Honess, R.W.

Primary structure of the herpesvirus salm1r1 genome

J. Virol. 66 (8), 5047-5058 (1992)

92333688

1321287

2 (bases 1 to 112930)

Albrecht, J.

Direct Submission

Submitted (31-JAN-1992) J. Albrecht, Inst. fuer Klinische und

Molekulare Virologie, Friedrich-Alexander Uni, Loeschgstrasse 7,

D-8520 Erlangen, FRG

Location/Qualifiers

1..112930

/organism="Salm1r1 herpesvirus 2"

/mol_type="genomic DNA"

/db_xref="taxon:10381"

complement(220..714)

/gene="STP-A11"

complement(220..714)

/gene="STP-A11"

/note="ORF 01"

/codon_start=1

/evidence="experimental"

product="salm1r1 transformation-associated protein"

/protein_id="CAA45623.1"

/db_xref="GI:60321"

/db_xref="SWISS-PROT:P18347"

/translation="MARLGGDDPDENSGDPHPNTERSDGDPPTPLPVLN

ACRGRPYKCLGHRPQESGCRPTLSAVGLPTSGSSSHLSPTVGLSAVRV

SGCGAGSEEHYAEVGSLSHSEHDEGKCTDCSVTILLVITLVLLITIGLMIVM

FKKM"

complement(3969..4532)

/gene="DHFR"

complement(3969..4532)

/gene="DHFR"

/note="ORF 02"

/codon_start=1

/product="dihydrofolate reductase"

/protein_id="CAA45624.1"

/db_xref="GI:60322"

/db_xref="SWISS-PROT:P09503"

/translation="MVQALNCIVAAVQNMKGKQGNLMPRLMDFKPRKRTTSSV

PKQNLVIMGRKTFWSPDKNPRLKGRINVLKSKELKPLPRAHFLAKSLDALKLTE

Query Match 0.1%: Score 21: DB 1: Length 37000;

Best Local Similarity 100.0%: Pred. No. 1.5:

Matches 21: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

CDS
 /note="ORF 03
 similarity to ORF 75 and EBV BNRF1"
 /codon_start=1
 /protein_id="CA45625.1"
 /db_xref="GI:60323"
 /translation="MLVHNLAEQILPHERLATSVLEHGLQVTSNPRTTTCV
 VVNSPNASLEPLVSKTLOSVPKLPFEPCSTQSFSGPHLOGSOTFSDVDV
 VKNLSMTEPOGPENAFVETVETVETVETVETVETVETVETVETVETVETV
 VTPQDRLEMDVDASAVSAPLSDPLMTNKLNLGTSOYVFKRCAAKVVE
 KNSRLAISNIDVNPWSSTNMLYDLHALEKLIYSFGSETPSLTSVNNAAOHV
 VPMFSACQIGHVWQILQTHLSTLGLSPKMLQAHNLKCSSMHIQGFLLVPRD
 LSHILPQRTIYNGLISTSLQITNNANEHPLODKTYIOLGNEFYHKOGLCOGSG
 KEIGSILTALAFIDSVKTYPGTIVGMSTSLPVASKAKLAACVQOQGRILVSLP
 POYVATLPPSPNSRVENKMLKQVFPNLTSLDIIAIXNNITDAOALKATCYAAC
 RKKIGLLHLKTEVYDNTVERPPIILFRDRKPKFPLSSFTSTTFLEERLMDOL
 NLKDTILKLEHPSVCKEFTVNHDKLISGRVARTSVGMQLPVSDYSILVPMHC
 TEEVENPMDYEDTIDSHQVEEAAVAGISAGESTILTQADLVGTIRATTEAL
 NLSMWPNNIGNVILDSITLPTAHVSTLQVMEATKFCALRVSCFTANAEH
 GASIVASAIYNTLDVSKCTIPDLKFNNSFLITTEKDYSLFGVAOQILEKTEIEI
 PSATSPVLMKKMLSVLOTLIKDSVYSGHVSQGLVATYAAEMALSQGGKVRVYHG
 EDAIKFICSTPGVYIEVQSKRTYVOQFLHSENNIQLIGESTSLITSISQNLRL
 VHEPDLFESAMRSFSDACPCQIHPRPTRMQIATVPKCPVPCSRHHVIVLLNN
 SVPHGLNLAIEAGFQPRVLVSIHQPSKTNVYDPHTWGFYIGASNVODEDYGML
 IAOIKSHVAFORDLTMLAKPDVFSVAILGACELFYNAIGNKPSPDIYMTGVNS
 SRKFSERMSVITPESTKAIAFOSLKNLPCWTOGHLKFKPKMLMEESGVNS
 SMFGYSLSSGPAONPLPINCENYAGVCSADGRHALLHDPCLNNLMOWVYLE
 NPPLKYSPPKTMELDKMGITVQASAPPSRSDPLRSFV"
 join(10912..11773,11774..11966,11967..12013)
 gene
 /gene="sccPH"
 join(10912..11773,11967..12013)
 CDS
 /gene="sccPH"
 /note="ORF 04b"
 /codon_start=1
 /evidence=experimental
 /product="complement control protein homologue"
 /protein_id="CA45627.1"
 /db_xref="GI:60325"
 /translation="MYTLHYICLVSCVYFWTLSCPTRNQVSVKYVNLNYSQPY
 PNGTILHYTCRBYAKRPVQYVTCVNGNNTVPRCKCKKCKSTPDLINGRTVGMILY
 YGSVITTCNSGYSILGSTTSACLKRGGRVMTPPPICDTRKCKPPQIANGTHTN
 VKDFYITLDVYVSCNDETKRLITGSSKICSETGSMVNGETKCEFIICKLPQVANA
 YVEVRKATSMQYLHINVKCYGFMLYGETPNCNHWSPAIPECKMISSPGDMRG
 INSNEENSTPSCGECACPGSNYPIS"
 10912..11964
 gene
 /gene="mccPH"
 10912..11994
 CDS
 /gene="mccPH"
 /note="ORF 04a"
 /codon_start=1
 /evidence=experimental
 /product="complement control protein homologue"
 /protein_id="CA45626.1"
 /db_xref="GI:60324"
 /translation="MYTLHYICLVSCVYFWTLSCPTRNQVSVKYVNLNYSQPY
 PNGTILHYTCRBYAKRPVQYVTCVNGNNTVPRCKCKKCKSTPDLINGRTVGMILY
 YGSVITTCNSGYSILGSTTSACLKRGGRVMTPPPICDTRKCKPPQIANGTHTN
 VKDFYITLDVYVSCNDETKRLITGSSKICSETGSMVNGETKCEFIICKLPQVANA
 YVEVRKATSMQYLHINVKCYGFMLYGETPNCNHWSPAIPECKMISSPGDMRG
 INSNEENSTPSCGECACPGSNYPIS"
 <10912..11773
 exon
 /gene="sccPH"
 /number=1
 11774..11966
 Intron
 /gene="sccPH"
 /number=1
 11967..>12013
 exon

CDS
 /gene="sccPH"
 /number=2
 complement(11995..12285)
 /note="ORF 05
 KRF1"
 /codon_start=1
 /protein_id="CA45628.1"
 /db_xref="GI:60326"
 /translation="MTEIFLHAKKHLQAEENNSNDPVYEIOTPLSECNRNT
 SLNDSYDVCYEDMDYDGCAYIRLASRVYDQLRFGNDSHIEYIG"
 12584..15970
 /note="ORF 06
 KRF1"
 /codon_start=1
 /product="major spDNA-binding protein"
 /protein_id="CA45629.1"
 /db_xref="GI:60327"
 /translation="MATKTAQPSADNLGSRAPVPCGYIYVYKEGFPKREASLLGNK
 NVGASMSPLSDLTVESNFSNVAVHKIDMTLLVRSAYHREALVFEFTDLE
 PIVGGLDILCDARSLEGTNEVPTDLRDYDVKOLAYPEYSDSCFMAVYVEG
 FKRLVGNLVPIIAGGLKQVINGRAVRPIYDEDLFSKSHHLPRPIPSVSKLH
 DSVETSLAQRIRDPESVIRASEKOSIDQYKALATVNSKDSLOSIVYQODASAMV
 IDYIAELMSTIGLSLEAPQDCAVLDITSMFIFETAEEDRTAIDQNMAMSVH
 VYHLSTSLVXILATINKOTQSNKSEQVNYNFMQHGLAYADATQRENGEPASG
 APKFSQGYTLVILALASFSPLRLANRCVYMOFCOHKSTNANYSDQYVGTAAAS
 DLCELOGCTPACICHTLFLRYLDRPPVYSGORDPYVTVGVSGQINDLMFGNATF
 FRKEDAEVONAMSEKTYTWMOLONVENVKLTGWEGVYSGSLIDIOSLETFEDI
 DNVYDESVKFMNCKIKNINPEETIKYHNVHVCNENMOCAPMFLNFKYSVLA
 IIDDTCLPIAMTYEQDNPSICAMPSEMLKHYOTIYTNKSSCLDGLVLTSHKTYH
 TDMFCPLINDLSQIVPMKQVRLAKALVPTTIKIKNAIVSNSEMTTDSG
 FIKSAIKDSYIVTGYMKFLNSLHVMFPNNAISALYMHFSOKOLVPLGISRE
 NMVELANNVETSSKMHDDMNVDIIPTTLITLYAKVNLNNTILRTCGQTOFYATLQCL
 LPTLOISATEYHVLIDOSIMSDVHLSIKDKHALVOTILKEDIATYKORPIVT
 VPLVANKYTGINGNTQIPCCNGLFGMGVGRVDNLIPDSTGFERONNSYMRBRHVM
 TPVAVHVKKNSLNLTPEVETIRKNVQNIPEDKNLTINFDNVYLEIKVCGDSCEN
 ITEDDLQFTIGETIYMSDEIWSRFQITLTSAGAWSVENVTKYLGCKNCKEKEFEVY
 EEQLSCVPQDIEEFAPATLSTLAASRRKRTISLSDIDL"
 15977..18016
 /note="ORF 07
 KRF2"
 /codon_start=1
 /product="transport protein"
 /protein_id="CA45630.1"
 /db_xref="GI:60328"
 /translation="MAOHAAVYSQIYGLTIDVSLITFVDPAHINKTYTKNTEINK
 IYIQINPLHNNITESTLSVYELQHLNKLKIVLETFSAHLSDYMYEENHTLSAP
 CSRHKSTVFOYNNCCSVAKCIIINDIEITFSKESLPSFCIRSCDLKRGHNHYDIFLG
 HLKGVSPILPDTIYLSNIPQYICLNHMMPLNGESLPSIMCVNCKHVCKOLNPEPI
 QGMFENELQORHIIYESNKKOEQNOTCSIDNORDSLKSNHTIIFENISAVLELS
 NLIVYSGAHKRCANVENTSEMAKILSYEAKMONTYKICKNTHFEDPKYKPIPISI
 FCGGTSVVDPIYKSLKDCSLAPMKRAYVQILKONELFYVANKILIGGEDVHAA
 SAYPLSDKATIVPDDVLDHARAKRYLQKTYKDKLSLYTCLQYGLAVSNTLSMR
 VWGGAVIDELVKLKNHLEPRDOFTSLDMVHCETDVTGENSKYINLVLYSQLSSEH
 ISSLTLOFKYKLITGLPSQVSEFPLSEPMALALCDLDAALPHKLLITTEMIPSTIEP
 KDWQSOTYKNTFYITSTDLNSIQEAMFIRELIVLSVLYNEVLEKNLVFSALNEK
 NCVNLSPNOFCSSIYLYTDESSPLIYVENQGVFDDVLAALYVHHLQLSGNHGT"
 18006..20432
 /note="ORF 08
 KRF1"

Query Match 0.1%; Score 21; Db 1; Length 112930;
 Best local Similarity 100.0%; Pred. No. 1.7;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 43415 CCTATGAAAACTATTAAAG 43435
 Db 45964 CCTATGAAAACTATTAAAG 45984
 RESULT 23

[illegible]

CDS
complement(4121..5533)
/note="orf4"
/codon_start=1
/product="transactivator"
/protein_id="AAG27214.1"
/db_xref="GI:11036585"
/translation="METSASTSCSDIMACVCDSDMSLSPEDDPIIDDFOLEVQWMAE
SVPSVQIDDEAGEELTTEETPNPADVCEADRYVTOFNPESKALSGYHKDEK
LATESDNIPRTNPIHAYTNGERSPKMYNQSRKQRESMRKGRYSGRDRSP
SKHPRRTDAEYVRNERSRDYIROIStOKLEQARSTLKIAGLSISTNVEFTN
VMKILGRMTTTFEEDGNIKEHESKOGCGPTREENTSMALMGKIKLOTOTYR
VSIKILGRMTTTFEEDGNIKEHESKOGCGPTREENTSMALMGKIKLOTOTYR
NKLKLGPMRCCLLRDGGELSTPEELLHROFSDITCMPTFMFVVISRVTAVL
RGDCIATEDISSSAQVLEETPGSCAGVLESITTHGRYGIDECRCWPERPET
HHKGFECSTFENTVNAPN"
complement(5643..6656)
/note="orf5"
/codon_start=1
/product="unknown"
/protein_id="AAG27224.1"
/db_xref="GI:11036595"
/translation="MQALGKTEHETIYCLMTYLLFVLAWTSRIQFRNVCVATAPY
OGKVIWNLVSSLIYVTNHSLELDLSYDSCRDILNGDSILPTVSSPLHEK
IRVVLGRNCRAMMCVHLKTIITNLEFVAYLOCRRVRMGPRKACEITSPSTYS
LQYTVSTVSTFLKFPYKRLKLEHESVORNAISSMFPDIPISFLCNKLIGLLIAR
EIPVHISGCVLLTGIVTPCSLIYPLVRIIVAMMFTGLIFGVEMVACVRSKNEN
NENNSTVNPRLGHVTCACCATVIGLAVKCIYVAVFAIIVEMHEQHOVSLFW
HIR"
complement(6661..9906)
/note="orf6"
/codon_start=1
/product="DNA helicase-primase complex component"
/protein_id="AAG27235.1"
/db_xref="GI:11036606"
/translation="MEALEKSOTIRILFATKCAVSCLOLLTGOISRPVYLSYTA
TADLVPEEGADKEVPTKRIKRLDGPVKTSSNYTHGKRVRIITLIGVITGAT
KARIMPVFCESKEGDIJNLCKSLMEGEPLOTRLSLELHEDFALHAIIOCLLT
THRASPRTKCKVANKYKNDGLIQNKMERDHLISLVAHERNVLARIYVNGESC
TPFVPAFFGPEKTLVLAIRYFLOLETSTYMTVDKYLQAIKDLLEYTVNGERAN
LSGYSIDLIFFEKISAFCCSSMYKRGIVANAPYISRSISIDVSESYITITND
RKLGRVSDREFVDYIYLAIFECFPMKROIKEHLNVCISVEQVPIIAMSRLGQAVD
NEPTHRSRVININYSKNVCDERTLTNMAVYIKRTYAIYKSCSLDYVIGIC
DSAISLTHRIDIEKVGKLGMLSTKSTINNVCSNDSDVSEALIKANQANSIN
SHKPAWENHSITRTLFECSINIGNNSLATYKSPQALLGCTKISGPIPYRISL
PQGRSFPALIVDFMCVTDITQNMELSMESITGKELPLCFRDMKVTMELATVAC
CSGIASSIPDEOMYINRMELNSTLAVSNITLDVDFYKAIIPKGVLAGRAFFHGA
LTAVOLFECSAVDINSYPCVYKSCNITESMCDVDENCDIVENVYNDVETIVE
MNDVDEMLCDIYNNIDQYTKSESETIPDIYNTNTSCNKLGRFCITVPPPIYL
TGPTSLKAIKIVQAVLLENDPVKMGKYLKDFSIDTGYVSHGSLRLPFESVTH
NTTEYGRLLPPIYIPDVCSILSEFISAHNSPENHFHSPKSPFNDDITIVLINITGEVA
DFPERKVAYNKEVEGTPVKSLEKTLQSHGSLTVDAHTAFTIDSIVISLIIQYIHLF
PGRREVSMTSSKCIYVRDMVLLQTLCTSGOGCTCRYPHGRGRTPRNHISL
RVDHNRSLVSSQCCFATKCDNRNMTITFLQPLNGRIGVNHHTETIER"
9917..10612
/note="orf7"
/codon_start=1
/product="unknown"
/protein_id="AAG27244.1"
/db_xref="GI:11036615"
/translation="MHRICAGLCGTRVPLEDSTYEYRKGPGSGPALRLQLQALAM
VNMLLPAPVTIEDVYTSADNRRLVRAAPALARTYAACSRNLECRQHFSENPSLNS
VTKSHIDQSRLADTCLAIATNLVLSVSGSLTVDATDQITRMVAEEVAVSIIM
EKTGLVDNOCGVNMLTFPAPGNIAPCSEDETRHNITKPTFGKSRNKRVSSESOYH
SNVPSRKEHEHV"
10761..10872
/note="reiteration 1"
complement(10881..12068)
/note="orf8"
/codon_start=1
/product="durfase"
/protein_id="AAG27245.1"
/db_xref="GI:11036616"
/translation="MNNSEQFEAMIAAENRETRTGILERRORSENYRDEILLDVGMA

CDS
RNSDFNCALDGDGCMQPVVLANNRKLTLPDSAMECGDFYIGRLDGVKASTPNKY
ALLLRCHISNDKNTDVFIANGVYIDSGRCAIVLYKKKNTIIRGCDIATVLLPY
KLATSYLVNVDNSLDVLAEMGVCEKIAMKLFNDVNNVAITGEGCIRASHCNYTE
THVIRILFSTNLEKRSKREVDAGYVCAPEITVYPARTITVYPTIOLRVNNMDAY
IFGRSSKRVICVITLPTWYINGSLCEPITFNATSSNIVYKGEIAQVYVLEHRNQS
HKKDILNNEFEPFSSIFGNHTIEKLNSPDVYPMWHTTMMNYIAPPSDRGNKGFSST
DVE"
12037..12300
/note="orf9a"
/codon_start=1
/product="membrane protein"
/protein_id="AAG27247.1"
/db_xref="GI:11036618"
/translation="MASNCSLEMLLLLSVFTSAHTTHKLPREHNFMAASGARGV
IDGSAIATFEFVASLGVCAITLALAYNACRFLPTRSVLRSTW"
12405..13310
/note="orf9"
/codon_start=1
/product="unknown"
/protein_id="AAG27246.1"
/db_xref="GI:11036617"
/translation="MASPDGDRIRSRNAVRRKMDAQVNVNYPYVCKPRNPPRSVVY
GPPDSDSLGTYATVETESPLETYGDSGVDRKRTMISNNSDODDEDEVI
AAFEARLKHBEVDAYENVQHGNAQSRMIOKHNRDVDSKRAPPGAGAJASGRPLS
FSTAPKNTTSAMCGPTPAYNRVFCEARIRIAAQAQAAASMSNPRNNAIEDRL
LAGTVVTRTHHEGINTLIQVANDLELGGKPRDKQSTARRKKEIVKDTODEPVAQVKN
SRGTQPVSGTSRATRSYKRPDGRK"
13537..14757
/note="segment protein: ORF10"
/codon_start=1
/product="transactivator"
/protein_id="AAG27183.1"
/db_xref="GI:11036554"
/translation="MEHNGAFDVEQMHNRHLQAFINDPDESILGDVQENAGSLYS
SVQCTPRPRASPAVLYQOLINDHSEGRITALLTCEMEDIFSCPLMEDYITDPI
IVSTNPSDELLIESLETPERINLTGCDPSPSTTELPMTVENVQNTFFTELR
VREKAYRLLILCYKSLRLHLOGISIRSSVGARSODCEKHYITGFKOSIRLRYREVA
KLARVLAHLITVYTRQPSMRLEFQOOSYPDVFAKMMLENROFTCAFPITLCNHG
IVLEGLKSSORLREYVRRRQGLPLVRCALIEKGVPLVOREFSAMHPSRLGFL
THHAKAKDVSYSKHSQEPGNVVRDHPARVNNINIGSSVEAMIVSPPSDILPGD
PRLKLIKDVSDVP"
15076..17004
/note="orf11"
/codon_start=1
/product="unknown"
/protein_id="AAG27184.1"
/db_xref="GI:11036555"
/translation="MDSNTTISIPSNDSNEGELIDSDNDGIFITYMDAYOPPNEFS

Query Match
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	46123	ATCTTGACTGCTGTGCTTC	46143
DB	77268	ATCTTGACTGCTGTGCTTC	77288

RESULT 25
HEVZYXX
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS

HEVZYXX 124884 bp DNA linear VRL 09-SEP-1999
Varicella-zoster virus complete genome.
X04370 M14891 M16612
X04370.1 GI:59989
capsid protein; deoxyypyrimidine kinase; DNA polymerase; DNA-binding
protein; durfase; exonuclease; genome; glycoprotein; kinase;
nuclease; origin of replication; overlapping genes; polymerase;
protein kinase; ribonucleotide reductase; thymidylate synthetase;
unidentified reading frame.
SOURCE
ORGANISM
Human herpesvirus 3
Human herpesvirus 3
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Varicellovirus.

REFERENCE 1 (bases 1 to 124884)
AUTHORS Davison, A.J. and Scott, J.E.
TITLE The complete DNA sequence of varicella-zoster virus
J. Gen. Virol. 67 (Pt 9), 1759-1816 (1986)
JOURNAL MEDLINE 86306657
PUBMED 3018124
COMMENT Data kindly reviewed (07-SEP-1987) by Davison A.J.
FEATURES
source Location/Qualifiers
1. 124884
/organism="Human herpesvirus 3"
/mol_type="genomic DNA"
/db_xref="taxon:10335"
88. 89
misc_feature /note="rLUL boundary"
complement(588..593)
/note="polya signal (ORF1)"
complement(589..915)
/note="ORF1 (AA1-108)"
/codon_start=1
/protein_id="CAA27884.1"
/db_xref="GI:59990"
/db_xref="SWISS-PROT:P09266"
/translation="MSRVSEYGVPEGVRESDDSDTSVFMVQHTLMQNNAFLVQTR
PPVLIPLVDVPPRRSRKASQILKQMDELQVGLVQLMATLALVTYIAFVHTRA
TSCKRE"
1134. 1850
CDS /note="ORF2 (AA1-238)"
/codon_start=1
/protein_id="CAA27885.1"
/db_xref="GI:59991"
/db_xref="SWISS-PROT:P09267"
/translation="MHVISETLAVGHVPAFIMSGTILVRSLNATAEENPASEKRLR
VLAQRVDLPGGSTLHITCTKTYITIGKSKPEGRSLALIGRAMTPGGARFTILA
MEKRSITLIEGCTGLHLPLSMGTPLFTHGSSNDLCLMRGNITDMHQRLEMFEN
LAQNTETPCITSTLQCNLTEDSGEALTTSDRPLPTLAQGRPTVSNRIGILKGGP
RQOPVCHRVRFAPETREGVLM"
1857. 1862
misc_feature /note="polya signal (ORF2)"
complement(1890..1895)
/note="polya signal (ORF3)"
complement(1908..2447)
/note="ORF3 (AA1-179)"
/codon_start=1
/protein_id="CAA27886.1"
/db_xref="GI:59992"
/db_xref="SWISS-PROT:P09268"
/translation="MDTGTASESSQPIRYNLKPPLASFTQVTPPLAETWTCPANS
HAPTPSLYGVKRLCALRATCGRADDLHAFILGIRDRPSESPMIVDQPFCLINS
ORLLPEMANNTICDAPFSATQOMMLESGQLGVHLAALIGYHCHCKSPSABECWTGAS
EAYDHVCGGKARAAVGL"
2157. 2782
misc_feature /note="polya signal (ORF4)"
complement(2783..4141)
/note="ORF4 (AA1-452)"
/codon_start=1
/protein_id="CAA27887.1"
/db_xref="GI:59993"
/db_xref="SWISS-PROT:P09269"
/translation="MASASIPDPDVSTCEDFMNLIPEDSDFALEVTDMADEAI
GSTPESDSTSRIVYERTADYANPRYSKRGRESYHNHNPCTLVVLPDSNHG
GRDVEGYARIEGRHSRSRYTOSKRHSDRLSNRRRPTTPAMTGTENDDTH
DESYRLFRSKARERIRKEYDIPVDRTGRALIEVYAGASVTIDSRHIDEETEK
LYVRATTOEGSMASGCGPFGIKONTSPMELMLYCHELXRPESIKMSRLARALRE
RYIRGSLLEALSDDELFTWIKMLAKNLPYTNPIVATSKLSLELKLKLPVR
CLLNNDNDGSRLLPELLRQRFSDITCTTYMFYMARIANIVVGRSGPVEYDYS
CNVOYLOEYTPESCLAGVLEALITHORECGRECTLTWAGHLSARPYGKFKCSTP
NC"
4252. 5274
CDS /note="ORF5 (AA1-340)"
/codon_start=1
/protein_id="CAA27888.1"
/db_xref="GI:59994"
/db_xref="SWISS-PROT:P09261"

/translation="MQLGKTEHFHIMCLSHANFTLYTRKVFREHCYATTVI
NGGPVWGSNNSLITVTEFNHSTFDLGSQYDSCRENLSGDVAKTASIPDLKD
IRIVLQRMCHAYMCVOLKMFAMFVGMVQFRRIRMPSPRSCELSIPSTYS
LNVYTVISNILLGYPTFKLARKLDCVSMRDCMSVFYNDLPSFYMHGVTLLML
EYVAHISGCIYLLTGLVAYTPCALLYPTVIRLAWVCTLAIVELISVRRKPTKD
NLNHNHNGIRICCTCCATVMSGIAIKCFYIVIRALAVIFMHEQRQVSLFSES
ENSGKH"
complement(5326..5577)
/note="ORF6 (AA1-1083)"
/codon_start=1
/protein_id="CAA27889.1"
/db_xref="GI:59995"
/db_xref="SWISS-PROT:P09270"
/translation="MDKSKPTIRLLPATKGCASISLSLLILGQISTEPLVYVSTWT
PDLDDVFNKNGREITQVLPTRKPREVDENQIMHLFCSADVAVIYLLIGFSTG
DVRSRVWPIFFCCFQTDFTDFKALYKALMGAPANPIISITLICTSTFPIHSVIO
MTYTHLNKRGSLDNGICITFATCLCKLVKSVKRODLSYAHKEQVLAAYRRLYWG
YGCSPMYIVRFGSEKTLIATRRYLLTDTPDSYVLEMPIDYDLAKIDPLFYQVPA
LPNCSSYNISDLSLPKLSMFCSSYTGTGTRKNNLSYILORIHDPTEIHAHSEYI
TNDKGLKVPDRFVDYITLAHECFNRKQIADLQAVIYSDVNRVPLKSSNLGR
ATANEFNHVHSLMRDYLKKNVICDVTGELGPKYITKTYTSLYAAKPSKFI
GYCDLATITLIRVENIEKQSPYGMSTIPSNPFGDELSNEPDSGVSAEALNANFA
NDTPNOSGRGPTSPGITKILFLFSAATGIAHDVSIISYKPLBALIGHSEVTPM
PYRVVALPHGAQAFVIANDTMWSITNRYTLPHEARLIADLKQIKNPENVASLRDM
OCTLLSYKKNYSKTSNIPKDOTLYNNELFNTRLITTNLITVDYDPIHRDPIGI
LHAGMAPFRGIIITAMQLPPKAVVNPKNDCPCTFYTACPEPVEVLEDDNLDITSH
SIDIFYENGELTYCEVENTEDVWFEDTQVTSVETHADVSNNENLHFTLPCKCKE
IGFRVCVPIPNPYALVGSSYLKGFQIILQOAVILEREVEYIGPYLRDSFIDTGYS
HGHSRLPFFSKPTTYTGTAVGOLLPEYVDEQIDILAEVTSIRNANFHSRPOSN
VPYQFILHNHAGEFYAEFFERKVARNKQISSPISILTKLKEGVCLAFATLEAVD
STLESIVHIANHPRGRDREYTLTSSKQIAIKRMDVLTLOCGTGFCPLRPHNG
RRAPRTFYSLRDHNHRLCISLAQCCFATKDCSNRHTITFTLEVNPYPLTSS"
5607. 9386
CDS /note="ORF7 (AA1-259)"
/codon_start=1
/protein_id="CAA27890.1"
/db_xref="GI:59996"
/db_xref="SWISS-PROT:P09271"
/translation="MOTVCASLCGRARITPEPSTYEVRYNTHPGCALILRLOEALTA
VWLLPAPLPLEDVVASADNTRRLVQAOLARLYASNCINIEKLTKEHTEPDSGILNA
VWSHMSNKRRLADMCILAAITHLVLSYGVADVTDAIDVQOTLMTPESEVMSVDVLL
EKLTVGARPOASFDVSHNHELISIAKGENVGLKTSYIKSEADQISEIKPLLEVSQNN
TSNLTKKTYPTETLQVLPVLPKQDQVFTTPAIKSHVMLV"
9394. 9399
misc_feature /note="polya signal (ORF7)"
complement(9426..9431)
/note="polya signal (ORF8)"
complement(9477..10667)
/note="ORF8 (AA1-396)"
/codon_start=1
/protein_id="CAA27891.1"
/db_xref="GI:59997"
/db_xref="SWISS-PROT:P09254"
/translation="MNEAVIDPLELEFSAVNTGDMFCQSOTIPNRLAKDTLIEVOPECAD
TLOCVLDDVSRHROPILLRNHKKLELPSKVTGRGFEVQMOLELVKSPAPNEVALL
TQCKPOLADENEFVANGVITAGVGVGSALILYVTLPIGLTLYLPVYKRO
SRILPKNVLKHDPIFKSTQVOPLSNPSENYEKPYIPERADISTYQCGPLRDSKEX
HIDVPLTYKHIIINPKQEDAGVDICVNLVYLRKNFETIVLPIIDMDPLRHSINAY
IFGRSSKRSRGIGIEPTAMPAGECHKFYVYNLTGDIIRKTGRLAQVILLIDHNTQIF
LKHVNSNIAFPALIRKCGIPGVQVYFTKIDLLATPBERGTGFGSDKTEINDVF
LKH"
11009. 11917
CDS /note="ORF9 (AA1-302)"
/codon_start=1
/protein_id="CAA27892.1"
/db_xref="GI:59998"
/db_xref="SWISS-PROT:P09272"
/translation="MASSDGDRLCRSNARRRKTPSYSGQYFARSRVYVGGPPDSD
SDGYITTVGADSPSPYADLYFEHKNTTTRVQPDNDSSEDDFIDIVVAIFRFR
LRHEIVEDAVYENPLSEKPSRSFTKNAVNAKFLDPSPPRAPGAGALASGRPISFT
APKATVSSWCGPTPSYKRVFCVAVRVAAMQAKRAEAMNPNRNNAELDRLLTG
AVIRITVHEGLNLIQANENDADGEGASVSKRGHNHKTGDLQCGMGNEPWAYQVRRPKS
RDIQDTTGRTITNRSRARSASRTDTRK"

```

misc_feature      11959..11964
                  /note="polya signal (ORF9)"
CDS
                  /note="ORF10 (AA1-410)"
                  /codon_start=1
                  /protein_id="CAA27893.1"
                  /db_xref="GI:59999"
                  /db_xref="SWISS-PROT:P09263"
                  /translation="MECNLSTGHEPSTDTNRSKTEQAVVDAFDESLFGVADSGIFET
SLYSHAVKAPSPMPVAPKILYQOLIRDLDFSEGPRLSCLFTWMDLFSCEPIND
LYSDMWLSPDPDVIISTVSKDHEVENFTTGSVRLSPKOPICLIPVYEVQDS
FTVRLARERAVKLVVTCSTIRYLGAKRTTIGLNTQNDQAKAYLRQSLIR
YREVAARLRLVHLVLTVTRFSMLRSLASQAHDPFALKEFTWERQFCALRP
VICNHGIVLEGGKPLTASALREINRRRELGLPLVRCGLVEENKSPVQQPSVHLR
RSVGLTHHKRLKLDAYAVKHPQEPHVRADHYAKVENKNGSSLEAMILAPSPSS
EILGDPPEPPGCFILR"
misc_feature      13416..13421
                  /note="polya signal (ORF10)"
CDS
                  /note="ORF11 (AA1-819)"
                  /codon_start=1
                  /protein_id="CAA27894.1"
                  /db_xref="GI:60000"
                  /db_xref="SWISS-PROT:P09263"
                  /translation="MQSGHYNRQRQRQRISSNTDSPRHTGTRKSTWYTHPPI
LSNSELVAVQELINSEMDQSSDSDDEPGYALHHSITNGSEONTSTSRHEIRIFK
LTERANEENINTDAIDDEGAEEGAEDDAIDDEGAEEGAEDDAIDDEGAEEG
EAREDAIDDEGAEEGAEEGAEDDAIDDEGAEDDAEDDAIDDEGAED
YFSVOVCSRDADQVFTLDEPISYTDLRIAKYMERAVSKELNVSKCEPVTITS
MLAHNGDESWFMARECTREYITVQGLDPIHLRIQDTSRMTPOILPTIPALPM
TLGELLIFPIEFMAQPIISERILVEDVFLDRASSKTHYGPBMNSVALPYNAGM
VQHIPEFYVSVLRVQGTALHMHMLSTACASINRISHGDLGLDPAIRISAN
CIFLRDNFGVDPGCMLEHDLAGLPREAVPDYQVLTQLVLPNPGPVAVIMRPFGL
AYMPELRATISEPSTLVRYATGHMELAEVFLSRHSLKPOFTPTREMLAFETILY
VTGGGGLNMCIRATAMYLTAAPYHSASAYANQESLPYIYIPNSDLCDLEVILLGE
VDLPVCESTATTATHELTGEAYRIATINWIERADCKESETDLKMSATLGLLQ
RVLGHANLLLLTSGALYGGCSYIIPRGILDAVNTLMLASPLVYAHQTLTSGWKDD
DAMQTLGIRPTDVLPRQDRIVQASPIENMFVGLTETIYPRQPIPSVDLAENLMO
YRNEILGIDKWSYAMHLIRKY"
repeat_region    13937..14242
                  /note="reiteration R1"
Query Match      0.1%; Score 21; DB 1; Length 124884;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 61676 CATAGTATGCGTGGCTGCC 61696
    |||||||||||||||||||
Db 96832 CATAGTATGCGTGGCTGCC 96852

RESULT 26
AB097932      125078 bp      DNA      linear      VRL 13-DEC-2002
LOCUS      AB097932
DEFINITION      Human herpesvirus 3 ORF62 gene for IE62 transactivator, complete
cgs, strain: The Oka vaccine.
ACCESSION      AB097932
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
Gomi,Y., Sunamachi,H., Mori,Y., Nagaike,K., Takahashi,M. and
Yamanishi,K.
TITLE
Comparison of the complete DNA sequences of the Oka varicella
vaccine and its parental virus
J. Virol. 76 (22), 11447-11459 (2002)
MEDLINE
PUBMED
12388706
REFERENCE
2 (bases 1 to 125078)
Gomi,Y., Sunamachi,H., Nagaike,K., Mori,Y., Takahashi,M. and

```

```

FEATURES
source
1..125078
/organism="Human herpesvirus 3"
/mol_type="genomic DNA"
/strain="The Oka vaccine"
/db_xref="taxon:10335"
/note="synonym: varicella-zoster virus"
complement(105189..109121)
/gene="ORF62"
complement(105189..109121)
/gene="ORF62"
/complete="1"
/product="IE62 transactivator"
/protein_id="BAC4481.1"
/db_xref="GI:2665421"
/translation="MDTPMQRSTPQAGSPDTLEMDLIDDAANAAEHARVYTSQ
PDDLLEGENVMVGREHEIYSIVSGLQPEPRDEYGEELTDODIVCEGDIXGSP
VILDAEVFHTFRSEAGAREPTGADRSLETYSGLKRLASRKPMPMNDERTGTPPP
QAFSPVSPASPVGDAGNDQREDQRSIPROTGTGNSPLPSVHRDQTSISGKPG
DEQAGHAAHSGKADVLQKTOPRQAGKSPKKTTLKVKVLPARKGPGVPPVQOLYV
LSDSPVAKGAKADLPETDTPRKRKHARCRITPRVPGRSSGKPRATLPGRSNAP
PIEDDSVEKKPRKRSREYSSSSSSSSSGSSSEDEDDPRVYSGSETTGRSGRSNAP
SPNSDSDSDSDGSTRQNTQPGTRISGDPRIKTKRLAGEGRORQKSFSLPRSR
TPILIPVSGPLMDGSPWGSAPLPENRVRFGSGTRGHWDEAVRAARAYES
TERXPILVPEGLMPARQYRALINLIYCPDDPIAMLONPRLTGYNALNFOYKLLP
GRGATVAGSVASPVHVEAMTGEMLALPHAAHVAASNRDRQKHEFILOSIRP
AFPMAPKATGSSPARISRGHSPPTPTQPPDPQPSAARSLSVCPPDRLRPR
KRKQSPRESLIDKIRETPVADARVADHVYSKARKVSEPTITGSPVVDPAVIT
MLDPGENGFRIRIPGALHTPPVSOQAKATCTPETIRLVDDLPFLPAMRALFS
DPAALAIARREGGGRRCPPSGVGLARRCAAMQIDPEDVRLIITYDLPGLGD
INPLESTLATDGPSPWSPSRGGLSVLAALSNRLCLPSTHAMGNTGPPDYSAVNA
RGVLLSTRLDAPAGAVEYGLSRALSRRLVLDVALRPMGDDGALQHYVVA
PARPDQAVVRWPDQAVTEGLARAVFSPGASPARIETAFANLYPQEPOLICLR
GNVATVYCTRACPKTRVPSREYRYVYLPQPDGCDLARSGLDLAGAADPDEAN
HSHRANKRGALALRFVFLPEGRRPGAGENDVFTMVRFCRHALLLEDPAPLEL
VLPPVAGRSVALYASADEARNALPPIPRVMPPQFGAETVLESDGTRAFGHGGS
ERPAETQAGRQRTADDERHALPEDDVEVCEDMDEGCGDGDGAPGSSFGVSYS
VAPGVLEDRVRGKRPVAVKVELLSSSEDEDDVWGRGGRSPQSRG"
BASE COUNT      33768 a 29398 c 28263 g 33619 t 30 others
ORIGIN
Query Match      0.1%; Score 21; DB 1; Length 125078;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 61676 CATAGTATGCGTGGCTGCC 61696
    |||||||||||||||||||
Db 96706 CATAGTATGCGTGGCTGCC 96726

RESULT 27
AB097933      125125 bp      DNA      linear      VRL 13-DEC-2002
LOCUS      AB097933
DEFINITION      Human herpesvirus 3 ORF62 gene for IE62 transactivator, complete
cgs, strain: The Oka parental.
ACCESSION      AB097933
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
Gomi,Y., Sunamachi,H., Mori,Y., Nagaike,K., Takahashi,M. and
Yamanishi,K.
TITLE
Comparison of the complete DNA sequences of the Oka varicella

```


vacine and its parental virus
 JOURNAL J. Virol. 76 (22), 11447-11459 (2002)
 MEDLINE 22276345
 PUBMED 12388706
 REFERENCE 2 (bases 1 to 125125)
 AUTHORS Gomi, Y., Sunamachi, H., Nagaike, K., Mori, Y., Takahashi, M. and Yamashita, K.
 TITLE Direct Submission
 JOURNAL Submitted (11-DEC-2002) Yasuyuki Gomi, Kanonji Institute, the research foundation for microbial diseases of Osaka university, research division, 2-9-41 Yahata-cho, Kanonji-city, Kagawa 768-0062, Japan (E-mail: ygom@email.biken.or.jp, Tel: 81-875-25-4171 (ex 620), Fax: 81-875-25-4843)
 FEATURES
 source
 1. 125125
 /organism="Human herpesvirus 3"
 /mol_type="genomic DNA"
 /strain="The Oka parental"
 /db_xref="taxon:10335"
 /note="synonym: varicella-zoster virus"
 /gene="ORF62"
 /complement(105166..109098)
 /gene="ORF62"
 /codon_start=1
 /product="p62 transactivator"
 /protein_id="BAC4482.1"
 /db_xref="GI:2665423"
 /translation="MDTPPMRSTPQAGSPDTELEMLDAAANAAEHARAVYTSQ
 PDLLLEGNGVAGREHEIYISVSGLOPEPTEDEGELEFDODVDEGQDGLMGP
 VTPLAEVHTRESEAGAREPTGADRLSELETSGLTKARSPKPMNGEGRTPPEP
 OAFSPVSPAPVGDAGNDQREDSIRPQTGTGNSPGILPSVYHNRQOSISGKRP
 DEQAGAAHSGGVVLQKTRPAQKSPKKTILKAVPLIPARKPGVPVPGVQLYH
 LDDSVPAKAKADLPETDTRPRKHDAGITPRVGRSGGPRAFALPGRSNAP
 PLIEDDPVEKPKRSRETVSSSSSSSSGSEDEDEPRRVSGSETTSRSGREHAP
 SPNSDDSDSNDGSKTQNIQPCYRSISGDDPIRTKTLAGEPGRQKSFELPSR
 TPIIPVSGPLAMPDGPMPGASAPLPSNRVRRPSETGHEHEDAAVRAARYAS
 TEVPLVPELDGRADGQRAILNLYCPDRPHAWIQNKLTGVNALNOFTKILP
 GRAGTAVTGSVASPVHVEGAMATGELALPAAAVASRTIDAQNHFIQSLR
 AFASMAVPEATGSSPARISKRPSPPTPATQPDQPSAAASLSVCPDDELRTPR
 KRKSQVESRSLDKIRETPVADARVADHVVSKARVSEPTITSGVPVPAVIT
 MPLDGPAPNGFRIRPGALHTPVPDQARKACPEETIARLVDPLFTAMPALSF
 DPGALAEIARAGRGDRRGVEALRRCAAMROIIPEDVRLIITDPLPEDF
 INGPLESTATDGPSPSRGLSYVALASRLCLPSTHAMAGMTTPDVSANAL
 RGYLLSTDLAFAGAVETLGSRLASARRLVLVDALERPDPALSGQHYVYRA
 PARDQAAVVAMPDSAVTEGLAAVAFASRTGPASFALEAFALYGEQPLCIR
 GGNVATVCTRAGPKTRVPLSPREYQVYLPQDGTAKLARSRGILGADPVEAA
 HSHRAANRWGLGALRPVLPBGRPGAAGPEAGDVPTWAFRCRHALLPEPAAEPL
 VLPVAGRSVALYASADEARNALPPIPRVMMPPGGAETVLEGSQGTFRVGHGGS
 ERPAETQACRORRTADREHALLPDDMWEGCEDNMSDEGGDDGACAPSSFEVYS
 VAPGVLRDRRVGLRPVAVKVELLSSSSSSEDEDVWVGGRGSPPOSRG"

REFERENCE
 AUTHORS
 TITLE
 JOURNAL J. Virol. 66 (5), 2763-2772 (1992)
 MEDLINE 92219360
 PUBMED 1313901
 REFERENCE 2 (bases 103034 to 111027; 127191 to 135300)
 AUTHORS Schwyzer, M., Vlcek, C., Menekse, O., Fraefel, C. and Paces, V.
 TITLE Promoter, spliced leader, and coding sequence for BICP4, the largest of the immediate-early proteins of bovine herpesvirus 1
 JOURNAL Virology 197 (1), 349-357 (1993)
 MEDLINE 94025583
 PUBMED 8212570
 REFERENCE 3 (bases 111028 to 114234; 123984 to 127190)
 AUTHORS Schwyzer, M., Wirth, U.V., Vogt, B. and Fraefel, C.
 TITLE BICP22 of bovine herpesvirus 1 is encoded by a spliced 1.7 kb RNA which exhibits immediate early and late transcription kinetics
 JOURNAL J. Gen. Virol. 75 (Pt 7), 1703-1711 (1994)
 MEDLINE 94292919
 PUBMED 8021599
 REFERENCE 4 (bases 66900 to 96900)
 AUTHORS Vlcek, C., Benes, V., Lu, Z., Kutish, G.F., Paces, V., Rock, D., Letchworth, G.J. and Schwyzer, M.
 TITLE Nucleotide sequence analysis of a 30-kb region of the bovine herpesvirus 1 genome which exhibits a colinear gene arrangement with the UL21 to UL4 genes of herpes simplex virus
 JOURNAL Virology 210 (1), 100-108 (1995)
 MEDLINE 95313343
 PUBMED 7793062
 REFERENCE 5 (bases 1 to 31444)
 AUTHORS Schwyzer, M., Slyger, D., Vogt, B., Lowery, D.E., Simard, C., Laboisiere, S., Mistra, V., Vlcek, C. and Paces, V.
 TITLE Gene contents in a 31-kb segment at the left genome end of bovine herpesvirus-1
 JOURNAL J. Microbiol. 53 (1-2), 67-77 (1996)
 MEDLINE 97164286
 PUBMED 9010999
 REFERENCE 6 (bases 1 to 135301)
 AUTHORS Schwyzer, M., Paces, V., Letchworth, G.J., Mistra, V., Buhk, H.J., Lowery, D.E., Simard, C., Bello, L.J., Thiry, E. and Vlcek, C.
 TITLE Complete DNA sequence of bovine herpesvirus 1
 JOURNAL Unpublished
 REFERENCE 7 (bases 30801 to 67800)
 AUTHORS Schwyzer, M., Vlcek, C., Lowery, D.E., Bello, L.J., Meyer, G. and Mistra, V.
 TITLE Gene contents in a 37-kb segment centered in the UL part of the bovine herpesvirus 1 genome: the last gap
 JOURNAL Unpublished
 REFERENCE 8 (bases 96901 to 99695)
 AUTHORS Letchworth, G.J. and Kutish, G.F.
 TITLE DNA sequence of the BHV-1 UL1 to UL3.5 genes
 JOURNAL Unpublished
 REFERENCE 9 (bases 114235 to 122983)
 AUTHORS Goltz, M., Buhk, H.J., Broll, H., Lewin, M., Mankertz, A., Boerner, B., Borchers, K. and Weigelt, W.
 TITLE Nucleotide sequence of the HindIII O and K fragments located in the US region of the bovine herpesvirus 1 genome
 JOURNAL Unpublished
 REFERENCE 10 (bases 121402 to 123983)
 AUTHORS Schwyzer, M.
 TITLE Glycoprotein E and US9 genes of BHV1
 JOURNAL Unpublished
 REFERENCE 11 (bases 1 to 135301)
 AUTHORS Schwyzer, M.
 TITLE Direct Submission
 JOURNAL Submitted (08-SEP-1997) Institute of Virology, Faculty of Veterinary Medicine, University of Zurich, Winterthurerstrasse

Query Match 0.1%; Score 21; DB 1; Length 125125;
 Best Local Similarity 100.0%; Pred. No. 1.7;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61676 CATAGTATGCTGGTTCGCC 61696
 |||||||||||||||||||
 Db 96682 CATAGTATGCTGGTTCGCC 96702

RESULT 28
 BHV1GGEN/ c 135301 bp DNA 1linear VRL 07-APR-2000

LOCUS BHV1GGEN Bovine herpesvirus type 1.1 complete genome.

DEFINITION AJ004801.1 GI:2653291

ACCESSION AJ004801.1 GI:2653291

VERSION complete genome.

SOURCE complete genome.

ORGANISM Bovine herpesvirus type 1.1

Viruses; dsDNA viruses, no RNA stage; Herpesviridae;

FEATURES
266A, Zurich CH-8057, Switzerland
Location/Qualifiers
order(1..4014,102918..111027,127191..135300)
/organism="Bovine herpesvirus type 1.2 (strain K22)"
/viflon
/mol_type="genomic DNA"
/strain="K22"
/db_xref="taxon:31519"
order(4015..9664,15010..22094,26636..102917,
114235..123983,135301)
/organism="Bovine herpesvirus type 1.1 (strain Cooper)"
/viflon
/mol_type="genomic DNA"
/strain="Cooper"
/db_xref="taxon:10323"
9665..11962
/organism="Bovine herpesvirus type 1.1 (strain P8-2)"
/viflon
/mol_type="genomic DNA"
/strain="P8-2"
/db_xref="taxon:10324"
order(11963..15009,22095..26635)
/organism="Bovine herpesvirus type 1.1 (strain 34)"
/viflon
/mol_type="genomic DNA"
/strain="34"
/db_xref="taxon:31517"
order(111028..114234,123984..127190)
/organism="Bovine herpesvirus type 1.1 (strain Jura)"
/viflon
/mol_type="genomic DNA"
/strain="Jura"
/db_xref="taxon:31518"
<1..472
/note="3' part of intron spliced out from transcript over
covalently joined genome ends, leading to immediate-early
RNA 1.5 and cIrc protein"
235..430
/rpt_type="DIRECT"
/rpt_unit="235..248
466..1280
/product="LRI.1 (cIrc)"
/note="transcribed from alternative late promoter"
/evidence="experimental"
486..1229
/note="immediate-early and late myristylated protein
(viflon)"
/codon_start=1
/product="cIrc protein"
/protein_id="CA06078.1"
/db_xref="GI:2653292"
/db_xref="GI:2653292"
/translation="MGARASAPAGPAPAHVLLDALSGGRIIDRGDEAVFVSCPT
RPVYHHRGRGTATTPVHFVGRATYALLPCKKFLYIMRGAVYGYEPTTGLHLADS
LHDPLTTAGLQQRDLCLDVLVDADMDPVFTTPELITELADPAPPPPSAARS
TLRRASMRPRTFCPHQLAEGSILDLCSPEQAAAGCSLLPACDSGDACPCDAGE
TARDCTADAARAPSPGALSRYSSVRSYVF"
1259..1264
/gene="cIrc"
1259..1264
/gene="cIrc"
1259..1264
/gene="cIrc"
/gene="UL52"
/note="synonyms: UL53, UL54"
complement(1649..1654)
/gene="UL52"
complement(1658..2860)
/note="early BICP27 affecting mRNA processing (cell
nucleus)"
/codon_start=1
/product="UL54 protein"
/protein_id="CA06079.1"

/db_xref="GI:2653293"
/db_xref="SPTREMBL:001354"
/translation="MADPEIATISTASESDLSFGSDREDEPAPSLAPALRSVGO
VRKRLGAGDEPMPAPPGGASGGGGAEEAPRARARPRRRPRRRPRRRPAP
ORSGPAPKAREALATSSHGGGAARSISSLALASLAEARATAEYRTAVFAA
RLDLMRPVONGEPFAAGVSPMAVLDGAGDPEGRVWETIMFGRDLYRMEYR
PHAQAARALRLDLVLRANLVDALASDECTWCKFLTKNLRLTADPILVAGAVL
ENLRKLAPFLRCYLRGLPSLELCAARLSLATPASYMEFVRLARLSRAVSGAE
CVPLETVTGADAPPEEYIPGCVAGLIDALDTHKQADSMCKLVANFTLVVYHMK
YFCNLETF"
complement(3040..4038)
/gene="UL52"
/codon_start=1
/product="glycoprotein K"
/protein_id="CA06080.1"
/db_xref="GI:2653294"
/db_xref="GI:2653294"
/db_xref="SPTREMBL:065816"
/translation="MLGGRTVNLALALTLTAHLALMLWALAARCCRCACVATARN
GSLRMELRSPAAVYVWGANNATLAADAPCRHAAVQHIPLGLDGDALHGRVAVAG
ARDCRAYLMCAQARGGLMLLYVAFYLVQERMFGLCRNDADFLSPGYTLNAAA
ALAAVHGHPYTKLARLMCELSARRALADVFLDPLPGCARRPALPLAEGFARLG
ARIAAGSVGITHPCAAAPPLYIKTMVAVYALFAGLEIVSLYRKPRRRRCCTGAGG
GDGSEGRKVCVCCSTLLAGLVKALYLAATYGVYIALHLHYHNLRLRLGQF"
complement(4013..7237)
/gene="UL52"
/codon_start=1
/product="component of DNA helicase/primease complex"
/protein_id="CA06081.1"
/db_xref="GI:2653295"
/db_xref="SPTREMBL:065817"
/translation="MDGPALDELALQILVATDCAIGFSLMLNGQEPGCAVVS
NMPGRLACLGESBNDVALADARLVFYLGGPGGSAATPRLARLVILQOR
AGRARARRTPROGPTRARARARARARARARARARARARARARARARARAR
ARVGEQOTVRSALRARPARGRGASLYIHHEHTVAAVRYLNSCATPWFELSKRG
PGEKTLVLAIRFYFQABRAGDATTYDQAVRDLATYVAAPNPGGLAPPDVSTA
ALANCCRSRGARVAGAPVYAATITEDGLAVRCLREITIDHRSKVADDEFVA
YVYLAYEGENRQITELRAVYITEPDEGELAPRLAGVSRLEKRAVAFERHVA
QFNQSYIEONVAAVVRLPATAEVARTYRLAATANGGRTICDGAALRAA
LDHLEGOARNGVNLHAGPASAASVGPGLADLRVAGPAGSPATPACGVSKR
LLELAAAARAGAPHLDFGARGTATPYRYVELPRGQAFVAPVADATYVA
ALDDEVAVYVAAAASGSRALYERORARLALLTERAACAGSDRSGLCPAP
RDQYTVRNELEFNRLAVTNVLVDVRLKPLPRGRDLHGMRFRKALALALAP
ETIADAMPAPRCFFKYSACPSAASNLGDGASVMAAPDADWDYESLAEAGA
QYSCEDVSDPAGAPBETGEGAGSALATACGCDKMGFRAVAVPAPVYIAGGP
TLKGIARLVQAVMLERPAFAMGRYLRFEAFVAAAYTHGSLRLEFFGKPDAAV
GRMLPPIVYPERCDVAAAFMAHRDHHFHFHAPAPAGGRERARRHAYGGEYVSFE

Query Match 0.18; Score 21; DB 1; Length 135301;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 42218 GTGACGGCGCGCGGCCAG 42238
DB 62787 GTGACGGCGCTGCCGCCAG 62767

RESULT 29
AF049081/c 425 bp DNA linear VRL 02-AUG-1998
LOCUS
DEFINITION Simian foamy virus strain SFVdab, integrase gene, partial cds.
ACCESSION AF049081
VERSION AF049081.1 GI:3377494
KEYWORDS
SOURCE
ORANISM Simian foamy virus
VIRUSES: Retrovirus; Retroviridae; Spumavirus.
REFERENCE
AUTHORS Henelle, W., Switzer, M. M., Sandstrom, P., Brown, J., Vedapuri, S.,
Schable, C. A., Kahn, A. S., Lerche, N. W., Switzer, M.,
Neumann-Haefelin, D., Chapman, L. E., and Folks, T. M.
TITLE Identification of a human population infected with simian foamy
JOURNAL Nat. Med. 4 (4), 403-407 (1998)

MEDLINE 98206861
PUBMED 9546784
REFERENCE 2 (bases 1 to 425)
AUTHORS Switzer,W.M.
TITLE Direct Submission
JOURNAL Submitted (17-FEB-1998) HIV & Retrovirology Branch, CDC, 1600
Clifton Rd, Atlanta, GA 30333, USA
FEATURES
Source
1. .425
Location/Qualifiers
/organism="Simian foamy virus"
/mol_type="genomic DNA"
/strain="SFVdab"
/db_xref="taxon:11642"
/cell_type="peripheral blood lymphocytes"
/note="from an SFV-infected baboon"
<1. .>425
/codon_start=3
/product="integrase"
/protein_id="AAC28078.1"
/db_xref="GI:3377495"
/translation="LLOGQYPKGYPKQYNKLOEGHVIYVERNGIRIIPKADRSITII
LOAHNIATGRDSTFLKYTSKYMNPENKRDVVKIROCKOCLVTQNAVLTAPILRPE
RPLKPFDFEYIDYIGPLPPSGYLHVLVVDGMTGFVWL"
BASE COUNT 132 a 82 c 82 g 129 t
ORIGIN
Query Match 0.0%; Score 20; DB 1; Length 425;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 65512 TGGTAGAGGATGAGCTTTA 65531
|||||
Db 129 TGGTAGAGGATGAGCTTTA 110
RESULT 30
LOCUS AY131198 1772 bp mRNA linear VRL 14-SEP-2002
DEFINITION Human herpesvirus 8 ORF45 mRNA, complete cds.
ACCESSION AY131198
VERSION AY131198.1 GI:22857925
KEYWORDS
Human herpesvirus 8 (Kaposi's sarcoma-associated herpesvirus -
Human herpesvirus 8)
Human herpesvirus 8
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Rhadinovirus.
REFERENCE 1 (bases 1 to 1772)
AUTHORS Bachinsky,Y.H., Dovrat,S., Moore,P., Chang,Y. and Sarid,R.
TITLE Identification and expression of the Kaposi's sarcoma-associated
herpesvirus-encoded open reading frame 45 protein
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1772)
AUTHORS Bachinsky,Y.H., Dovrat,S., Moore,P., Chang,Y. and Sarid,R.
TITLE Direct Submission
JOURNAL Submitted (12-JUL-2002) Faculty of Life Sciences, Bar-Ilan
University, Ramat-Gan 52900, Israel
FEATURES
Source
1. .1772
Location/Qualifiers
/organism="Human herpesvirus 8"
/mol_type="mRNA"
/strain="BC-1"
/db_xref="taxon:37296"
518. .1741
/codon_start=1
/product="ORF45"
/protein_id="AA06003.1"
/db_xref="GI:22857926"
/translation="WAMFVRTSSSTHDEERMLPIEGAPRRRPVYKFIPTPPPLSLPG
FGRPGYAGPTVIDMSADPDVAFEDTSPSPATPDLDIISPOSSGSEYDEDEDEDE
EENDVDEDEDEDEGEPADFPQPLSHLRPLARPLRTPKPAVVAVGRVRSSTDAESE
ASMGVNSODDGEFSPAGLSPSDEGVALLEPMAATGTCAGYSPASRNSVGTGSSPY
SDPDGSPWRRLRAAPTAIVLTISDSDDSSNSPDVNNEAFTDARFISHQPSSEE

DGEDEGVLSORIGIMDYGOKRROSTASSGSEDEVVRCOROPNLSRKAVASYIIISG
SPTDEPSSANSVIYSPSSTKHLEPTQSPSTSAHSISGSTITTASRCSDPRIILAST
PPLCGNGANMPMD"
BASE COUNT 411 a 516 c 489 g 356 t
ORIGIN
Query Match 0.0%; Score 20; DB 1; Length 1772;
Best Local Similarity 100.0%; Pred. No. 4.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 64741 GTGAACCAATCCAGCAG 64760
|||||
Db 192 GTGAACCAATCCAGCAG 173
RESULT 31
HPV59VG 7896 bp DNA linear VRL 10-FEB-1999
LOCUS HPV59VG
DEFINITION Human papilloma virus type 59, complete viral genome.
ACCESSION X77858
VERSION X77858.1 GI:557236
KEYWORDS complete genome.
SOURCE Human papillomavirus type 59
ORGANISM Human papillomavirus type 59
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
Papillomavirus.
1
REFERENCE 1
AUTHORS Rho,J., Roy-Burman,A., Kim,H., de Villiers,E.M., Matsukura,T. and
Choe,J.
TITLE Nucleotide sequence and phylogenetic classification of human
papillomavirus type 59
JOURNAL Virology 203 (1), 158-161 (1994)
MEDLINE 94303229
PUBMED 8030272
REFERENCE 2 (bases 1 to 7896)
AUTHORS Choe,J.
TITLE Direct Submission
JOURNAL Submitted (25-FEB-1994) J. Choe, C/O Hajo Delius, DKFZ - Abt. ATV,
Im Neuenheimer Feld 506, 69120 Heidelberg, FRG
FEATURES
Source
1. .7896
Location/Qualifiers
/organism="Human papillomavirus type 59"
/mol_type="genomic DNA"
/db_xref="taxon:37115"
55. .537
/gene="ORF putative E6"
55. .537
/gene="ORF putative E6"
/codon_start=1
/protein_id="CA54849.1"
/db_xref="GI:557237"
/db_xref="SPTREMBL:O81964"
/translation="MARFEDPQRPYKLPDLSITLPIHLDIRINVCVKGLQEREV
FEAFANDFIYVRCDTPYAACICISFYARVELLYVSDSYGELAEETPLHLL
IRCYRCLARPLCPTDKLKHITERRRHNIAGIYTGCCRCRTPARHLRQQRARSTLV
"
542. .865
/gene="ORF putative E7"
542. .865
/gene="ORF putative E7"
/codon_start=1
/protein_id="CA54850.1"
/db_xref="GI:557238"
/db_xref="SPTREMBL:O81965"
/translation="MHGPKATLCIDIVLDEPQNYEVDLVYEQILPDSSENEKDEPD
GVNHPILLARAEPRHNIVCVCCKNNQDLVYETSDGGRALQQLFMDLTLSFVCP
CAAND"
872. .2806
/gene="ORF putative E1"
872. .2806
/gene="ORF putative E1"
/codon_start=1
/protein_id="CA54851.1"

```

/db_xref="SPTREMBL:Q081971"
/translation="MALRRSSDNKKYLLDPSPYAKVSTDEYVTPGISIFPHAGSSRLLT
VGHHYFVKPKKGGNGQDVPKSAVYRVFRVYLPDPNKGFLPDNTYVDPNSORLVNAC
VGVATIGRPGTGVGLSGHPYLNKLDDETSNHWASAVDTKDRDNTVSDYKQOLCIIG
CVPAIGHEWMTGKGLPPTVVOGDCPLELINTLEDGMVDTGCGAMFKLLODKS
EVPALDIOSICKYDPLQMSADAVDSMFCFLRREOVAFRHPWNSGTMCGDLPESLY
IKGDIRANPSPSYLTSPPSGSVTSDSQLFNKPYLHKAGSLNNGICHHNQLFELY
DPTSTNLISVCASSTTSLPNVYTPTSFEYAHNVEEFDQLEFOLCKITLTEMVSYI
HNMMTTLIEDNEFGPTPTPLSLDTEFRFVQSAATCCDTPAPVQODYDYLKKEWPV
DLKRFESADLQGFGRKFFLLQLGARPPTIGPKRRAPAPSTPSPKRVKRRSSRK
"
a 1457 c 1594 g 2372 t
0.0% ; Score 20; Db 1; Length 7896;
ity 100.0% ; Pred. No. 5.3;
ervative 0; Mismatches 0; Indels 0; Gaps 0;
ATTGGAATAATATT 58578
|||||
ATTGGAATAATATT 3696
9028 bp DNA linear VRL 17-MAR-2003
cell lymphotropic virus type 1 isolate Tan90 from Central
Republic, complete genome.
1 GI:5106411
lymphotropic virus 1
lymphotropic virus 1
Retroviruses; Retroviridae; Deltaretrovirus.
s 1 to 9028)
N.N.K., Herve, V., Sherman, M.P., Durand, J.P., Mathiot, C.,
J., Love, J.L., Leguano, B., Sironusi, F.B., Dube, D.K., and
and phylogenetic analyses of a new STLV-I from a naturally
tantalus monkey from Central Africa
192 (1), 312-320 (1993)
s 1 to 9028)
Love, J.L., Dube, D.K., Leon-Ponte, M., de Perez, G.E.,
L., Bianco, N. and Polesz, B.J.
Submission
d (27-JUN-1998) Medicine, SUNY HSC Syracuse, 750 E. Adams
acuse, NY 13210, USA
Location/Qualifiers
1. 9028
/organism="Simian T-lymphotropic virus 1"
/mol_type="genomic DNA"
/isolate="Tan90"
/db_xref="taxon:33747"
/country="Central African Republic"
/notes="Isolated from a Tantalus monkey"
1. 755
802. 2088
/codon_start=1
/product="gag polyprotein"
/protein_id="AAB3692.1"
/db_xref="GI:5106412"
/translation="MGQIFSSASLPIPRPGLAHNHLNFIQAAVRLPSPSYGH
OLKRFKALLETAPMPCINSRSLASLPKGTGRGVNELTHLLOQDAITQVESA
PSSPTLPDPSPDPTPIPRPYVEPTAQLVLEPHHGPAPSHRPMQMDQAIQVESA
GAGSPGQGTIRLVNVOGDPKADLDLIQYCSSLVASHQQLDSLSELETGRT
GYNPLAGLGRVQANPOOQGLKREYQQLAAFAALPGSAPKSPMSIQLGDELPYT
FVERLVNALVNLGDPGPGKDPILRSILASVNAKKEOKLQARGHTNSIPLMEPRCA
TWPDKTKVLYVQKPPKPNQPCRFSGKAGHSRQCTORRPPRHALCDDPTHKRDC
PRKPAISDPEPEEDALLDLPTDIPHRKNSIGEV"
2253. 2753
/codon_start=1

```

/product="protease"
/protein_id="AAD39694.1"
/db_xref="GI:5106414"
/translation="MTVLPIALFSSNTPLKDTVLGAGGQODHFKLSTPLVRLP
RTPLVLSCLVDFTENMMATIGFALDLOCGGLYLPKAGPVLPIPIVPAVLGIEHL
PPPEISQFPLNQNARSRCNTWSGRPMQALSNPIPGQELIYOSLKKPMEGDSSTT
CGPLTL"
2990..6643
/codon_start=1
/product="reverse transcriptase/envelope protein"
/protein_id="AAD39693.1"
/db_xref="GI:5106413"

/translation="MQLAHILQPIQAFSQCTILQYMDLILASPSHKDQLLSVTM
ASLISHGLPVSEBNTQQTPTGKFLGQIISPMLHYAVPPIRSNALPPLQALIG
BIOWSKGTPLOPLHSLYCALQRIQDIPDOICLVQOVSLVLRQALSNQCSRL
VQVPLGLMLTLTGTTTVOOSKOQMLVHAPLPHTSOCPPGOLASAVLIDK
VLOSGLCLOTIHNIISTOTEDQFIOTSDHPSPILYHSHREKILGAEGLMNTF
LKTAPLAPVKAIMPPLISPIYIINAACIPSDGSTSAAYILMDKHLISQSPFLP
PKSKORAEELGLHGLSSHSRCLNIFLDSKYLYHRLTLALGTFOGRSQAPFO
PLPLLSKRVYLHHRSHNLDPDTRLNALTDALLTPVQLSPALHSLTHCGOA
ALLOGATTEASNLRSCHACRKNPNQOHMRGHIRGLPNHIMOGDITFEKNT
LYRLHWVDTESGATATOKKETSEASISLQAIYAGKPNYINTNGPAYISODE
LDMCPPLAIRHTTHVPNPTSSGLVERSGILKTLKYFTDKPDLPMQNALSTLMT
INHLNVLTHCHKTRMOLHSPRIQIPETBSLNGQTHYFKLEGLMSROKQQA
LOEAGAPLIVYIASSAQMITPRLKRAACPRVGAAPTPKKTITNMGKRLTILF
FOFCELLIGDYSPECCTLTIGVSSYHSKPCNPAQVCSWTLDLASDAQALPCTGA
LVSYSSHYATSLYLFPMIRKPNNGGGYSASISDCSLKCPYLGQSWTCPTGA
ISSPYMKFOOVNFOEVSRLINLHFKSCGFESLIDAGYDPIMFLNTEPSQLP
TAPPLPNSNDHLEPISIRPKSKLTPVOLLOSTNYTCIYIDRASLTHVLYEP
NVSYPSSSTPLVPSLALPAPHLTPNNMTHGCMPOIALYSSPCHSLIPPSLS
PVPILGSSRRVAVVAVVLSALMGAGMAGTCSMSLASRSLHVEDDISLTO
ALVKNHKLKIAQYNAQNRGLDLFWEGGLCALOECCFLNITNSHSLDERP
PLENRVLTGWLNDLGLSQWAREALQGITLVALPLVLIAGPILQRLPLPSRVR
HPHSLINPESCL"
7618..8355
/codon_start=1
/product="tax protein"
/protein_id="AAD39695.1"
/db_xref="GI:5106415"
/translation="MRKYSPPRNGMEPTLGOHLPTLSPPDGLRQNLVYLMGDSVY
CLVYOLSPITWLPPLPHVIFCHPGOLAFPLNMYKMEELLYKLSLTGALLIPE
DLPTLLEQPARAPVTLFAMONGLLPHTSTLTPEGLIWTPTDGPVMSGPKDQOPS
LVLOSSEFIHFKPOTKAYHPSFLSHGLIYQSSPFINHLLEETININIVSLFNKEA
NDTPHERQISPGLEPPRAEKHFRFREV"
8274..9028
BASE COUNT 2087 a 3150 c 1703 g 2088 t
ORIGIN

Query Match 0.0% Score 20; DB 1; Length 9028;
Best Local Similarity 100.0%; Pred. No. 5.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 79649 GGGGCAACCACTGAGC 79668
|||||
DB 4355 GGGGCAACCACTGAGC 4374

RESULT 33
AF083424 108409 bp DNA linear VRL 07-JAN-2000
LOCUS AF083424
DEFINITION Ateline herpesvirus 3 complete genome.
ACCESSION AF083424
VERSION AF083424.1 GI:4019231
KEYWORDS
SOURCE
ORGANISM
Ateline herpesvirus 3
Ateline herpesvirus 3
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Rhadinovirus.
REFERENCE
1 (bases 1 to 108409)
Albrecht,J.C.
TITLE Primary structure of the Herpesvirus ateles genome
JOURNAL J. Virol. 74 (2), 1033-1037 (2000)
MEDLINE 20091363

PUBMED 10623770
REFERENCE 2 (bases 1 to 108409)
AUTHORS Albrecht,J.-C. and Fleckenstein,B.
TITLE Direct Submission
JOURNAL Submitted (11-AUG-1998) Institut fuer klinische und molekulare
Virologie, Universitaet Erlangen-Nuernberg, Schlossgarten 4,
Erlangen, Bayern 91054, Germany
FEATURES
source
1..108409
/organism="Ateline herpesvirus 3"
/mol_type="genomic DNA"
/strain="73"
/db_xref="taxon:85618"
/complement(join(90..730,1339..1507))
/note="T10; similar to T1P and STP-C of herpesvirus
saimiri C-488"
/codon_start=1
/evidence="experimental"
/product="tlo"
/protein_id="AAC95538.1"
/db_xref="GI:4019240"
/translation="MANPEOEHEEGKPPPLGDSGESEGPNIPODPTPGPPPIINS
KNEDYPPLENGPARKSPGPPGSGNSPPVLMVKNNGDRKODVSGGNSAPNS
VESKTSSSSSSGNENKCPDEBTOECITITTYIPWEDARKMLGVKIDSSDBEE
RSPENKYPKNIKLVNDGEMNPPGIPPODEPRANIGOKOSATSKNGPOITLNEAT
EVESQATDQOLNHRVEKVKITVICLIGIIVALLILFELGLFLLMK"
complement(2144..2264)
/product="HAUR 1"
complement(2752..2865)
/product="HAUR 2"
3224..6961
/note="orf03; similar to FGARAs"
/codon_start=1
/protein_id="AAC95537.1"
/db_xref="GI:4019239"
/translation="MLVLFHSYEALLPEELATSAILOPGLQVTSNHPVAGVY
VYVRHNASPLEPVGKFRFSYSPPTPTSPAEOLTSYSGQLSLDTPTTSRELVDI
LKLSMTFPOGKRNADIIERTICTRTTITICDINPTMHQHLKLCVPTGKLFKE
ILPOKSLNLOAPENARALSTPISDPLNVEKGVYTGEGFOTPNGLVYLMALHMR
KNSRLGIVLIDITWTWMSSTNILEGLNVEKGVYTGEGFOTPNGLVYLMALHMR
APLFPACOGTGHLSLAQSDMPEVTOAPOMKMLHALNLKCSMTTIGFQFVPSDL
ATIIPOKTIYNGSVSTALRTPVCAATASLREKLYLQIOLGNYNHYHLMQDSGK
EIGSLILASFPMDCVKTESGIVGMSYTPLESKAKATLANQCVQASARILLSLPM
QVTSKLAPSNSYTKHNKEVLKQHFENLITSDLIATINININABEALKTACDAGCK
FKKIGMLVHRKGTIVVDDRGDKPYKLOFDRKPKFPLKSPINITLLOGNTMSELD
LRDTFLEHPSVCKEYIVSHIDKLVSGVARTAVIGPMOLPVDYSIIVPYLOGN
NRDMGENPMDETIDRCVFEELAKPGICSSIGESTLIAQADLKIGTRATTEALN
LAMASNNIGSIIIOVATITPYTAQASIOVYMDTAKTFCALSVSCPTFAATDGG
ASIVASATVNPENAKCMFTPNLKHNSDILLPTPKRRNHRGSVVOQCGKRTIDLP
QATSETEBLKLQVICTLREDOSLVSGHSDGGLALVEMALISGGGVARYVQGE
DTLOFLSETPQIVIEVSTKLXYVQGLNLRNVDGLOLVGKICISPFLEAVSONSIDM
SEPLDSLROIWRKESDACEADQVPOPEMHIITVLPKCPGAVGCFHSHVYLLPHNS
VPHGLISAIAGFQPKLISIDHPYOTNSIDITVYPAKFEFIVAGSNMOEENIGALK
AOLKSHVALORDFERIMAKLPYCVCAICAMACCELLFYKTTGYNKPSTPYMCVANS
EKFBRSNINITYIPENTKAIAROSIKNSLIPQWGTCTHRYHHRKMLEKMAEHGVSS
MEYGHNLASGPQOHTPLTPNGSNATAGICSDGRLLALHDPISLNNICOMPYPPTD
PPLKXSPKTYMFLDLHKWGITVQASPPPSRTDPLSLVP"
7470..8552
/note="orf 04a"
/codon_start=1
/product="complement control protein homolog ceph"
/protein_id="AAC95530.1"
/db_xref="GI:4019232"
/translation="MHTLVIYFIILPCVIEFWSSSCPRKRRNYSLRAYVNTNSSGSY
PNGTLQVTCRKGYIGROIQVTCVNGMIVPNEQKRCSTPADLLAGWTVYVGNLY
YGSVTVTCNNGVYOLGSPSCILGPGRWMMRPICETIKETKPPATLGGVHTN
IKKEYTYVDANTYSCNDETKTLNPGSKOSFGRGAPDDEETKKEFYVCKIPIYANG
HVEVAKISNNVQIOTVINIKCKGRFLQSETPMKACNGWFPALPCECAPAPRGMPI
IDSGEDTSPSGRNCNOCNTSVSTNITVTTTGTHTSHIYPTGKNYKLPQGVAVIIL
TTGSIILAIILTGVALHRCRLRMFVP"

CDS
/note="orf 06"
9205..12591
/codon_start=1

/product="major sRNA binding protein"
/protein_id="AAC9533.1"
/db_xref="GI:4019233"
/translation="MATKATOPADNIGSRAPYAGAGYIYVYKKEGPEOASLLGN
NYGADMSPLISGLTVEANSPFNKAVHKKIDMTLTSVSAVHREAIYVFNFTNET
PIFFEGGLDLSGDARNLFGYTSFTRHDLKIDIKDAPPTTODSCMSVYVES
FBERLFGNVLPIISOGKVOINGEAKVPIYLEDLFSKSHLEPRFIPYSKTLH
DSLFTSIAGLRIDVESYIRAI EKOSIDQYKLAIVNSKHEALQVACODASAMV
IDICIAELASISGLSFLTEPOERCALDYTSWIPEDTETEBGRKAIIDMMAMVH
VYTHLESTNSVLYTKINKOTONKSDONINSYFMOHGSYAAEATONGEPASG
AVKNGSGYTLFHALASSEPHLARSYVMOFOHOKSTTNSYVAVGYTSVAVS
ELCELOGKCPACIHTLFRYLRKDRPPLSSRRDPYVGYGSOYNDLMGNAT
PREKEDDMQNTCEKTYTQILQNVKELATIGTIGLSDLTIDIOSFLTEREI
DNVNDVEIKFNLCLVKNININRETIKGVHVLHYCCNVWQAPCAMPLNLEFKSYA
IIDIDICLPAVMIYEDNPGMMPSEMLKMHVOTITNFKSSCIDGLVGAHEKVAH
GMFCDFINVDALNGOIVPVKQVRLAKALITVPKTIKIRIVFNSNSMPEAIQAG
PIRSTKSDSYITGYPYKELNSLKHVIFPDAKISALYLMHPSKROIPVLEISKE
NITELANYTEASCKMHDNMVLDIPTTLAAKAVLNNTILTCQOTQYATLOCL
LPTLOYVSAETERYPHVLHQSITSVDYLSIKKQALIVOTLUKEDIATIGKHPITV
VPLVYVRYGINGNTQIFQCGNLGYPMGVBNLIPDSSGFRONNSAVMRRLTEM
PIVIANILKRTSNLNLFEVERTIRKNVOTIFDDKDNLIFDNNVIELVGLGESEN
MIEDLOFYLGDIYIIMSDIWSRFLITDTSQFWSVYTKILSGRKOEDCNLEFVGV
ESOLSCAPQIDEPFOATLSTIAAGRRKRRIHLSIDIL"
12598..14640
/note="orf 07"
/codon_start=1
/product="transport protein"
/protein_id="AAC9533.1"
/db_xref="GI:4019241"
/translation="MAOHIAANYSOIYGTLDVSVYTFVDPHSINKIFITNNOKINK
ITQIMPLQDDONVESTLSVLEHLNLNKLMTDITLKHNLNVEYTPNINISLSTP
CSNHLKIVQNNCSVSMCIINDIEIFLKSIFYCIRAHADYVGNKHTIDLG
HMGISLPIPLDYLSNICIYCLMELHMMIPNGESLOSMTSNTCHVONCNPVY
OGEFELLORHIVDTOKPEPTQCSINDIRDELSKLSHTIIEENTSAVLEIS
NLIVSSGTHCTONTENTSEIYKILSHETKMONRYKICKSTHFEDPKSISIT
FGGIGINSYDEVYKSLSDCSLAFKRAYQDILKONELFVNLNLIKGEDISEST
PVPISERAAVNEQVINDAHAKDAYIQKVTGDKLSLYACLDQGAVALSTLNR
WGCAYVDEIVAKLNFLEFDQFISLMDIHLSESVSGENSKYIKNLISQLSSEH
ISLTLQFOLITGLPLSONSVYPLPNTIALHCLDAAGALPHHKLITEMIPTEP
KDWVSQYKNEFTTISGDLNNIQQEVMFIRELVLSLYNRALEKNLOFVSNLEK
NCVKLSPNQFSQIYLYTEDRSPFLIYINQNGVFNFDVTLWVHHLQLSKKNDS"
14627..17050
/note="orf 08"
/codon_start=1
/product="glycoprotein B"
/protein_id="AAC9533.1"
/db_xref="GI:4019234"
/translation="MTLNRCVLLIYTFSTACQSTTPASSDENGKTPALKEKFRY
CSASTIGELREFNDRACPTSEDKVHREGILLVYKNIYPHIRKVRKYKLIATSVRI
NGWSRGVAITNKMELSAVPAKYEIMJMKNYCHNCMOLEVGLNASCYCDRGNKKT
VDLKPVDGLTGLATRYVSOPIFADAGMLVYKTRTVNCEIYEMFARSADPYTEV
TALGDVEVSPCDANSCPNASDVLSQVDFNHTVYVGNRATSOOHGRIRPAHTLD
YASWEAIKKTTSVCSMVFMGFORAIOEHDSHTYHINELTAGSTSEKTELASFSS
EYSCLSMDINSTITDKIGRVNNTYHPNTRQYKRTSGMLVQPIALITELAMIEA
TVVSPPLSTAHLSRTGRKRDVSAGSBNVLAQIOIAYKLOSIINNVLEELA
TWCRQVQRTMIVETAKINPNSVMTAIGKPSAALAGVLSVTCINDQVSVSIH
KSLKLTNNDVCSRPVTEKFNVSOLFQGLARINDEIDELSELSVSGCRNAAHEFTA
KNETHEKNYLHVELPLTNISITLDELFLGOLARINDEIDELSELSVSGCRNAAHEFTA
LETMEFEVYNQISIGIRKRDENSRNDRDIOPESELTADIGSKYKIVATASA
FSLFGGIVTIGLNFINKPLGMLTFLVCAIITLLVILLVARTNMSQAPRMIYPIGE
KSRSVYTPTEPEYIKOILGLMNMQOEEYKREHNASOPSLKRAVDALRRKRGK
QISTEDKMI"
17123..20152
/note="orf 09"
/codon_start=1
/product="DNA polymerase"
/protein_id="AAC9533.1"
/db_xref="GI:4019235"
/translation="MEFVNPYLTKLAGSKMLSCCTKOPICHLVPCFNPSPDRGIV
SVSSPAPTYFNGSENNVYLGNNOSMHLKRCQKTEPEVOSITHIYIVETYSSE
DRCNVDFKRFQNDIIPNGVYLKLGRTDLAGSAVFGQKIYEVYKPGVGNITILM
KQALNEKIGPCRCYQTEFLVKKIKLSRYDDDEHVPVYTTSSHSYKVSIVYVANGCE
IETINVDATIRFLIIDNNSTFGMTCKSACFRITNDSYTDIEFDGYNLDEFHAERT

EMPVYIMAFDIEICIEKGFPCAKNEGDILIQISCVFQWGYPTDRTKNMLSLGTCA
VEDSEVEYERPESEADMLHGFETILRDENVLETIGYNSNEDPLPIDRAQIYINIKLSD
YSRVKSGETFOVAMPKMDNGEMRSVSKISGIIIDIMYIVCKDLSLSNKLDTVA
DHICGAKKEDVYSKDLIPLMSDEGRKAGRCVADSVYVLCMLHEFKHVEISEIA
KLAKITPRVLTGQOOLIRVNSCCLAAARENVYLLPSNVNNTDPCGATVYPIPEY
NNAVLVYDRAVSLYPSIIQAHNLCTSTLIPNLSNINPYLKSSSYEFMSSSGIIRHYK
KTIQTLISLKLTLVWLSKRAIKQKLAOCEDDOTKTLIDQOOLATVCAVAGVFGV
ASGLDLCISLTAETVTLQGRTRMLERKSAFIEEMTVRIQELVPRKLNHEHAKRVYIG
HISNDLVEEGGYVDVTVRGRGLATFTSEKLENAPIKLESETPQCLLAKRVIYG
IISNDLKLKMGVLYRRKACFKVQATSSKLTNLLIDPEKAAOOLSKKDPVAFEG
GIDGFLYKVIDLINESYENLRQGVSMDDLTSEPRSSVKTENLPHLYKTKI
KROEPPQIHDRIPYVYQKTAICISMAEDPYVQHNPIARDLFXDLKHGVANI
IOCLFDSNKTVSVALNFSIFPLFSELSKSDSTET"
20192..21412
/note="orf 10: similar to Raj1 Lf1"
/codon_start=1
/protein_id="AAC9533.1"
/db_xref="GI:4019236"
/translation="MNPSTFNGRMTYVSSGLFSTISNNEIAPATPVARVPHLP
SISILDKRVSHGLVPTLQFOQYTSVPVAFGSDTSQPKPVLPMEISDFNPLVY
FVAGGPIILKRNELKRYEIVISPLTRDISSEYFPDNDYDLALAGFGRILENEN
IRGTPKRTNGSYVMLFRCERKIPLEVININEVKSDELIFESLLOEVTNNTYIMTH
MGSPKPDQIEVOVHNVNINPHELVKHALPWEIAPSGSITPIYLEAKIIPKSS
VEISSEFVRNGVLDVTRNQSALPVAASSHTTKYVYKQIYPIPIPLSTYVNPGRITF
IKRGCVAAVAPCFEYILKAPGQDCEDVTLDSOTSTHMSDVLIKPEGGPIVHAHHL
VKEINFTDEPMT"
21415..22632
/note="orf 11: similar to Raj1 Lf2"
/codon_start=1
/protein_id="AAC9533.1"
/db_xref="GI:4019237"
/translation="MATPIKIRVWRGSAKOSERKNYLFMSVSEHETITNNQ
EIIQLDDVYLACPSIREIYVQSGKRPFGSGRYGPGTITFVYVGHENYIKIP
MTISDQDELIFITFALCEIIPGSKIKITLPTFLKGLVTLGLCEDETSIMTS
CMGMYGIVSETPOVLKSEYITKNEPLPHMAOKTGRPNKMARVHTONVCEVN
STYKGDHITRLAOKSSEVDNFEPRVYIGTITNNKILAAQNHPIYFCPMDKQSGIP
IIVGDSIRTPADHAAVKNYNSSTYATNMTINCECPDHPHISDCMKPSPIY
INVTNLTNLTITSSGKIGEAFLKPLCKIKIISKKHVQPLPSAVTLPGVNTINS
NKPLADLTYYK"
complement(23207..24028)
CDS
Query Match 0.08; Score 20; DB 1; Length 108409;
Best Local Similarity 100.0%; Pred. No. 7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CDS
62322 TTAATGAAACAAAAA 62341
59155 TTAATGAAACAAAAA 59174
RESULT 34
AF319782 149696 bp DNA circular VRL 07-NOV-2002
DEFINITION Callitriche herpesvirus 3 strain CJ0149, complete genome.
ACCESSION AF319782
VERSION AF319782.2 GI:24762296
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
An Epstein-Barr-related herpesvirus from marmoset lymphomas
Proc. Natl. Acad. Sci. U.S.A. 98 (3), 1224-1229 (2001)
21107697
2 (bases 1 to 149696)
Rivallier, P., Cho, Y.G. and Wang, F.
Complete genomic sequence of an Epstein-Barr virus-related
herpesvirus naturally infecting a new world primate: a defining
point in the evolution of oncogenic lymphocryptoviruses

		/translation-"MSGRSFENPFLHCKNTCAKPKDEKYLRLIPDCKTPGARGVTDI RGEAPPLCFHNGTKIQVMHSHGVGRGMSKSCASNGCAEATDMERHVDIETEV QEKCAVIPSDBKQGVVPCGIVIKLGRREDGASVCINPGQADGYFSEPAVNIYV ALVEILKGFEDRTPCRMAVETVERSIMGYNTKMKYKILSHNSISHATSILK DKYCKIFENANDSRRFVLDNKEFTTPGWRGCRAMPRIIDRDSFADREDCVTDLS VITNDVSWPPIYMAEDIECLGEEGFPNATNEIDLIIQISCVLMSVGEPTSNRIIL TVGTCAEDIVEVEFEPEMDLIYAFQILRIIDNVEITIGYVNAFEDWPIILDRARI YGINPASLGRIGGVCEVRPNDAKMFRACTRISGVIDMYSVCKELISLD KLDYTAARILGTCKEDVHYKEIPLFRAPEREKRLGMCIDQSVLMDLHNHFTV VETSELAKINPCRRYLDGGOIRVSCILAAOKRGFLLPMPEDSPDRDYGATVY QPIAGFPNSVLYVDFASLIYPSITQAHNLCTYITVPEEGKRLDLRPGDYSESIS AGTFHFVKHIIHKSFLASLESMLAKRAIRKLLGACNDPRQRTILDKQDLAKICTN AVGTGVAHGLPCCLTIAETVTLQGRFMLERAKVYENLSLDLEKLAQCSATPMSE NPDGILRVYIGDVSLEIECSGSEEGVSALEPLARFTSSLEFAPISLEAEKIFSC LMLITKRKYGVLDGKITMKGVDLVKTACQVORTCRVLDLIGNDVYKRASTL SLRPTQSTFEGLEPGLDVIYINLEAYGDLRANRVPISLSTFTTELSTROISAYKSO MPLHLYOKTLARNEEPPQIHDRIPYFVVASARGSRGRTKRSEMAEDPSYTRHNI PIAVERHEKLLQGTANITLOCLFGNNPEVALSVQNTAGYPHO"	
CDS		17204..18121 /note="similar to EBV BILF1; glycoprotein gp64" /product="orf6" /codon_start=1 /protein_id="AAK38213.1" /db_xref="GI:1367647"	
		/translation-"MDETQIMGSPVLEEGGQCNSSYNTGSLFTGYMVEIIL IILLLFLILRLKDSIDMWLAVFMOTLMLLGLKIQEFSNTGLCMTOHMLMSIL LSEFHSGMAHRAHLMVSAKTIKPVSNRCIIMLLITVETLIVLAVSEAGISSML NRGNLCREGATCGAHRIOAQRACCVATITACVITATYKIMHTRISTRRITC NMFPTGICATCULLAARLVPRPREPNLGFPCSSLMTRYHAFGSLILLILLIYI WAHROFIDDKNILESTLVSRFRAFNPS"	
CDS		18132..19526 /note="similar to Raj1 Lf1" /codon_start=1	
Query Match	0.0%; Score 20; DB 1; Length 149696;		
Best Local Similarity	100.0%; Pred. No. 7.2;		
Matches	20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	48982 GGGGGCTTGTGTTAAGG 49001 		
Db	48615 GGGGGCTTGTGTTAAGG 48634		
RESULT 35	AF250284	232392 bp	DNA linear VRL 30-AUG-2000
LOCUS	Amsacta moorei entomopoxvirus, complete genome.		
DEFINITION	AF250284		
ACCESSION	AF250284.1 GI:9944523		
VERSION			
KEYWORDS	Amsacta moorei entomopoxvirus		
SOURCE	Amsacta moorei entomopoxvirus		
ORGANISM	Amsacta moorei entomopoxvirus		
REFERENCE	Entomopoxvirus B.		
AUTHORS	1 (bases 1 to 232392) Bawden,A.L., Glassberg,K.J., Diggaus,J., Shaw,R., Farmerie,W. and Moyer,R.W.		
TITLE	Complete genomic sequence of the Amsacta moorei entomopoxvirus: analysis and comparison with other poxviruses		
JOURNAL	Virology 274 (1), 120-139 (2000)		
MEDLINE	20396580		
PUBMED	10936094		
REFERENCE	2 (bases 1 to 232392)		
AUTHORS	Bawden,A.L., Glassberg,K.J., Diggaus,J., Shaw,R., Farmerie,W. and Moyer,R.W.		
TITLE	Direct Submission		
JOURNAL	Submitted (28-MAR-2000) Molecular Genetics and Microbiology, University of Florida, P.O. Box 100266, Gainesville, FL 32610, USA		
FEATURES	Location/Qualifiers		
SOURCE	1..232392		
	/organism="Amsacta moorei entomopoxvirus"		
	/mol_type="genomic DNA"		
	/db_xref="taxon:28321"		
		gene	500..1882
		CDS	/gene="AMVTR01" 500..1882 /gene="AMVTR01" /note="LRR gene family member" /codon_start=1 /product="AMVTR01" /protein_id="AAC02973.1" /db_xref="GI:9944790"
		gene	/translation="MELPVMELEIFPNVLDNDRKLPIDSKCIISKLILYKYNVSCIK EIKNFIMKELITANNYIKYSELEGIENTKLIKLYCYNTRIDSLKGIENLIKRLCYCE NTNINSLVYKNIINLELTCFETNITSLKGIENLNLKEPDSYTLILDSLKEIKNLI MLQNLNSHTIIVLSLEGIEINLNLKEDCSYTSINSKEIKNLINLKLDECEYNITS LKEQNLINLKLDCSYTKINSLEQNLINLKLDEHNITNITSLKGIENLINTKIN CSNINISLVYLELNTMLKNICYGINIDFEILKNLINLELDCSEFKIYSLKGIEN LNLKELEDCYTKINSKGIENLNLKLDOSYTKIDSLKOTKLNLEOHCYVTEL DSLKGIENLNLKLPFNHNTKINSKGIENLNLLEILYCANNITISLEGINLKLLE LYFNNTIIV"
		CDS	complement(1926..2108) /gene="AMVTR02" complement(1926..2108) /gene="AMVTR02" /codon_start=1 /product="AMVTR02" /protein_id="AAC02986.1" /db_xref="GI:9944803"
		gene	/translation="MILINSESYKSEYSSFFLLISVFNVSVKILRIFSKISLVFCL LTLELSTCEGIIIVY" 2273..2545 /gene="AMVTR03" 2273..2545 /gene="AMVTR03" /codon_start=1 /product="AMVTR03" /protein_id="AAC02975.1" /db_xref="GI:9944792"
		gene	/translation="MANEDMLNEIYIKLDVSLVYDKDLINGIANDKINKESNNYL LKSMECKCLIEMSYNYLSKDSLLEIKLLENFTFLKYIIOQNKN" complement(2542..2934) /gene="AMVTR04" complement(2542..2934) /gene="AMVTR04" /codon_start=1 /product="AMVTR04" /protein_id="AAC02987.1" /db_xref="GI:9944804"
		CDS	/translation="MFWLLILPSTICCEPKQSKYFCDIYDPCINNLMKSCNNNE VRVNNKCIOTSEYKNTGNTCHCKNKNLIPGIIHYNPLMCKNLSMCCFEEDNYIIV CTEONNKYIWKIDYNTDCKSILKIRY" complement(2971..3786) /gene="AMVTR05" complement(2971..3786) /gene="AMVTR05" /codon_start=1 /product="AMVTR05" /protein_id="AAC02988.1" /db_xref="GI:9944805"
		gene	/translation="MDYERNLINNRSLTFONDYKRYIYISILLIIIIIIIIIIYIIF AKKESATNNDSTKNTINIKNTISNNKMYMDEFNATIRYINKINKNSEQKIFEIA RSRTISLYNNITIDIDYDRGVADNNKMMITIDMCNDYDINIVVYIRLNCNDISR EIQNSFKYENYINIMFYNSKYNIDICYNNNNFGMYKKNKKIILNLTXTLSRL KYEMYHMLSHFIFIKHDFILNSYFPIEYVYNDKNEIDEERITVMEKNNIRCT" 3871..4416 /gene="AMVTR06" 3871..4416 /gene="AMVTR06" /codon_start=1 /product="AMVTR06" /protein_id="AAC02978.1" /db_xref="GI:9944795"
		CDS	/translation="MDFIKLQDIAIRSTIDNLNIPGLRKKINKNVCENCCMFENNN QITCNVCLKSCGNKLYNNLSIKFSYTKGYRENNKFNLLDLDIDCKKNTEICTECH KLTFNNNIDYVELRNIDSIDKVGVCFLIINILDCENRYLTNNYINSYNNYTL

```

gene      ILIILILLRFYIKKIFHIVSVR"
           Complement(8798..8892)
           /gene="AMVTR13"
           /complement(8798..8892)
CDS       /gene="AMVTR13"
           /codon_start=1
           /product="AMVTR13"
           /protein_id="AAG02992.1"
           /db_xref="GI:99444809"
           /translation="MGDEKGTQMYENIHRYDNEYLIFYYTKDFKHSKDKIDNNF
DVRKNIININIKINDFY"
           9826..10068
           /gene="AMV001"
           /db_xref="GI:99444524"
           /translation="MDFSILKTNFIEIFLISVGSIMISLANGLMIWISNI
SSIAFYFKRQYPLCQOCVFLLTITIGIYNNDKL"
           10272..10703
           /gene="AMV002"
           10272..10703
           /gene="AMV002"
           /note="putative dmpase"

gene      CDS
           /note="putative dmpase"

Query Match
Best Local Similarity 100.0%; Pred. No. 7.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      65766 TATATATATGTATAGATT 65785
         |||||||
Db       204744 TATATATATGTATAGATT 204763

RESULT 36
LOCUS   AF480884                241087 bp    DNA     linear     VRL 29-JAN-2003
DEFINITION   Chimpanzee cytomegalovirus, complete genome.
ACCESSION   AF480884
VERSION     AF480884.1   GI:19681028
KEYWORDS
SOURCE      Chimpanzee cytomegalovirus
ORGANISM    Chimpanzee cytomegalovirus
VIRUSES; dsDNA viruses, no RNA stage; Herpesviridae;
            Betaherpesvirinae; Cytomegalovirus.
REFERENCE   1 (bases 1 to 241087)
            Davison,A.J., Dolan,A., Akter,P., Addison,C., Dargan,D.J.,
            Alencor,D.J., McGoch,D.J. and Hayward,G.S.
            The human cytomegalovirus genome revisited: comparison with the
            chimpanzee cytomegalovirus genome
            J. Gen. Virol. 84 (Pt 1), 17-28 (2003)
TITLE
JOURNAL
MEDLINE   22421467
PUBMED    12533697
REFERENCE 2 (bases 1 to 241087)
AUTHORS   Davison,A.J.
TITLE     Direct Submission
JOURNAL   Submitted (05-FEB-2002) MRC Virology Unit, Church Street, Glasgow
          G11 5JR, U.K.

FEATURES
         location/Qualifiers
         1..241087
         /organism="Chimpanzee cytomegalovirus"
         /viralion
         /mol_type="genomic DNA"
         /db_xref="taxon:188763"
         1..687
         /rpt_family="TRL"
         /rpt_type=inverted
         1..297
         /note="terminal redundancy"
         /rpt_family="a"
         688..200038

```

CDS
/note="Region: UL"
714..1628
/codon_start=1
/product="R11"
/protein_id="AA00649.1"
/db_xref="GI:19881029"
/translation="MRNSTMLENPSTTHIPSEGGPLGYPVSRREDMKRGTEWIEGT
DYEDCMCMWGRFTLNRRPVYRLLOREGCDMNVRCRGMGFRAIDNPGMAIW
ROHLYELGGHGOROLDSPSGAEARGLRPLKPKPTDNNHLPICEPFGGFE
ARITSDLPHTNTHSNTHCHOTREHSPYODMRPDSSEEDSDPHGSAAYVELLED
DEVDLDPDTFYDETPTPEHEHNTNRERLATISGGDGLMGTPLHRHETHSDHELR
GMWARKGBERGAMPAETFTCPGRRPW"
6664..7191
/codon_start=1
/product="virion glycoprotein RL10"
/protein_id="AA00650.1"
/db_xref="GI:19881030"
/translation="MRVYLCSTLLLLAIGATAIHNDVCTSLDGGTRLICKCRNNNN
SNPKPTATSGHITCLANCTCKRYTEPLRLISLGIYSAMGAGSFATLLILVIFEV
IYSRRPADDDNGVEDEPFLAYRDLTKKLDKSHASKONTYERIPYRCQRLRDEBP
LITNEDDEEDNE"
7202..7900
/note="R11 family"
/codon_start=1
/product="IgG Fc-binding glycoprotein RL11"
/protein_id="AA00651.1"
/db_xref="GI:19881031"
/translation="MKRDLTLKYVSTAFCLISSAKPPTTALCPRLRPTYTTC
TRNRTLASRLNTGHSVSVRYALPGHKPTQMPICSTIDAAHSTTRDYRKARFICTR
HSMILYNTVVEDMGAVILDEYTDASEYFEFISRAVCEAVATCAEMKYLIDNRCOT
LKPACTINPPNDLRDMLNISICHAMIGLLIIVSLVGFLLRLRRVGVQNAVYRLSN
RDEPLLFQDASE"
7939..9021
/note="R11 family"
/codon_start=1
/product="glycoprotein RL12"
/protein_id="AA00652.1"
/db_xref="GI:19881032"
/translation="MSEICSVATLLLVALLSQTLEDNTNTSSVNTSTNDSNISPT
TSSPKATSPSPFTPLNTSTEXTLSNVSTHTPLTLLPTSTTSFHSFONITIT
EYSTYNLCNTEIYSSNSTESITATSCNTANTFPDNTTSTAIOITTTTEIYKAVY
TTVGRKESENVLHVNSTFONCTRTVWNHPYITTHKKRKNKPHTLCASSGHSYKH
NHHKLCLOCTPKNLFLFDLVNHSKXYIAECDGDNHAAQGFILTVNVAHTNTRYVC
OPKDTVTTRPISTHLFNQNYSGHYPGASNSHSGMAVGLFLMACVILFEFARVY
KKRYRLRDVSESEVYVYTRPEHD"
9123..10124
/note="R11 family"
/codon_start=1
/product="glycoprotein RL13"
/protein_id="AA00653.1"
/db_xref="GI:19881033"
/translation="MVDHFAITWTLLVFLILASGTVSSCHTSHSVSSTTVATTSNPS
VNTNSADTSNST
TTTTTYYTISTVPASPFTNTKFECDTATKWINITAKVGDVNTPPACNTSGKY
HTAAWTKVNTKETDLCLFEPDYISIPQAGICFCQHWQSMITIDVTENAGNYIVD
HGDGNHHYDKGYRLQVTSNHTTGTNRKCKPNDFTSTPDHKNKEKTIENEFGNMYD
OPTFPMGMAIWAAYVIVALLALVWGSRSSTVIYAGKPRYKLSKNKDPDEWASP"
complement(10256..10432)
/note="contains hydrophobic domain"
/codon_start=1
/product="UL2"
/protein_id="AA00654.1"
/db_xref="GI:19881034"
/translation="MRGDAVSLIYEDDLPLFGSGFNASHAYSPFVLGIFVTVVYV
WYLMWIKILRDNF"
10504..11097
/note="R11 family; contains hydrophobic domain"
/codon_start=1
/product="UL4"
/protein_id="AA00655.1"
/db_xref="GI:19881035"
/translation="MRRGWRKPPGGAATFKYGLLVYLSVSVYIGCIHYGAIDHAYD
RVKSGDNVTLTSPFYHLGSDNFWYKRNATGYVPCYSVKTITFPVDVAVECKHHMI

CDS
/note="R11 family; contains hydrophobic domain"
11469..11924
/codon_start=1
/product="UL5"
/protein_id="AA00656.1"
/db_xref="GI:19881036"
/translation="MELISYPMRGEFALCAPGHQYNSVTVTLVLCVAVSSLTAS
TSAAGSGYGNLILORALNSDPDPTTSLPRLQALPAHASSSGCFEFGYGLAIHA
AVNTAVLVEGLIFANFVHPQTIHGWRDLRDLHRTLGKRRTORLVNS"
12130..12981
/note="R11 family"
/codon_start=1
/product="glycoprotein UL6"
/protein_id="AA00657.1"
/db_xref="GI:19881037"
/translation="MPPRSFGCGGLNKVWICSLILVLYVCAAPGSPHMSRVRRQT
SLSLPSCSPVNCYGGDVSINSTIYPACNSTEMGRYNSFWPPLCOLMGHMRLSGO
NRLSLTCSROHLTLHSTSDGYTGTYGVGNCPHHHEIMKCFNLTVLAKPTTAAAP
TTTSVPTPLILITTRNTYVGVSPANTVLTSTMTTGTAGNASVANGMEYROYOPTSLA
QTHRRAPLNATNADVAVNTAVTASMGVLVLLLATVLYLPDLGLPQTANRRMRROGR
EEOHLIL"
13052..13693
/note="R11 family"
/codon_start=1
/product="glycoprotein UL7"
/protein_id="AA00658.1"
/db_xref="GI:19881038"
/translation="MAADPHTLMSLGLCKALMLISCLILVAFLLASSSTTTMYVY
SGPPGRPLSLANFTQDDDVHMYRLKGNSTVSLCSQWQDGVYIARSNLSCLPWL
ILFNMTVNDGLLYVNGTNGTSTYVNTYIGLOFAPKTKPKKTKTNRAKASE
RTGMSLFRYARBDLSYRRKDDNNIHLGLVAGLFLALYICLMGLKILCTH"
13799..14305
/note="R11 family"
/codon_start=1
/product="glycoprotein UL8"
/protein_id="AA00659.1"
/db_xref="GI:19881039"
/translation="MNVGQPPSPPEPSPSESTWNTTGGDGBRSVTTTVAVST
RPTTISAGKNASTSTRATPATTTRITTRITRYVTRTRNSGVYITRTTTPROPDCL
LRTQUSYHHTVOAOPKIAVHTVLLILFLFYLVILFCLRIPOKLYDKWNRNRGQ
VVVVTTEL"
14327..14860
/note="R11 family"
/codon_start=1
/product="glycoprotein UL9"
/protein_id="AA00660.1"
/db_xref="GI:19881040"
/translation="MEYFVSVLTYCNKLHEVPREVECKKVTYIGQNYSLKSTHW
SNSVSVHTVSSLYMCKERESNDAPENFVNTDIOCNCEEELLLELPTQYTAAYY
RGDYVPRCMLYSCYNTVAVNRREYAEKHPASSIWIPIPAVYTLILLISIKIKIQ
RWHEEMOYRYRDYVT"
14959..15657
/note="R11 family"
/codon_start=1
/product="glycoprotein UL10"
/protein_id="AA00661.1"
/db_xref="GI:19881041"
/translation="MPFGSYVNGCLFNFVLSANFKYFESEACEHTTYETHPILLG
GKPLGAGHOTAYWKHKCDSTNSNDKLPCLCYPPRNSKGKIDESAENFTFNYLCSN
STLILARMLTDAGEYCRKNSGRHDSNMTSMSCYRVIVPIRTKTSKPKBSGPTRYK
TYDANSVTLLLEEDPLFQTHRSTQNHAIWLFIAVIVIVILFEFKIPOKLPDKKL
HKSVAKTGHSFAH"
15758..16468
/note="R11 family"
/codon_start=1
/product="glycoprotein UL11"
/protein_id="AA00662.1"
/db_xref="GI:19881042"
/translation="KCHRLNFKCTSFYAAMICVPTSTDLOMACVEKARQGSVNT
FDIIRISGKNOSTYWRGSRYNADMKNCTGTGNIYHSTIRLNTYTCQKNFSLLIYNT
SEVSNKYITRTYRSTSTNSWSFDTCFKLTVIYKPKPKRTTTLKRPQEPVTKPKTT

CDS
VVDYRYSDEGATVNSPGIVSSQROSATITISWICLISIVIVILFVFRIPQKILLP
FMCPRKDEITLMIPTTEL
16623..18392
/codon_start=1
/product="UL13"
/protein_id="AAM00663.1"
/db_xref="gi:19881043"
/translation="MVVYSRGLTSTYLLPLLLCKVPLLLTWPSAHGLDIVDELSH
DYETISVFRAMQOVGFMLPAPLWGRSEIDEDPSSPAQADVDVRSPPRP
RLQSPYHNRPPPLPSGLRMQHELOFLQYRQOELLQREERQHQRRYRWR
RPTPEPPDPSPYPASSILPAPFAPASLANAEOLNARGSRASRGMASEPAS
SVEEOYRVRVGNVTRRRHHPOHRSYRRNLVANGRDSILLARLIHNOTRTGY
RCRYGRNRGSARRRDSGSGAAGHSGRAGSOLRRERYIVDIOLFRCGWT
RQASRIRTRREENTVMSDASRLRANFSRRITTYWQTVPGENPSAEGLAVPA
ADGVKETSQSMVTVTTEGERQKTEQVKAAGSEETIEKVFETDERVAEETKVE
EVQVVEEENNVVEETGEREDRDODAMIIWGEWWDLLDLETTAGCEVAVEK
EETTKGADADTDTVTYASSETTDDVDTQITNELPCELNNAEISSGRAVGTCPRRREGPHR
SEFRLGLMSHLARRAISVS"
18719..19780

CDS
Query Match 0.0%; Score 20; DB 1; Length 241087;
Best Local Similarity 100.0%; Pred. No. 7.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 61845 AACACACAGCGCTGCACCGA 61864
|||||
DB 155301 AACACACAGCGCTGCACCGA 155320

RESULT 37
AF061207 478 bp RNA linear VRL 02-APR-1999
LOCUS Sindbis virus isolate SAAR86 polyprotein gene, partial cds.
DEFINITION AF061207
VERSION AF061207.1 GI:3132537
KEYWORDS
SOURCE Sindbis virus
ORGANISM Sindbis virus
VIRUSES: ssRNA positive-strand viruses, no DNA stage; Togaviridae;
Alphavirus; WEEV complex.
REFERENCE 1 (bases 1 to 478)
AUTHORS Samuels,L.M., Lindsay,M.D., Poldinger,M., Coelen,R.J. and
Mackenzie,J.S.
TITLE Geographic distribution and evolution of Sindbis virus in Australia
JOURNAL J. Gen. Virol. 80 (Pt 3), 739-748 (1999)
MEDLINE 99190435
PUBMED 10092014
REFERENCE 2 (bases 1 to 478)
AUTHORS Samuels,L.M., Lindsay,M.D., Poldinger,M., Coelen,R.J. and
Mackenzie,J.S.
TITLE Direct Submission
JOURNAL Submitted (22-APR-1998) Microbiology, University of Western
Australia, QBIT Medical Centre, Nedlands, WA 6907, Australia
LOCATION/Qualifiers
source 1..478
/organism="Sindbis virus"
/mol_type="genomic RNA"
/isolate="SAAR86; South African isolate"
/db_xref="taxon:11034"
49..>478
/codon_start=1
/product="polyprotein"
/protein_id="AAC16287.1"
/db_xref="GI:3132538"
/translation="MNRGFSNMVGRPPFAPATAMRRRRROAAPMPARNGLSAQIOO
LTVASVAVIGQATRPOTRRPPROKQAPKOPPKPKKTKTEKKKKQKQAPKPKPK
RORAKTLADRLDVLKNEGSDVIGHALAMGKVMKPLHYK"
49..>478
mat_peptide /product="capsid protein"
BASE COUNT 147 a 149 c 121 g 61 t
ORIGIN
Query Match 0.0%; Score 19; DB 1; Length 478;

Best Local Similarity 100.0%; Pred. No. 16;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 71673 CCAAGACACACCGCAGC 71691
|||||
DB 274 CCAAGACACACCGCAGC 292

RESULT 38
AF123881/C 1511 bp mRNA linear VRL 11-AUG-1999
LOCUS Multiple sclerosis associated retrovirus element gag polyprotein
DEFINITION (gag) mRNA, partial cds.
ACCESSION AF123881
VERSION AF123881.1 GI:5726237
KEYWORDS
SOURCE Multiple sclerosis associated retrovirus element
ORGANISM Multiple sclerosis associated retrovirus element
VIRUSES: Retroid viruses; Retroviridae.
REFERENCE 1 (bases 1 to 1511)
AUTHORS Komurian-Pradel,F., Paranhos-Baccala,G., Bedin,F.,
Oumanian-Paraz,A., Sodoyer,M., Ott,C., Rajoharison,A., Garcia,E.,
Mallet,F., Mandrand,B. and Perron,H.
TITLE Molecular cloning and characterization of MSRV-related sequences
JOURNAL associated with retrovirus-like particles
VIROLOGY 260 (1), 1-9 (1999)
MEDLINE 99335590
PUBMED 10405350
REFERENCE 2 (bases 1 to 1511)
AUTHORS Komurian-Pradel,F., Paranhos-Baccala,G., Bedin,F.,
Oumanian-Paraz,A., Sodoyer,M., Ott,C., Rajoharison,A., Garcia,E.,
Mallet,F., Mandrand,B. and Perron,H.
TITLE Direct Submission
JOURNAL Submitted (26-JAN-1999) UMR103, CNRS/Biomerieux, 46 Allée D'Italie,
Lyon Cedex 07 69364, France
LOCATION/Qualifiers
source 1..1511
/organism="Multiple sclerosis associated retrovirus
element"
/mol_type="mRNA"
/specific_host="Homo sapiens"
/db_xref="taxon:89382"
/clone="GL2"
/note="multiple sclerosis patient
cell-free plasma"
<1..>1511
/gene="gag"
<1..1060
/gene="gag"
/note="encodes partial matrix and capsid proteins; gag
polyprotein (CA) has 3 potential glycosylation sites"
/codon_start=2
/product="gag polyprotein"
/protein_id="AAD48375.1"
/db_xref="GI:5726238"
/translation="LERTLENNQDQNTLRKKRPIFCSTAMPQYPLQGRWTLPES
SINRITLQDLFCRKSGKSEVPYVOTFSLRNSQCKCGICLPTGSPSPPYRS
VPSPTSTNDPPLATYQVKEIDGVNNEKRSANIPRLCLQAVNGGEGPAPVAP
FSLSDKQIKIDLKFSNDPDGVIDVLOGIQSDPLWRDILMLNLTPTNERSAAV
TAREFGDLWTLSOANNRMTTEERTTPGQGVSPVPHMTSEHGMCVCHLITCV
LEGRLKTRKKPMYSMSSTIQGKEENLTAVLDRLRLKHTSLSPDSIGQILND
KFTOSADIRKNKSLP"

BASE COUNT 481 a 361 c 341 g 328 t
ORIGIN
Query Match 0.0%; Score 19; DB 1; Length 1511;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 61342 ACATCAATATAGCGCTCAG 61360
|||||
DB 558 ACATCAATATAGCGCTCAG 540

RESULT 39
LOCUS MR008421/c 2359 bp RNA linear VRL 26-APR-2001
DEFINITION Murine rotavirus EC outer capsid protein VP4 gene, complete cds.
ACCESSION U08421
VERSION U08421.1 GI:475678
KEYWORDS
SOURCE Murine rotavirus
ORGANISM Viruses; dsRNA viruses; Reoviridae; Rotavirus; unclassified
rotaviruses.
REFERENCE 1 (bases 1 to 2359)
AUTHORS Dunn,S.J., Burns,J.W., Cross,T.L., Vo,P.T., Ward,R.L., Bremont,M. and Greenberg,H.B.
TITLE Comparison of VP4 and VP7 of five murine rotavirus strains
JOURNAL Virology 203 (2), 250-259 (1994)
MEDLINE 94330134
PUBMED 8053149
REFERENCE 2 (bases 1 to 2359)
AUTHORS Dunn,S.J.
TITLE Direct Submission
JOURNAL Submitted (07-APR-1994) Stephen J. Dunn, Stanford University, Medicine/Gastroenterology, 3801 Miranda Avenue, Palo Alto, CA, 94304, USA
FEATURES
source location/Qualifiers
1. .2359
/organism="Murine rotavirus"
/mol_type="genomic RNA"
/strain="EC"
/db_xref="taxon:28327"
/lab_host="Macaca mulatta"
order(1. .15, 2348. .2359)
/note="PCR primer binding"
10. .2337
/function="outer capsid protein"
/codon_start=1
/product="VP4"
/protein_id="AA050484.1"
/db_xref="GI:475679"
/translation="MASLIYRQLTNSFTVLDSEITIGAEKQSQSYVANGPFAOIC
YAPVWGEINSDSTVEPVLDGPTPIAFPOPEYIILSPVPGVAEETNVDNM
ITAIIEPNPTTSRYTIFGTEQLVENSSTDKMFIDELKTSVGSARYMILAS
GTLCAVAKHTDLYSYIGETPGAGVAFFEHFTNLTAHSDFYIIPMAQOSICTRY
INNGLPIONTRNVVARHLSARSIIITQAOANENIIVSKTSLEKQENRDIITRFK
ANAIKSGGIGYKWKSEISFPKANYQTYRMDGEVTAHTTCSVGNVNNDEFGALPT
DPVLSREVIKENSFYIDYWDSDQAFRRNMYVRSIADLNTVCTGCTGTFESIPVGO
WPAWTGAVSLRAGVTLSTQFTDFVLSLSRFRRLSVAPPSITRTVSGLYGLP
ADPNNGREYVELAGRSLISLVPSNDYQPIKNSVYRQDLERQELREENALS
QETALSQVLALPLDMFSMFSGIKATLDVAKGMATNMKFKSGIATSVSAMTES
LSDAASVSRSSTGTSISTSWMTDVSRAVDNDNTVSTOTATISRLRKEIT
TQTEGMNFDDISAVALTKTKLDKSVQIAPNLPDITVTEASEGTFINRSGYRVNNDEARE
TCTDGRFRAFRVDFFELPDYVQKFAADVESPYSALIDKTKLKNLNDNTGISKEDA
FSLRSPRYRLRTINGNPTIRNRITQQLMOCRL"

BASE COUNT 710 a 516 c 542 g 591 t
ORIGIN

Query Match 0.0%; Score 19; DB 1; Length 2359;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 59664 ACCTATTGTGAAAAAAGC 59682
|||||
Db 595 ACGTATTGTGAAAAAAGC 577

RESULT 40
LOCUS AF329888 2689 bp DNA circular VRL 15-MAR-2002
DEFINITION Maize streak virus strain MSV-E isolate MSV-Pat, complete genome.
ACCESSION AF329888
VERSION AF329888.1 GI:14794711
KEYWORDS

SOURCE Maize streak virus
ORGANISM Viruses; ssDNA viruses; Geminiviridae; Mastrevirus.
REFERENCE 1 (bases 1 to 2689)
AUTHORS Martin,D.P., Willmott,J.A., Billharz,R., Velders,R., Odhiambo,B., Njuguna,J., James,D. and Rybicki,E.P.
TITLE Sequence diversity and virulence in Zea mays of Maize streak virus isolates
JOURNAL Virology 288 (2), 247-255 (2001)
MEDLINE 21488909
PUBMED 11601896
REFERENCE 2 (bases 1 to 2689)
AUTHORS Martin,D.P., James,D. and Rybicki,E.P.
TITLE Direct Submission
JOURNAL Submitted (20-DEC-2000) Microbiology, University of Cape Town, Private Bag, Cape Town, WC 7000, South Africa
FEATURES
source location/Qualifiers
1. .2689
/organism="Maize streak virus"
/vifion
/mol_type="genomic DNA"
/strain="MSV-E"
/isolate="MSV-Pat"
/db_xref="taxon:10821"
/country="South Africa"
/note="Isolated in 1999 from severely infected Digitaria"
join(2682. .2689, 1. .2)
/note="conserved nonanucleotide at origin of (+) strand replication"
19. .2664
150. .455
/gene="V1"
150. .455
/gene="V1"
/note="MP: facilitates intercellular movement of viral DNA"
/codon_start=1
/product="movement protein"
/protein_id="AAK73467.1"
/db_xref="GI:14794712"
/translation="MDPOSANYSIPRPPTAPPAAGVPMHVGAVLSPALLCIYL
LYLWLDLILVLAARKRSTEEILFQSEAVDRSPITPTLETPAHPGPFVPSG-
466. .1207
/gene="V2"
466. .1200
/gene="V2"
/note="nuclear localized ss/ds DNA binding protein"
/codon_start=1
/product="coat protein"
/protein_id="AAK73468.1"
/db_xref="GI:14794713"
/translation="MSTSKRADEVOMNRSTKKASAPVKKTKGKADPSPLOIOR
LLHSGDMITVPSGSGCDLITVYRGSDEGRHRSITITVGVGDYHRYADAGACRYS
NRGTGVMVLVDTTPGGNSPSTKIDIFAPDLVAMPPTWKVRELCHEVVKRRWLET
METDGRIGSDIPPTNOSWPCRNIDIFKFTSGVGRYOMKNVNDGGAIGORALYM
VIAPGNGVTFTHAGQFRLYFKSVGNQ"
1203. .1207
/gene="V2"
complement(1217. .2520)
/gene="C1/C2"
complement(1217. .1221)
/gene="C1/C2"
1274. .1349
/note="origin of (-) strand replication"
complement(join(1364. .1789, 1882. .2520))
/gene="C1/C2"
/note="replication initiator/associated protein; required for initiation and termination of viral DNA replication"
/codon_start=1
/product="Rep"
/protein_id="AAK73470.1"
/db_xref="GI:14794715"
/translation="MASSSSNRSFLHRNANTFLTYPHCPENPEIISOKLMDLVARWNP

gene	/note="replication initiator/associated protein ORR1; possibly involved in cell cycle regulation"			
CDS	/gene="C1" complement(11705..2520) /gene="C1"			
repeat_region	/db_xref="GI:14794714"			
GC_signal	/translation="MASSSSNRSLRHNANPFLTYPHCPENPEITISOKIDVIAWRNP /product="Repa" /protein_id="AAK73469.1"			
BASE COUNT	663 a	615 c	719 g	692 t
ORIGIN				
Query Match	0.0%; Score 19; DB 1; Length 2689;			
Best Local Similarity	100.0%; Pred. No. 19;			
Matches	19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	69150 AGAAATCCAGAAATCATC 69168			
Db	2446 AGAAATCCAGAAATCATC 2428			
RESULT 41				
AF339477				
LOCUS	AF339477 4676 bp ss-RNA linear VRL 02-FEB-2003			
DEFINITION	Babanki virus strain Dakay 251 nonstructural protein 4 gene, partial cds; and structural polyprotein precursor, gene, complete cds.			
ACCESSION	AF339477			
VERSION	AF339477.1			
KEYWORDS	GI:28193938			
SOURCE	Babanki virus			
ORGANISM	Babanki virus			
REFERENCE	Viruses; ssRNA positive-strand viruses, no DNA stage; Togaviridae; Alphaviruses; WEEV complex.			
AUTHORS	1 (bases 1 to 4676)			
TITLE	Kinney,R.M. and Pfeiffer,M.			
JOURNAL	Nucleotide sequence analyses of the 26S mRNAs of viruses of the genus Alphavirus			
REFERENCE	Unpublished			
AUTHORS	2 (bases 1 to 4676)			
TITLE	Kinney,R.M. and Pfeiffer,M.			
JOURNAL	Direct Submission			
FEATURES	Submitted (23-JUN-2001) Abovirus Diseases Branch, Centers for Disease Control and Prevention, P.O. Box 2087, Fort Collins, CO 80522, USA			
SOURCE	Location/Qualifiers			
	1..4676			
	/organism="Babanki virus"			
	/virus			
	/mol_type="genomic RNA"			
	/strain="Dakay 251"			
	/db_xref="taxon:48540"			
	/country="Cameron"			
	/note="isolated in 1969; virus passage P7/SW2/BHK21-1"			
	<1..573			
	/codon_start=1			
	/product="nonstructural protein 4"			
	/protein_id="AA033324.1"			

[illegible]

hit population in Albania during the 1996 outbreak

JOURNAL
J. Clin. Microbiol. 40 (1), 316-317 (2002)
MEDLINE
21635047
PUBMED
11773144
REFERENCE
2 (bases 1 to 6745)
AUTHORS
Marturano,J. and Fiore,L.
TITLE
Direct Submmission
JOURNAL
Submitted (23-SEP-2001) Laboratory of Virology, Istituto Superiore
di Sanita', Viale Regina Elena 299, Rome 00161, Italy

FEATURES
Location/Qualifiers

1..6745
/organism="Human poliovirus 1"
/mol_type="genomic RNA"
/strain="3788ALB96"
/db_xref="taxon:12080"
5'UTR
CDS
555..>6745
/codon_start=1
/product="polyprotein"
/protein_id="AAL33795.1"
/db_xref="GI:18146571"

/translation="MGAQVSSQKYGAGHNSRAYGSGTINNTINYYRDSASNAASKO
DESDPSKFTPEPKVDVLTAPMLNSPIEACGSDRLANTLNGSTITTOEANSV
AYGRMPEYLRDSEANPDQPEPVAAREFTLEVSATKSKMMWMLPMTLRDMGL
FGQNMVYHILRGSGYTVHOCNAKSFHOGALGAVAPMCLAGSNTPTPTSYONAN
PGEKGFTEFTGFTDNNOTPARSEVLMITSSEMAPYAMARRPILITLNNCATIV
LPVNSLSDSMVKNHNMGIALLPLAPLINTNESSEPELITLTAPOCCENGRLIT
LPRQLGLPVNTPGSGNOYLTADNOSPCLDEPOTPIDIPGVKMMELAEIDTMI
PFDSATKKNMTMAYRVLSDPKPHTDIDILSLSPASDPLSHTMCEILNTYTHMA
GSLKFTFLFCGSMATGKLLVSAAPGADPKRKKEALGTHVIMDIGLQSSCTMVP
WISMTYRQTIIDSTFEGYISVFQRTIVPLSTPREMDILGEVSAACNDSVRLRD
TTHIEOKAIAOGLCOMLESMDNTREKVGASTRDALPTNTESSGPAHSKIPALTAV
ETGANPLPVDTQTRHVVOHRSSESSIEFPARGACVITMVDNASTSKDKLE
SVMTITTKDTQVLRKLEFFYSRDMFEFTVIANFETNNKALNOYOMVPPG
APVEKMDITYTWSNSPSIFTYTGAPARISVYVIGISNAYSHFYDFCSVPLKDS
AALDSDLGKASLNDGLTAVRVNDHNPVTSKIRYLPKHRLMCPPPRAVAY
YGPVDYKDGTLPLSTRKDLTYGYGHONKAVYAGYICNVHLATOCPLONAVSIM
NRDLIYDSKAGQDSTARCNQNTGVYCESRRKYVPYSPFTFOYWEANDYPAR
QSHMLIGHFASPGDCGILRCQHGVIITAGBGRVAFSDIDRLHAYEEAEQGI
SNYINSIGAARSGFTQOIGKISLSEIMSVSTTEKILKMLIKITISLGIITRYED
TTTVALTLALGCDVSPWOMLKKACDILEIPYIYIRODSWLKKEFTACNAKCLEVY
SNKISKFTDLMLKELIIPARNDLEFVTRKLOLEMLENDISTIHOSCPQEHQELFVN
VRLWLSISKRFAPLYAEAKRIQKLEHGNNYIOFBSKRIEPPCLVLVHSGGTTKSA
TNLJARIAIEKENTISLPPDSHFDGKQGVVIMPNQPEGADMLKFGOMTSTVE
FIPPMASLEEKILFTSNYVASTNSSRITPPVAHSDALARRAFDMIDIOIMGYSR
DGKILNMAATEMKCHOPANFKCCPLMGKALIOIMDKSRVRYSTIOITMIINER
NRSNIGCMCHALFOGRLQYKDLKIDIKITPPPECINDLLOAVDSQEVYDCERKGL
VNISQVQLERNINRAMTILQAVTFPAVAGVYVMYKLFAGHOGAYTGLPKKPNIP
TVRTAKVOGPGFDYAVAMAKRNIYATITGKGFMLGHDVAVLPHDSGETEIVID
GKEVEVIDAKALEDOVYLNGLIEITITVTLKRNKFPDRIPIHQITETMDGVLIWTSK
YPMNVYPVAGTVEOYVNLGROLIVTLAMNPPRAGCGGILTCGVKIDIMHAGNG
SHGFAALAKRSYFTQSGEIOIWRPSKEVGPVIANPSKTLPESAFHYEGVKEPA
VLTKNDPRLKIDFEPAITPSKYVKITPEVDYEMKAVDHYAGQLMSLEINTPOKLED
AMVGTDLAEALDITTSAGYRYVALGKKRDLNLTOKRDKEMORLMDYVGNLPTVY
VKDLRSKSYEOKESRLIEASSLNDVSEALMAGNLYAAFKNGDVYTGAVCGDDP
LFWSKIPVIMEEKLFAFDYTGDAISLSPAMEALMVEKIFGFGRDVYIYLNHSHH
LYKNKTYCVRKGMPSGSGSTIFNSMINLIRTLTKTYKGIIDDLH."

mat_peptide
555..761
/product="vp4"
762..1571
/product="vp2"
1572..3029
/product="vp3"
3030..3935
/product="vp1"
3936..4382
/product="protease p2-A"
4383..4763
/product="p2-B"
4764..5561
/product="p2-C"
5562..5921
/product="p3-A"

mat_peptide 5922..5987
/product="vp4"
mat_peptide 5988..6557
/product="protease p3-C"
mat_peptide 6558..6745
/product="polymerase p3-D"
BASE COUNT 2001 a 1577 c 1555 g 1612 t
ORIGIN

Query Match 0.0%; Score 19; DB 1; Length 6745;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 42568 GGTGATCATGATGATGCA 42586
DB 5362 GGTGATCATGATGATGCA 5344

RESULT 43
LOCUS AY056702/C
DEFINITION Human poliovirus 1 strain 3914ALB96 polyprotein gene, partial cds.
ACCESSION AY056702
VERSION AY056702.1 GI:18146570
KEYWORDS
SOURCE
ORGANISM Human poliovirus 1
Virus; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.

REFERENCE
1 (bases 1 to 6745)
AUTHORS Marturano,J. and Fiore,L.
TITLE Investigation of the presence of recombinant polioviruses in the
hit population in Albania during the 1996 outbreak
J. Clin. Microbiol. 40 (1), 316-317 (2002)

JOURNAL
J. Clin. Microbiol. 40 (1), 316-317 (2002)
MEDLINE
21635047
PUBMED
11773144
REFERENCE
2 (bases 1 to 6745)
AUTHORS Marturano,J. and Fiore,L.
TITLE Direct Submmission
JOURNAL
Submitted (23-SEP-2001) Laboratory of Virology, Istituto Superiore
di Sanita', Viale Regina Elena 299, Rome 00161, Italy

FEATURES
Location/Qualifiers
1..6745
/organism="Human poliovirus 1"
/mol_type="genomic RNA"
/strain="3914ALB96"
/db_xref="taxon:12080"
5'UTR
CDS
555..>6745
/codon_start=1
/product="polyprotein"
/protein_id="AAL33796.1"
/db_xref="GI:18146571"

/translation="MGAQVSSQKYGAGHNSRAYGSGTINNTINYYRDSASNAASKO
DESDPSKFTPEPKVDVLTAPMLNSPIEACGSDRLANTLNGSTITTOEANSV
AYGRMPEYLRDSEANPDQPEPVAAREFTLEVSATKSKMMWMLPMTLRDMGL
FGQNMVYHILRGSGYTVHOCNAKSFHOGALGAVAPMCLAGSNTPTPTSYONAN
PGEKGFTEFTGFTDNNOTPARSEVLMITSSEMAPYAMARRPILITLNNCATIV
LPVNSLSDSMVKNHNMGIALLPLAPLINTNESSEPELITLTAPOCCENGRLIT
LPRQLGLPVNTPGSGNOYLTADNOSPCLDEPOTPIDIPGVKMMELAEIDTMI
PFDSATKKNMTMAYRVLSDPKPHTDIDILSLSPASDPLSHTMCEILNTYTHMA
GSLKFTFLFCGSMATGKLLVSAAPGADPKRKKEALGTHVIMDIGLQSSCTMVP
WISMTYRQTIIDSTFEGYISVFQRTIVPLSTPREMDILGEVSAACNDSVRLRD
TTHIEOKAIAOGLCOMLESMDNTREKVGASTRDALPTNTESSGPAHSKIPALTAV
ETGANPLPVDTQTRHVVOHRSSESSIEFPARGACVITMVDNASTSKDKLE
SVMTITTKDTQVLRKLEFFYSRDMFEFTVIANFETNNKALNOYOMVPPG
APVEKMDITYTWSNSPSIFTYTGAPARISVYVIGISNAYSHFYDFCSVPLKDS
AALDSDLGKASLNDGLTAVRVNDHNPVTSKIRYLPKHRLMCPPPRAVAY
YGPVDYKDGTLPLSTRKDLTYGYGHONKAVYAGYICNVHLATOCPLONAVSIM
NRDLIYDSKAGQDSTARCNQNTGVYCESRRKYVPYSPFTFOYWEANDYPAR
QSHMLIGHFASPGDCGILRCQHGVIITAGBGRVAFSDIDRLHAYEEAEQGI
SNYINSIGAARSGFTQOIGKISLSEIMSVSTTEKILKMLIKITISLGIITRYED
TTTVALTLALGCDVSPWOMLKKACDILEIPYIYIRODSWLKKEFTACNAKCLEVY

SNNKISKIFIMWLEKRIIPQARDKLEEVTKIKOLEMLENOISTIHQSCPSQHOEILFNN
 VMLWSISKRFAPLVAEAKRIQKLEHGINNYIOFQSKHRIEPCILVHSGPSTTKSVA
 TNLIAALAEKENTISLPPDSHSGYQOQGVAVINDPQNEGADMKLFCQWVSTVE
 FIPMASIEEKILFTSNVLAISTNSRITPTVAHSDALARRAFADMDIOIMGEYSR
 DGLKLNMAATECKNCNCHOPANFKCCPLWGAALQIOMDSRVRYSIDDIITMIINER
 NRSNNGNCEALFOGPIQOYKDKIDIKITPTPECCINDLQAVDSQSEVADYCEKRMU
 VNISQVOLEARNINRAMTILQAVTTFAAAGVAVYWKLFAGHQGAVTGLPKKPNIP
 TVRTAKVOGPGFDYAVAMAKRNIIVATTGKGFETMGMVNDNAVLEPHDSPEETIYID
 GREVEYIDAKALEDOVGNLEITIIVTLKNEKERDRIKPHIPIOTIETNDGVLITVNSK
 YPMNVYVAVTEOGVNLNGROLIVTLKNEKERDRIKPHIPIOTIETNDGVLITVNSK
 SHGFAALKRSYFTOSOGIOMIRPSKEGYVIVNAPSKTKLEPSAFHYPFGVKEPA
 VLTQNDPRKLTDEFEAKIESKYGNKTEVDEYMEKAVDHAGOLMSLETIKPMOCIED
 AMKGIDGELALDITTSAGPYVALGKKRDKILINKOTRDKEMORLIDITGINLPIVTV
 VDELRKSKVEQGSRLIEASSLNDVSAMRAFGNLVAFKHNKPGVITGSVAVGCDP
 LEWSKIPVLMEEKLEAFDYTGDAISLSPAMFALKMVEKIFGGRVDYIDYLNHSHH
 LYKNTYCVKGGMPSCSGTISFNSMINNLTLLTKTKYKIDLDHL"
 555..761
 mat_peptide /product="VP4"
 762..1571
 /product="VP2"
 mat_peptide /product="VP2"
 1572..3029
 /product="VP3"
 mat_peptide /product="VP3"
 3030..3935
 /product="VP1"
 mat_peptide /product="VP1"
 3936..4382
 /product="protease P2-A"
 mat_peptide /product="protease P2-A"
 4383..4763
 /product="P2-B"
 mat_peptide /product="P2-B"
 4764..5561
 /product="P2-C"
 mat_peptide /product="P2-C"
 5562..5921
 /product="P3-A"
 mat_peptide /product="P3-A"
 5922..5987
 /product="VPg"
 mat_peptide /product="VPg"
 5988..6557
 /product="protease P3-C"
 mat_peptide /product="protease P3-C"
 6558..>6745
 /product="polymerase P3-D"
 BASE COUNT 2002 a 1575 c 1555 g 1613 t
 ORIGIN
 Query Match 0.0%; Score 19; DB 1; Length 6745;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 42568 GGTGAATCATGAGTTGCCA 42586
 |||||||
 Db 5362 GGTGAATCATGAGTTGCCA 5344
 RESULT 44
 AY056703 6745 bp RNA linear VRL 04-MAR-2002
 LOCUS Human poliovirus 1 strain 4019ALB96 polyprotein gene, partial cds.
 DEFINITION AY056703
 ACCESSION AY056703
 VERSION AY056703.2 GI:19073875
 KEYWORDS
 SOURCE Human poliovirus 1
 ORGANISM Human poliovirus 1
 Viruses; ssRNA positive-strand viruses, no DNA stage;
 Picornaviridae; Enterovirus.
 REFERENCE 1 (bases 1 to 6745)
 AUTHORS Marturano,J. and Fiore,L.
 TITLE Investigation of the presence of recombinant polioviruses in the
 hit population in Albania during the 1996 outbreak
 JOURNAL J. Clin. Microbiol. 40 (1), 316-317 (2002)
 MEDLINE 21635047
 PUBMED 11773144
 REFERENCE 2 (bases 1 to 6745)
 AUTHORS Marturano,J. and Fiore,L.
 TITLE Direct Submission
 JOURNAL Submitted (23-SEP-2001) Laboratory of Virology, Istituto Superiore
 di Sanita', viale Regina Elena 299, Rome 00161, Italy

REFERENCE 3 (bases 1 to 6745)
 AUTHORS Marturano,J. and Fiore,L.
 TITLE Direct Submission
 JOURNAL Submitted (04-MAR-2002) Laboratory of Virology, Istituto Superiore
 di Sanita', viale Regina Elena 299, Rome 00161, Italy
 REMARK Sequence update by submitter
 COMMENT On Mar 4, 2002 this sequence version replaced gi:18146572.
 FEATURES
 source
 1. 6745
 /organism="Human poliovirus 1"
 /mol_type="genomic RNA"
 /strain="4019ALB96"
 /db_xref="taxon:12080"
 <1..554
 555..>6745
 /codon_start=1
 /product="polyprotein"
 /protein_id="AA133797.1"
 /db_xref="GI:18146573"
 /translation="MGAQVSQKVGAGHNSNRNAYGSGTINTYNTYRDSASNAASKQ
 DFSQPSKFEPEKDVILITAPMLNSPNIACGYSDRVINLTGNTSTIQAASAV
 AYGRMPEYLRDSEANVDQPTPEPVAAMFVTLFVSWTKESKGMWKLPNLRDMGL
 FQGNMYHYILGSGYTVHVOGNASKFEHOGALGVAVPEMCLAGDSNTPTPTSYONAN
 PEKGGTFTGTFPTNNOTTPARSPVIMTTSSEMAPYAMARRPPIIINRTNNCAIV
 LPYVNSLSDSMVKHNNMCIATLPLAPLANESSEPIITITTIAPMCCERGNLRT
 LPRLOGLPVNMTGSMOYLTAADNFQPCALPEFDVPPIDTIGEVKMMELAEIDMTI
 PPDLSATKKNTEMRYVOLSDKPRHTDDPLICLSIPASDPRLSHMLGELINLYHMA
 GSKLTFELFCGSMATGKLIVSAPPAGAPPKRREAMGTIVINDIGQSSCTWVP
 WISNTFYROTIDSFTFEGGYISFYQTRIVLSPREMDIGFVACNDPFSVRLRD
 TTHIRKALIAQIGOMLESMINTVREKYGASTSRALPTESSGSPHAKELPALTAV
 EFGANPNIPVSPDTQTRHYVHORSRSSESIEEPAPGACVITIMYDNPASTSKLFL
 SYWKITTYRTVQLRKLEFTTSRDMEETVITANFTETNNGHALNOVYOQIMYPRG
 AVPEKWDYTWQTSNPSIFETYGAPARISVPPVGVISNAVSHEYDGSKVPALDOO
 AALGDSLGAASLNDIGILAVRVNDHNPVTSTKIRYLAKRKHRLAMCPRPRVAV
 YPGVDYKDGDTLAPLSTKDLTYGQHOKAVYTAQYKICNLAHQEDLOAASIMM
 NPDILIVDSKAGQDTSIARCNCTGYGSESRKRYVSEVGPPTQYMANVYPARY
 OSHMLIGHGFAAPGCGGTLRCOHGIVGITTAGGEVLAFFSDIRDLAAEEEMAGGI
 SNTYNSLGAARSSGFTQOIGDKTISELTSVWSTTTEKLNKLIKITSIGITTRNED
 TTTVATLTLALGCDVSPWQMLKKKADILIEIYVIRGDSWMLKKEFEACNAGKLEWV
 SNNKISKIFIMWLEKRIIPQARDKLEEVTKIKOLEMLENOISTIHQSCPSQHOEILFNN
 VMLWSISKRFAPLVAEAKRIQKLEHGINNYIOFQSKHRIEPCILVHSGPSTTKSVA
 TNLIAALAEKENTISLPPDSHSGYQOQGVAVINDPQNEGADMKLFCQWVSTVE
 FIPMASIEEKILFTSNVLAISTNSRITPTVAHSDALARRAFADMDIOIMGEYSR
 DGLKLNMAATECKNCNCHOPANFKCCPLWGAALQIOMDSRVRYSIDDIITMIINER
 NRSNNGNCEALFOGPIQOYKDKIDIKITPTPECCINDLQAVDSQSEVADYCEKRMU
 VNISQVOLEARNINRAMTILQAVTTFAAAGVAVYWKLFAGHQGAVTGLPKKPNIP
 TVRTAKVOGPGFDYAVAMAKRNIIVATTGKGFETMGMVNDNAVLEPHDSPEETIYID
 GREVEYIDAKALEDOVGNLEITIIVTLKNEKERDRIKPHIPIOTIETNDGVLITVNSK
 YPMNVYVAVTEOGVNLNGROLIVTLKNEKERDRIKPHIPIOTIETNDGVLITVNSK
 SHGFAALKRSYFTOSOGIOMIRPSKEGYVIVNAPSKTKLEPSAFHYPFGVKEPA
 VLTQNDPRKLTDEFEAKIESKYGNKTEVDEYMEKAVDHAGOLMSLETIKPMOCIED
 AMKGIDGELALDITTSAGPYVALGKKRDKILINKOTRDKEMORLIDITGINLPIVTV
 VDELRKSKVEQGSRLIEASSLNDVSAMRAFGNLVAFKHNKPGVITGSVAVGCDP
 LEWSKIPVLMEEKLEAFDYTGDAISLSPAMFALKMVEKIFGGRVDYIDYLNHSHH
 LYKNTYCVKGGMPSCSGTISFNSMINNLTLLTKTKYKIDLDHL"
 555..761
 mat_peptide /product="VP4"
 762..1571
 /product="VP2"
 mat_peptide /product="VP2"
 1572..3029
 /product="VP3"
 mat_peptide /product="VP3"
 3030..3935
 /product="VP1"
 mat_peptide /product="VP1"
 3936..4382
 /product="protease P2-A"
 mat_peptide /product="protease P2-A"
 4383..4763
 /product="P2-B"
 mat_peptide /product="P2-B"
 4764..5561
 /product="P2-C"
 mat_peptide /product="P2-C"
 5562..5921
 /product="P3-A"
 mat_peptide /product="P3-A"
 5922..5987
 /product="VPg"
 mat_peptide /product="VPg"

```

mat_peptide      .5988. .6557
                  /product="protease P3-C"
mat_peptide      6558. .>6745
                  /product="polymyrase P3-D"
BASE COUNT      2000 a 1574 c 1556 g 1615 t
ORIGIN
Query Match      0.0%; Score 19; DB 1; Length 6745;
Best local Similarity 100.0%; Pred. No. 21;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      42568 GGTGAATCATGAGTTGGCA 42586
          |||||
          5362 GGTGAATCATGAGTTGGCA 5344

RESULT 45
AF463399/c      9538 bp      RNA      linear      VRL 01-NOV-2002
DEFINITION      Potato virus Y strain MN polyprotein gene, complete cds.
ACCESSION      AF463399
VERSION      AF463399.1 GI:19716315
KEYWORDS
SOURCE      Potato virus Y (PVR-MN)
ORGANISM      Potato virus Y
                Viruses; ssRNA positive-strand viruses, no DNA stage; Polyviridae;
                Potyviruses.
REFERENCE      1 (bases 1 to 9538)
AUTHORS      Fellers,J.P., Tremblay,D., Handest,M.F. and Lommel,S.A.
TITLE      The Potato virus Y MNr N1b-replicase is the elicitor of a veinal
                necrosis-hypersensitive response in root knot nematode resistant
                tobacco
FEATURES
            source
            1. 9538
                Location/Qualifiers
                1. 9538
                    /organism="potato virus Y"
                    /viral
                    /mol_type="genomic RNA"
                    /strain="MN"
                    /db_xref="taxon:12216"
                    /note="acronym: PVR-MN"
                    1. 9186
                        /codon_start=1
                        /product="polyprotein"
                        /protein_id="AA195713.1"
                        /db_xref="GI:19716316"
                        /translation="MATVSTICFGSEFECKLPYTPASSGCAEERVVLAADPFKDL
                            AQLSTRLSROEHATVRLKNGYVYRYKDTDLAROKLEKKERDERPOAASIV
                            SKISTAGDPPSKIEPOTPKGYITTPRYKATKTSIPKLTSSQMHLLIQVRRISA
                            KGSVHLNKRKAHVEYKEILGTRATVATHAMGARRVDFRCDMWTLCKLCLART
                            DMSNOVRTNIRKDSGYILNAGSLGHFGSGGLFVRSHEBKLDARSRYTOS
                            VDSMWQFSDAENFMKGLDGNMARLRYPSDHTCIAGLPVEDCGRIALMTHTSLPYK
                            ITCPTCAQOYANLPASDLKLLHKHARDSLGSQKDFVYVYKLEHLEHTPEYD
                            LNIELFNEIFKSGEKQSPKKNLBYLNFLPKCKRNTAHENQVQSLLELAROKN
                            RPDNIKRGDISFRNKLKSAKAMNLYLSCDNDLDKNAFLMCGREYHARFYSFEE
                            IDPAKGSAYEIRKHPNGTKRLSIGLVPLDLAERQMKGDYRKQPSVSKRTSSK
                            DGNVYVPCCTLLDGSAAVESTFYPTKHLVIGNSDQKFDVLPKDGSEMUYIAOG
                            YCINVFLLAMLIINVSSEDAKDTKVKVRCMCPKLGTPWPMDLATCAQMRLEYPDVH
                            DAELPRILVDHETQCHVYDSFSQTTGYHLLKASVSQLLIFANDELESDIKHRYG
                            GYPMACPELGSTISPRREGVYMSBSAALKLLKGTFRKRYNRQLLDPEYLLIISIL
                            SFGITLAMNNVSEFELAVRLMNEKOSTIMIASLALRVSAETLLAQRVIDAA
                            AVDLDATCDGFLNLYLPTALMVLQVYKSNRECDOTLKAGFSSYMSVQYIMENY
                            IOLLDANDKDLTWREKLSATWHSYAKRATITRYIKPTGRADLGLYINISPOAFLGSI
                            ORVKTAGSLNERFNNTKCVNISSEFIRIRFRLPLTVFVNSLVIYSMTSYVA
                            MGSITIIDORAKYRREIELMQIEKNEIYCMELVYASLQRLERDPTWDEYIEYLKSVNO
                            IYOPAOACMEYEDVHQRTSPVKNLQVYAPMALYINFDARSQCVFKTLNKRGV
                            LSLDHEVHQSLVDIKNFDERNEYIDELSEDITRISVLDTKRSDMWDROIOMGH
                            TLPHYRTGEHFMETLRATAVQVANDIAHSEHLDPLVRGAVSGSKSTGLPVLVAGSV

```

```

LLEPTRLAENVFKQLSSEPEFKKPTLRNGNSVFGSSPSISIMTSGFALHYFANNRS
OLNOENFVLEDECHVLDPSAMAFRSLLSYVTHQCYLKASATPVGREVFETQOPKVL
IYEDSIFQAFVADAGSKTNADVIOGSVULVYVSSYNDVDTLAKTLTKNNMVKVD
GRTMKHGCLEITVTKGYSKPHFVAVANNIENGTBGTIDIVNPGKLVSPFLDIIDNSY
AYNKISVSITGERIQRGLRGYRFRKKIGIALIFTEBGTIIEIPMTASEALACPAIYLP
VMTGAVSTLIGNCTAROVKTIQEFELSPFIQNVADHGSMPVYHDLKRYKLRND
MPLCDOSIPYRASSWLSAGEYKRLGVLDVDDVQYIAFHIREVPKLIENMLERIV
KRYDCLFSPISASSISKIATYLRDLFALIPRTLIVERLLEERIKQSPFSLIDEG
CSMSFSIYVNTVLRARYAKDYTAENIOKLEVRSQLKFSNLDGACDENILIKRES
LOFVHQAATSLAKDLKIGVKKSLVYVDLIAGAVGIGLMWSPRTOSEVYVOH
OGRKNSKRIQALKFRHARBRKAGFELDNNDDTIEEFGSAYRKKKGKGTTYGMGRSS
RRFINNGFDPTEYSFIQFVDPDLGAQIEENVYADRDQERFSEVRKMYVDDLEIM
QALHSNTSIAHAYFRKDWSDKALKVDLPNPNPLICTKTQIKAFPEPEBELQOTGAV
EVDVDDIPOEVEHEAKSLMRGLRDFNPIAQIVYCRKLVSEFGTSELVIGGAYIIA
NHLPFRSYNGSMSEVMSHGTFRKKNLSIYVPGRODILIKMPDFPVPOKLEFR
APONERLCIYNGTNOEKYASSLITETSTTVYVPGSTPEPKHMLEDDHCGCLPVYSTA
DCLVGIHSLANNVOTTYNSAFDEEFESKYIRTNBHEMTKSWYINPPTVYMGPKL
KESTPGLGKFTTKLVODLIDHVVVEQAHNSAMYEALGNLQAVAAKMSOLVTKHIV
KECGRYKFEELVDTEAEAFRPLMDAYGKSLNBDAYIKDLMKSKPIDVGIIVDDA
FEEAINRVYIYQMHGFOKCAVYTDQOEIFKALNMKAAGAMYGKKKDYFHFETDAD
KBEIYVOSCLRLYKGLGIGMNGSLKAEKKEKILANKRTFTPAFLDTLLGKVCVD
DENNOFYSKNIECQWYGMTRFYGGWDLRLRLPREMVCYDADGSGQFDSLPYLYINA
VLIINSTYMEDVGLQMLRNLYTELITPTIPSTPDVYKRRGNNSQSPSTVVDNSL
MVLAMHVALIEKIEFEEDMTVCFFVVGDDLLIATNEKESILDRLSQHSDELGN
YVSSSTRKKEELMFMSHRGLIEGVYVRLLEERVSITLQMDRADLPBHRLEICAA
MIESWGSELTHQIRRFYSMLIQOOPFAIADEGKAPYIATSLARKLYMDRAVDEEL
RIETEMVVALDDDESDSYEVHNOANDPTIDAGESSKKDAPGSGIOPPNKAKDQV
NAGTGTAVAPRIKATITSKMRKPSGAVGLNLTLDLOVAPQOIIDSNRATROSOEDT
WYEAIRVADIDIEETEMPYVNLMPWCIENGLSPNTINGWYMDGSEVOEYFLKPYE
NAKPLRLQIMAFHSQAEVYIEMRNKKEPYMRPYGLVRLRQTSLARVAFDEYVTSR
TPVRAREAHQIKKAALKAQSQRLEFLDGVSTOEBNTHTEEDVSPSMHLLAGVKN
M"
1. 825
    /product="p1"
mat_peptide      826. .2472
                  /product="HC-Pro"
mat_peptide      2473. .3471
                  /product="p3-6k1"
mat_peptide      3472. .5373
                  /product="CI"
mat_peptide      5374. .6825
                  /product="6k2-N1a"
mat_peptide      6826. .8391
                  /product="N1b-replicase"
mat_peptide      8392. .9183
                  /product="CP"
BASE COUNT      2981 a 1737 c 2257 g 2562 t 1 others
ORIGIN
Query Match      0.0%; Score 19; DB 1; Length 9538;
Best local Similarity 100.0%; Pred. No. 22;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Search completed: September 29, 2003, 17:28:43
 Job time : 25977 secs

THIS PAGE BLANK (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sv model

Run on: September 29, 2003, 17:28:46 ; Search time 1072 Seconds
(without alignments)
12605.660 Million cell updates/sec

Title: us-09-831-000-1
Perfect score: 40001
Sequence: 1 tcccacgggtcgcacacg.....agcgttgaataacacgac 40001

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 189188 seqs, 168911627 residues

Word size : 0

Total number of hits satisfying chosen parameters: 378376

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	34377	85.9 133719	1 AF083501	AF083501 Macaca mu
2	31222	78.1 130733	1 AF210726	AF210726 Macaca mu
3	33	0.1 130733	1 AF210726	AF210726 Macaca mu
4	33	0.1 130733	1 AF083501	AF083501 Macaca mu
5	26	0.1 108409	1 AF083424	AF083424 Acelline h
6	23	0.1 133661	1 U93872	U93872 Kaposi's sa
7	23	0.1 137508	1 KS075698	KS075698 Kaposi's sa
8	21	0.1 7433	1 HPA18F	M59808 Hepatitis A
9	21	0.1 7436	1 HPA24A	M59810 Hepatitis A
10	20	0.0 207	1 AY149710	AY149710 Hepatitis C
11	20	0.0 222	1 HPCNS5AD	L23464 Hepatitis C
12	20	0.0 222	1 HPCNS5AE	L23465 Hepatitis C
13	20	0.0 223	1 AY149712	AY149712 Hepatitis C
14	20	0.0 224	1 AY149695	AY149695 Hepatitis C
15	20	0.0 224	1 AY149697	AY149697 Hepatitis C
16	20	0.0 224	1 AY149699	AY149699 Hepatitis C
17	20	0.0 224	1 AY149703	AY149703 Hepatitis C
18	20	0.0 224	1 AY149713	AY149713 Hepatitis C
19	20	0.0 224	1 AY149715	AY149715 Hepatitis C
20	20	0.0 224	1 AY149717	AY149717 Hepatitis C
21	20	0.0 226	1 AY149724	AY149724 Hepatitis C
22	20	0.0 253	1 AF388468	AF388468 Hepatitis C
23	20	0.0 253	1 AF388469	AF388469 Hepatitis C
24	20	0.0 253	1 AF388473	AF388473 Hepatitis C
25	20	0.0 253	1 AF388475	AF388475 Hepatitis C
26	20	0.0 253	1 AF388516	AF388516 Hepatitis C
27	20	0.0 318	1 AF506554	AF506554 Hepatitis C
28	20	0.0 323	1 AF506566	AF506566 Hepatitis C
29	20	0.0 337	1 HECS07267	HECS07267 Hepatitis C
30	20	0.0 339	1 AF506542	AF506542 Hepatitis C
31	20	0.0 339	1 AF506546	AF506546 Hepatitis C
32	20	0.0 332	1 AY257434	AY257434 Hepatitis C
33	20	0.0 336	1 AB081064	AB081064 Hepatitis C

34	20	0.0	337	1	D14179	D14179 Hepatitis C
35	20	0.0	337	1	HPCNS5A22	D14214 Hepatitis C
36	20	0.0	339	1	AF515972	AF515972 Hepatitis C
37	20	0.0	340	1	HC061361	U61361 Hepatitis C
38	20	0.0	340	1	HPCT1	D10078 Hepatitis C
39	20	0.0	378	1	AF506608	AF506608 Hepatitis C
40	20	0.0	391	1	AF506582	AF506582 Hepatitis C
41	20	0.0	392	1	AF506586	AF506586 Hepatitis C
42	20	0.0	678	1	AY100081	AY100081 Hepatitis C
43	20	0.0	681	1	AF516375	AF516375 Hepatitis C
44	20	0.0	682	1	AF516377	AF516377 Hepatitis C
45	20	0.0	683	1	AY100067	AY100067 Hepatitis C

ALIGNMENTS

RESULT 1																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																				
----------	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--

ORPENYVESVPSISGVLGIAISLIMCMLFTTRCNENSSSTNSVASQSYTOPSH
NQRNTNCSRHRTYRNAHQESIELEPMQHTSEDSQCVLLEKKNAYAGPOENIT
NEVMEQYDDVYKNI EGT SYEDNEVMEHMDPTINFNFNYSGLILEEVEDEVYMELEN
OYHGLELNDHNEYNHLEMLMEIOYDML" complement(2692...3258)
CDS /note="orf 2: similar to kaposi's sarcoma-associated
herpesvirus ORF 2"
/codon_start=1
/product="dihydrofolate reductase"
/protein_id="AAD21331.1"
/db_xref="GI:4494909"

/translation="MDITVNCIVAVDEOLGIGKNTMPWPIRLNEMMYEOKMTSPSY
VGEKNVIMKRTWESIPERKRPVLRNITILSRLEPRPHGAHPLATLIDARFVYR
OYKLKEQNTWAVIGKSVSEVSLNKCPLKLYITRIMESFCDFEFSINFETMYL
SEIPGKDTNFEEENGIRKYKFOYERKNFK" 3676...5613
CDS /note="orf 4: similar to kaposi's sarcoma-associated
herpesvirus ORF 4"
/codon_start=1
/product="complement binding protein"
/protein_id="AAD21332.1"
/db_xref="GI:4494910"

/translation="MTEKLPFLFLHAIMYVHCENCKRPHFTEYRVKSNTEKDYV
GETAELICRGVYNTNKLITTECLONGTWSPTNPPCDKRCPTPADILNGAHHGGD
NALFKGSIYECNEGYDILGSIYRFGCIOTENVNDSNPCEIOKCIKPRVENS
DYLNODYNTGDAITFKCSLYTLVGSTTLVCSNKNWSFPCVLMVCESPQIDN
GYIDIGSRARYNHQSITVCKSDGINAVGPELTICTNTWVPLKCYLVNNSPTM
PETMPEPTPPDYOKINLSTAKTATTPNAFTVTVSPKDVTCVKRPHFEFVKAEN
DKERYSVASVELICRPGFTKMQSTVSECSNWTAPNAPKCHRKCKPTEOELLNGE
YIVSGEAPFYGTNITKYKNEGOLIGSMVRIKDKDLTSDMPEAPKCIIEKCK
PPQITNKGHYKNTDFEYOXLDITVPECSNDRFSICGDEMTCTISMTNMPRCQDITC
SAPNIAHKLITGSSSVYKKGQSVTIGCTGFTLIGSEITCKDSSMDPLPTCPAY
SMPSDTPKPTKNTPTPEAPKPNTPVGNTHPPKPPNPPIAPPMSKWRHVVIL
LFAVASLFLVLAALYCCFLK" 6045...9443
CDS /note="orf 6: similar to kaposi's sarcoma-associated
herpesvirus ORF 6"
/codon_start=1
/product="ssDNA binding protein"
/protein_id="AAD21333.1"
/db_xref="GI:4494911"

/translation="MASKGNAGOPLEDNOSGRAPIGACGYVAYSKODEPPEASILG
NRPSGSGFSLPILYGLTVEHEPPLTYAAKRYDITTLAVKTCFHEHYVFNASL
FRPYDGTGNEICEEARALRGYOTIERGPHSNMNPBECQLPDRDEMLGYVTE
GFERLRMGCLVAVFOTQOYVINGROAFKVP/LDEDIEFAPHGHRMPEFTHKDSAYL
YDSLFTSIAGLRKLDVAVIHATEKQFMDHYIAKTVQAKQFSTLLPKTTDSSSH
IVDSVAELALSYGCMFLECPQDACELYNDSMPITFDCDSPEARVNLLEWSEAOAY
HVAQGLFAANSVLITKVOQAPRGQKDVVNSFLOHGLGFLNEATIKENSSEAF
KGVSNALDSSFTPHLAYASPSPLILAKLYYMOFLQHKSTNOAEMVHYVGT
AANSEMTICGNTPATCINTLFEYRIKDRPRAVYTPPORDPYVYVGTATNDIEILG
NFASFROBEDGNPADEHPKITYMOLCOTYETKLSAIGITEDHNVNLTNIOSELR
VEFKIDISIVDEVMKFNMSIKNNFNEHVSVAHILQFCNVYWOAPCAVFNLSLY
KSLMIIDODICLPYCMYEDBNPAMGLIPSEMLKMHIEOTLNFKAACLDGVLTCGE
LKIVHRMFCDFEPTDAGSNGMLAPFKMOYIARAMVYPKSIKNNIISNTGASE
AVOSGFAPCTGRTDYVYAGPYKKEINSIRALPDDTKATLXYLHKISQNKPVK
DYDDELAELYSYKINSLAPEFTNVIDVPSDMSARITKNCALIRACQIOFYAT
TILCFLPYLOTTIDEEYTHVLSAIAINAVYLAIEIKRIALIVQTTARQVAAATGR
RPVITPVVAVKRYGVNGNNVHFCGNLGYFAGGVDRNMLPESSPERKTKQVAMLR
RHVMMTPIDILIRAGQOTISTEASVSKSYQALLLEDKNDPMLKSVILELIRHLG
KGCODLSEDOYVILGDYCM/LTDEV/LTIDNIAOSGVPTIEDAGALIEDQDADILQ
FVSDDIATASQCPBEOPLPPSAGALLACKKRKINMLSDLD." 9468...11528
CDS /note="orf 7: similar to kaposi's sarcoma-associated
herpesvirus ORF 7"
/codon_start=1
/product="transport protein"
/protein_id="AAD21334.1"
/db_xref="GI:4494912"

/translation="MARELALVLAQSLAVALDLSVIFADRSIDGARILTKTQIEN
LNRDLPLREONSVETSLIEVHLAKNIEDLIGELERSLRQYSREFEFLHLE
PECHYSTVFOFGGLIDVNMCLINDVELLCRISLSEFYCIGANESLHCLNLF
LSTLRGISPIHPPLVYTVPCVOCILREIELVPOGSSILAVLADRHCDHCKRVARE
PIHGFETELSQLGKLVTKRSDATQHGVRSSADQDRESSLAIODHNIKRVASIAHE

CDS

/note="orf 8: similar to kaposi's sarcoma-associated
herpesvirus ORF 8"
/codon_start=1
/product="glycoprotein B"
/protein_id="AAD21335.1"
/db_xref="GI:4494913"

/translation="MIMTRRLRLRAVWVIAIGTAVGENVTPPKATYKPPCP
STPPENPRPAAEFKFCVCSASATGELFRNLKTEGTGCTGDEILWAFKNIV
PHIKVRYRKYVATSVYRGMTEAVTGRQEVLRPVQYRTEINMDPTJOCCFSSRN
VNGIVNTYTDDEFTNQYFLODPVEGLDNTDQYRSQVLYTTPHCFQYRVTYVNC
EIVMIAARSAPYSFVIALDITVAVSPEFCHNDSTCSVAETENGELKARVILNTTYD
PATROPTTEFVAFDSEGYVSKMAEDKSAVCALITMKTPEPRAIOTTHERSYHVA
DVTATFTSPLSQVNTFGETPCLNDVLOKTLNATIKLSHDHANGSOXYETEGLE
LIMOPLEPLSLADEMRLENGTTPAPPTTSTANVRSSVGENEATDOLAPQOFAY
DKLRASIKVYLEELSRACRQVODTYWVMEISKINPTSVMTAIYGRVPSAKFQDAI
SVTCVANDQASVSIHKSIRTPSGICQSRPAPFRILNSTLTKGOLGSPNEILLD
NOVESCCKCHFTIASVITYYQDYFVKINTSEISTETPALNSTEPENIDFRV
IELYSRAKRLKSGSVFDEIEMFERENYTOQALGREDLDTDLNDRALDISEIV
ADLDQVATIRMTIYPIDIDMOPSGKQVQEOEKNIAGHQIOQDERRRILDEOQSAS
LFRASDGLKFRFGYKPLENEAEQEMSK" 14122...17166
CDS /note="orf 9: similar to kaposi's sarcoma-associated
herpesvirus ORF 9"
/codon_start=1
/product="DNA polymerase"
/protein_id="AAD21336.1"
/db_xref="GI:4494914"

/translation="MDFPNYILGPRGRPHSHRTDAPAPAGAGVAPPVYCLILPA
CLTRPGAGMIPVITPEPPYFENGARGDVLILAKERSWTRADRPAVPDQDOSTIF
HAYDVETTYAADRCAEYPSRFQDIIIPSGVTLKLTGTEGTSVAVNFQOYFYA
KVPAGINVTTHILOQALKNATAGAACGSTRVNRILIKTYDVABAPYTEILSSGML
STLSDRLVACGCEVESNVDAVRFEVDHGGTGTGWSVCAPIRLAARDRTALEP
CSMEDLSVOADRSMQPPRYATVADIECTGEGAFGAPIRDGAAYVIOISVETREGAP
NPNILTSVGCDDIPPTDVLPEPSEYDMLVSEFAMIRDEPVDITGYNINSPLLYL
ITRASYVNLNBYETIKTGSTIEVEHPRGGGSGFMSKYIATGIVPDMQVCR
EKLISDYKRLDVTARQCLGGKKEVSKDIPLESRSGSGAKVSGCVMSVYLMVL
LKMIMHIEISEIKLAKIQARVLTGQOQIRVSCLEAARENFTLPVPTPGQGG
YOGATVINPIIGFDEPVLVYFASLVSIIQANILCSYTAIRHGDILHAPNPDY
ETFVLSGPMVFEVKKHRESILGRLTYWLEKRAIRRTAACDPSLKTLLDQOLA
IKYCNVNGYGTGVASGLPCINIAETVYASATGSAKVSVALYLTEDORTLRE
VTARHGAFRVYIGDTS/LTADCGI/SAEASARCDLARIATD/LPPT/KLEAKET
FKCLLLTKRYIGVLLNDKRWMGVDLIRKTAQEVQERAILDLVLHDEPKAA
RLCKLRPHAVYEEDLPAGFETKIEVENASVATDILNSVY/PEQ/LTFESTELSR/CDDV
TTN/PHLAVQOKLASRCEELPOVDRIRIPYVVDVAGSKSLDAHPDYVHQHQPVAV
DLYEDKILVHAGN/LQCLFGNNAPTVAILXN/LNVPYKLES" 17261...18511
CDS /note="orf 10: similar to kaposi's sarcoma-associated
herpesvirus ORF 10"
/codon_start=1
/product="unknown"
/protein_id="AAD21337.1"
/db_xref="GI:4494915"

/translation="MLVNELSVLGDMEVTFPHGRSEFVNITRLQTKHGIGVARYL
PFSIDLOHOFARGLVTRLKELPFSDCAVALIPDGSAGDADARAAPGVLDSSRP
LTWVWNASGRHTIRFCLFLKPIDLERLAVYFENGESGDETPKPCATCETSLPGSP
LRVGEASQTSFHSFVAVPPANSVACLILRLIRAPDPAEVLGDSGPVLPHTHGIGVYA
SGCNVCKASVHTLSPSRCKTAQMEIYIAPRDNALVYILOSQSPVLPHTHGIGVYA
DAEKTTOPGSAEYRVOLITROQCAANGDAFLVTGVAPEPLVYVTTALLSGCTTHL
RLFNPNCTPTTIKRDITLVAAAPCPVVRVLSADADAPDVLASPTGALSTNAFTIPVG
FPGVVASACHVTSINDGNCVBERNH" 18520...19749
CDS /note="orf 11: similar to kaposi's sarcoma-associated
herpesvirus ORF 11"

Query Match	85.9%;	Score 34377;	DB 1;	Length 133719;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 40001;	Conservative	0;	Mismatches	0;
			Indels	0;
			Gaps	0;

[illegible]

OY	80820	GGATGAAACAAGTCGGTCCGACCCCTTGATGTTACATCGTCCGGGTATAAAAACAACCTT	80879
Db	80820	GGAAATGAAACAGTCGGTCCGACCCCTTGATGTTACATCGTCCGGGTATAAAAACAACCTT	80879
OY	80880	CTGTACCGCATACAGACGAGTTCGACACGTAACGAGTCTCATGGAGATGGGCGCAT	80939
Db	80880	CTGTACCGCATACAGACGAGTTCGACACGTAACGAGTCTCATGGAGATGGGCGCAT	80939
OY	80940	CGACGGGATTCGGCGCATGCGACCGACAGACACAGGGCGATCTGTGCATATCTTAGTG	80999
Db	80940	CGACGGGATTCGGCGCATGCGACCGACAGACACAGGGCGATCTGTGCATATCTTAGTG	80999
OY	81000	GTTGCTCTCCAGGTTTGGGGACCTTCGAAAGCTCTAGATATATCCACCATATCAAAA	81055
Db	81000	GTTGCTCTCCAGGTTTGGGGACCTTCGAAAGCTCTAGATATATCCACCATATCAAAA	81059
OY	81060	CTGTACGGGATTCGGCGATGCGACCGTATACGTCCTCATGCTTGTAGTAAGACCT	81119
Db	81060	CTGTACGGGATTCGGCGATGCGACCGTATACGTCCTCATGCTTGTAGTAAGACCT	81119
OY	81120	TCATTTCCCGGTTTCCAGGTTCTTCACGCAAAATGCGAGTCCGTAAGGATTAATCAACA	81179
Db	81120	TCATTTCCCGGTTTCCAGGTTCTTCACGCAAAATGCGAGTATCGTAAGGATTAATCAACA	81179
OY	81180	CACCTTCTCGCACTTTTGTGCTAATAACCTTAGATCTTCTGGCAAACTGCAGTCAA	81239
Db	81180	CACCTTCTCGCACTTTTGTGCTAATAACCTTAGATCTTCTGGCAAACTGCAGTCAA	81238
OY	81240	CGACCCCGGAGCGGTAAACAAGTCTCATCTTGGAACAACAACCGGTGGCCAG	81299
Db	81240	CGACCCCGGAGCGGTAAACAAGTCTCATCTTGGAACAACAACCGGTGGCCAG	81299
OY	81300	CGAGGACGGGACATGATGTCGACTCGACACCGGTATTCAGCATAAACGTTGAGGCCAA	81353
Db	81300	CGAGGACGGGACATGATGTCGACTCGACACCGGTATTCAGCATAAACGTTGAGGCCAA	81355
OY	81360	CGGTCTCTCCAAATATAGAAAGTTAATTGATGGCCCCCTGGACCGCATGCTCGCGCA	81419
Db	81360	CGGTCTCTCCAAATATAGAAAGTTAATTGATGGCCCCCTGGACCGCATGCTCGCGCA	81419
OY	81420	CAGCCTGTTTGTGTCATCGAGCTCCGACCAATACCGTTGGGGTAAAAACCCGTCCTTC	81479
Db	81420	CAGCCTGTTTGTGTCATCGAGCTCCGACCAATACCGTTGGGGTAAAAACCCGTCCTTC	81479
OY	81480	TTTTCAGCTCCAGACCCACCCCTGATGTCGTAATTGGAACCTACTGATTTAAACCAAGCACT	81539
Db	81480	TTTTCAGCTCCAGACCCACCCCTGATGTCGTAATTGGAACCTACTGATTTAAACCAAGCACT	81539
OY	81540	GAGTTTGGTGGGAAGACATAGATTACACTTGCACAACTTACACCGTTCGGGCACAGA	81599
Db	81540	GAGTTTGGTGGGAAGACATAGATTACACTTGCACAACTTACACCGTTCGGGCACAGA	81599
OY	81600	GGCGAAACAGTCTATATCGAGACACCGGTCGCCCATAGGCTTATTAATTAATTAAAGCT	81655
Db	81600	GGCGAAACAGTCTATATCGAGACACCGGTCGCCCATAGGCTTATTAATTAATTAAAGCT	81659
OY	81660	CTCGTATACCTTTTGCTGTCATGTCGTAAGAAATCATCTTTCTCGTAATCTGCCAT	81719
Db	81660	CTCGTATACCTTTTGCTGTCATGTCGTAAGAAATCATCTTTCTCGTAATCTGCCAT	81719
OY	81720	AGTGGGACGGTTTTCGCCCTGACATATGCTCGCATGTTGCAGTATGTCATCAAAAACT	81779
Db	81720	AGTGGGACGGTTTTCGCCCTGACATATGCTCGCATGTTGCAGTATGTCATCAAAAACT	81779
OY	81780	TCTGCGTAATTCATACGAGACCGATCTGCACTTCTTGTTCACCGGAGACCCGCAACAAG	81839
Db	81780	TCTGCGTAATTCATACGAGACCGATCTGCACTTCTTGTTCACCGGAGACCCGCAACAAG	81839
OY	81840	TCTTGTCCTCATCTCCCAACAACATCCGGGTAGTCGCCCGATTTGGACCGGGGCAACA	81899
Db	81840	TCTTGTCCTCATCTCCCAACAACATCCGGGTAGTCGCCCGATTTGGACCGGGGCAACA	81899
OY	81900	GCCAGGCCCTGATATCGACTCCACAGGCCGCCCATTTCCGCTATTTGGAGACTTGACGAGTC	81959

Db 81900 GCCAGGCGCTGATATGACTCCACGGCGCCGCAATCCGCTATTGGAGTTACGGATC 81955
QY 81960 AGCTCTCAAGACAATGAAACCCCTTGCTGTACAGGACACAGTTCAATAATGTCTAAAT 82019
Db 81960 AGCTCTCAAGACAATGAAACCCCTTGCTGTACAGGACACAGTTCAATAATGTCTAAAT 82019
QY 82020 GAGGAGTCAATGTCCTTAACATATGCTTAAGACTATCAAACTGTCTAGGGAGAGA 82079
Db 82020 GAGGAGTCAATGTCCTTAACATATGCTTAAGACTATCAAACTGTCTAGGGAGAGA 82079
QY 82080 GTGACAAACACCTGGGACCTCAATATAATTTTGGAGTGGGCTATGACCCGCTTCCTC 82139
Db 82080 GTGACAAACACCTGGGACCTCAATATAATTTTGGAGTGGGCTATGACCCGCTTCCTC 82139
QY 82140 TGGTATGATTAACCCCATCGCCACCATATTTCAGAGAACAAACACTTCAGATACAAAC 82199
Db 82140 TGGTATGATTAACCCCATCGCCACCATATTTCAGAGAACAAACACTTCAGATACAAAC 82199
QY 82200 ACTTATTTACAGATAGAGGCGCTCACCGGCTTCACAAAACCGGTGCGCGCACAGTTAA 82259
Db 82200 ACTTATTTACAGATAGAGGCGCTCACCGGCTTCACAAAACCGGTGCGCGCACAGTTAA 82259
QY 82260 CATTAAACATTTAGCGGGGAGCAACGCGCGCCACAGACACTGTCGACAGCTGAATATT 82319
Db 82260 CATTAAACATTTAGCGGGGAGCAACGCGCGCCACAGACACTGTCGACAGCTGAATATT 82319
QY 82320 AGCGGTACAGTGTCTTTCACCTCCGCTCGGCTGTAGTACGCCCCCAAAATATAGTTAA 82379
Db 82320 AGCGGTACAGTGTCTTTCACCTCCGCTCGGCTGTAGTACGCCCCCAAAATATAGTTAA 82379
QY 82380 ACACAGCTTTGGAGAGCGCGCTCGCTCGGAGATGTTCTGGCCATGGCTGCATATAG 82439
Db 82380 ACACAGCTTTGGAGAGCGCGCTCGCTCGGAGATGTTCTGGCCATGGCTGCATATAG 82439
QY 82440 TCACCAAGTTAAATGACGACACAGCGCTTGGCGCACAGACAGCCCAACCGCCCGTAA 82499
Db 82440 TCACCAAGTTAAATGACGACACAGCGCTTGGCGCACAGACAGCCCAACCGCCCGTAA 82499
QY 82500 GATTGACGTTTCCCTTGAAGCAAGCGCCAGGGAATGCCCAACATCTAATGTAATGCCG 82559
Db 82500 GATTGACGTTTCCCTTGAAGCAAGCGCCAGGGAATGCCCAACATCTAATGTAATGCCG 82559
QY 82560 GAGGGGTGCGGCCCAAAAGCGCAACCGCGCAAAAGATCTTATCCAGGAAGCGCAACGCC 82619
Db 82560 GAGGGGTGCGGCCCAAAAGCGCAACCGCGCAAAAGATCTTATCCAGGAAGCGCAACGCC 82619
QY 82620 TCGGCTGGAACCTCTGCTAAGTGGCTGGAATCTCGGAAACCACTGCTGCTGGGATC 82679
Db 82620 TCGGCTGGAACCTCTGCTAAGTGGCTGGAATCTCGGAAACCACTGCTGCTGGGATC 82679
QY 82680 GGTGCGGCGCATATGTCCTTGAAGGCGACGTTCCGACATGGAGACACAGATGCCG 82739
Db 82680 GGTGCGGCGCATATGTCCTTGAAGGCGACGTTCCGACATGGAGACACAGATGCCG 82739
QY 82740 TTGGAGATTCAGTCCACCTTCACCACTCTGTCCCAATAAAGTAATTAATTAATC 82799
Db 82740 TTGGAGATTCAGTCCACCTTCACCACTCTGTCCCAATAAAGTAATTAATTAATC 82799
QY 82800 AGCATCAACACATGTTTACCCCGGCTCCACCGACACAGTGTACCGAACCAGCGGCGCA 82859
Db 82800 AGCATCAACACATGTTTACCCCGGCTCCACCGACACAGTGTACCGAACCAGCGGCGCA 82859
QY 82860 ACCGGAACAACTTATTCACGGGCTCTCGCGCAACCCCGTAACTAGACAGTATGCCG 82919
Db 82860 ACCGGAACAACTTATTCACGGGCTCTCGCGCAACCCCGTAACTAGACAGTATGCCG 82919
QY 82920 GAGGCTGTATCGCAAGAGACACAGACCTACAGGTATTTGTAAGGGAATGATTCGG 82979
Db 82920 GAGGCTGTATCGCAAGAGACACAGACCTACAGGTATTTGTAAGGGAATGATTCGG 82979
QY 82980 CATCTGCGGATATGAGTGCAGAAAGTGTCTTATGTAACGTCGCAACAGGTTGA 83039
Db 82980 CATCTGCGGATATGAGTGCAGAAAGTGTCTTATGTAACGTCGCAACAGGTTGA 83039

Db 82980 CATCTGCGGATATGAGTGCAGAAAGTGTCTTATGTAACGTCGCAACAGGTTGA 83039
QY 83040 CTATGCCGATATGGCGCTGGATAGCCAGTTTTCATCTCTTACCGGTTAATCCCGCA 83099
Db 83040 CTATGCCGATATGGCGCTGGATAGCCAGTTTTCATCTCTTACCGGTTAATCCCGCA 83099
QY 83100 GCGCGGTGCAAGATGGCCCTGGATGCAAGTACTCAATAAATGTTTTTTCGGCTCC 83159
Db 83100 GCGCGGTGCAAGATGGCCCTGGATGCAAGTACTCAATAAATGTTTTTTCGGCTCC 83159
QY 83160 TCGACTTCCTGCTCCCTCTGTGTATTCACAGATGGAGTAAAGTCTTCTCCG 83219
Db 83160 TCGACTTCCTGCTCCCTCTGTGTATTCACAGATGGAGTAAAGTCTTCTCCG 83219
QY 83220 TCAACCCACCGCATTCGCGGATGACGACTGTCTGCAAGTATCAACACAGCTCTCA 83279
Db 83220 TCAACCCACCGCATTCGCGGATGACGACTGTCTGCAAGTATCAACACAGCTCTCA 83279
QY 83280 AGGCTGATATGTTTGGTCACTCGGACCGGCTCATATCTTCCGCGGTGACGGCAA 83339
Db 83280 AGGCTGATATGTTTGGTCACTCGGACCGGCTCATATCTTCCGCGGTGACGGCAA 83339
QY 83340 TGCCAAACCTTGTCAAGTTACCTCTGACAAAGCAGCTGAGACCTTCACAGACCTAGCG 83399
Db 83340 TGCCAAACCTTGTCAAGTTACCTCTGACAAAGCAGCTGAGACCTTCACAGACCTAGCG 83399
QY 83400 TGGCAACGGAACCTTGTGCTATGTCGTGAGACAGTACTTAACTTATTTATCT 83459
Db 83400 TGGCAACGGAACCTTGTGCTATGTCGTGAGACAGTACTTAACTTATTTATCT 83459
QY 83460 GTGCTGACTCTCGCGCGGGAAGTTGTGTTATAGACACCGGGAAGATATATG 83519
Db 83460 GTGCTGACTCTCGCGCGGGAAGTTGTGTTATAGACACCGGGAAGATATATG 83519
QY 83520 GTTCTGACACAGCTGCTCTGACAGACACACAGAAATAGAACTTGTGGCTCTCT 83579
Db 83520 GTTCTGACACAGCTGCTCTGACAGACACACAGAAATAGAACTTGTGGCTCTCT 83579
QY 83580 GGGCACAGGCTGCTGTAGAGATACAGTGTGCCCGCTTGCACGGCGCATGGCTCTG 83639
Db 83580 GGGCACAGGCTGCTGTAGAGATACAGTGTGCCCGCTTGCACGGCGCATGGCTCTG 83639
QY 83640 GTCCCGGAGGCGGGGAGGCTTCTCATGAACCCATGAAGTTAAATTTCTGTTAG 83699
Db 83640 GTCCCGGAGGCGGGGAGGCTTCTCATGAACCCATGAAGTTAAATTTCTGTTAG 83699
QY 83700 AGAGGAACATGACCTCTGTTGATATATCAACATTAAGTGTAAACCGCGGTACA 83759
Db 83700 AGAGGAACATGACCTCTGTTGATATATCAACATTAAGTGTAAACCGCGGTACA 83759
QY 83760 GCGTTTCCCTGTTCTTATATGACGTACACCTCGGTTTGTGCGGTAGCTATGTC 83819
Db 83760 GCGTTTCCCTGTTCTTATATGACGTACACCTCGGTTTGTGCGGTAGCTATGTC 83819
QY 83820 CCGTGTATACGGGACAGCATGCTTATTTGCTTATGCTTGTGCGGCTGCTT 83879
Db 83820 CCGTGTATACGGGACAGCATGCTTATTTGCTTATGCTTGTGCGGCTGCTT 83879
QY 83880 CACGATCTGAGATGGAACACAGACAGTGAACCGGTGCATAGAAACACAGATGACG 83939
Db 83880 CACGATCTGAGATGGAACACAGACAGTGAACCGGTGCATAGAAACACAGATGACG 83939
QY 83940 GATGGGAACCGGGCGGATGCAAGCAACACTCTCGCATTTGGAGCTGTATGCA 83999
Db 83940 GATGGGAACCGGGCGGATGCAAGCAACACTCTCGCATTTGGAGCTGTATGCA 83999
QY 84000 GTGCGCAAGCGCAAAATTAACCTGAAATCTCAACGCGCAAAAGGCACAATTTGAT 84059
Db 84000 GTGCGCAAGCGCAAAATTAACCTGAAATCTCAACGCGCAAAAGGCACAATTTGAT 84059
QY 84060 GAGGCGAGGCGCTTCTGGAGCCCGAGACAGATGTGCTGCGGCTGATCTGCTG 84119
Db 84060 GAGGCGAGGCGCTTCTGGAGCCCGAGACAGATGTGCTGCGGCTGATCTGCTG 84119

Db	86280	GCTGTGAACAAACATAAAGAAAGGAGCGACAGCTGTGGCGCTTTGGCGCTCCTGTCAAGATGAA	86339
QY	86340	CCCCGCGGGTACATTTACTTCTCCTCCATACGGTGCAGGGTATGATACAGATGTGCTTC	86399
Db	86340	CCCCGCGGGTAACTTTACTTCTCCTCCATACGGTGGAGGGTGAATACAGATGTGCTTC	86399
QY	86400	CGTTGTTCCGAGACACCGACACCCGCTCCAGACGGTCCCTGCTCCCGCTGTCACTCC	86459
Db	86400	CGTTGTTCCGAGACACCGACACCCGCTCCAGACGGTCCCTGCTCCCGCTGTCACTCC	86459
QY	86460	CGCGGCAACCGTGTGTCATCATCTGCACATCATATTGGACACAGCTAGCAGAACTTCAG	86519
Db	86460	CGCGGCAACCGTGTGTCATCATCTGCACATCATATTGGACACAGCTAGCAGAACTTCAG	86519
QY	86520	GGCAATGGGACATCCCATGTATTTTGGACTAGTATGACAGGGCAATGAAATCCAGCC	86579
Db	86520	GGCAATGGGACATCCCATGTATTTTGGACTAGTATGACAGGGCAATGAAATCCAGCC	86579
QY	86580	ACACTTCACGGGCGGGACATCTCCTGGAGTTGGGCAATCTCGCAGCTCCTCCAAATTAAG	86639
Db	86580	ACACTTCACGGGCGGGACATCTCCTGGAGTTGGGCAATCTCGCAGCTCCTCCAAATTAAG	86639
QY	86640	CACAGATTCGACAGCCTCGAGCGGCTCGAAGCCGAGCTCATAGTAAATTTTCAGATA	86699
Db	86640	CACAGATTCGACAGCCTCGAGCGGCTCGAAGCCGAGCTCATAGTAAATTTTCAGATA	86699
QY	86700	GTGTCATATGCCGTCAATGTTGGCTTTCCAGTATTTTACACAGATTTCCAGACTCCGT	86759
Db	86700	GTGTCATATGCCGTCAATGTTGGCTTTCCAGTATTTTACACAGATTTCCAGACTCCGT	86759
QY	86760	CATAACACAGATCAAACTCTCTGCGATGTTTTCTGACGGGCTCGAAATCTGCCCCGTGC	86819
Db	86760	CATAACACAGATCAAACTCTCTGCGATGTTTTCTGACGGGCTCGAAATCTGCCCCGTGC	86819
QY	86820	AAATTCGACAGGAAATCACTGGGAGCGAGCGCAAGAAACGCTAAATGATTTATCGGCACA	86879
Db	86820	AAATTCGACAGGAAATCACTGGGAGCGAGCGCAAGAAACGCTAAATGATTTATCGGCACA	86879
QY	86880	ACACAGGTGTCCGGAGCGTTTGGGATCAGGAAGGCCACATATACGCACACCGAGCGCG	86939
Db	86880	ACACAGGTGTCCGGAGCGTTTGGGATCAGGAAGGCCACATATACGCACACCGAGCGCG	86939
QY	86940	TCCGAAATTTGAACCTCCGACGTTCTCTCCAAAGTAAAAAAGATACCTCAACAGCCCC	86999
Db	86940	TCCGAAATTTGAACCTCCGACGTTCTCTCCAAAGTAAAAAAGATACCTCAACAGCCCC	86999
QY	87000	TAGCACAAGGTTGCGCAGAAAGTCTGAGATCGCTTTGGATTCGTTTAAACGGAGAC	87059
Db	87000	TAGCACAAGGTTGCGCAGAAAGTCTGAGATCGCTTTGGATTCGTTTAAACGGAGAC	87059
QY	87060	TCCTCAGTGGCGCCTTAGCCCTCGGCGCGCTGTCTCTCGAANAACATCCTCTCGAAGCGA	87119
Db	87060	TCCTCAGTGGCGCCTTAGCCCTCGGCGCGCTGTCTCTCGAANAACATCCTCTCGAAGCGA	87119
QY	87120	ACTGCCCATGGAACAGTATGCAACAGTGTGGTCCGAGTATGACAGATTCGAGCC	87179
Db	87120	ACTGCCCATGGAACAGTATGCAACAGTGTGGTCCGAGTATGACAGATTCGAGCC	87179
QY	87180	CACCGTAACCTCAGGAAGCAATTGAAAGTCTGTAATCTTTTCCCGAGAGCCGCCCGCG	87239
Db	87180	CACCGTAACCTCAGGAAGCAATTGAAAGTCTGTAATCTTTTCCCGAGAGCCGCCCGCG	87239
QY	87240	CTTGCTCGGGGGGTACGCTCCCTCAAAATACCTGTAGATCTACCTGCATATTAACATCT	87299
Db	87240	CTTGCTCGGGGGGTACGCTCCCTCAAAATACCTGTAGATCTACCTGCATATTAACATCT	87299
QY	87300	AATTTCTTAAATTTTCGGGCACTGTAACCGGTTTACACAGCCACGGGCTGAGCAAAA	87359
Db	87300	AATTTCTTAAATTTTCGGGCACTGTAACCGGTTTACACAGCCACGGGCTGAGCAAAA	87359
QY	87360	ATGCTCAAAATATCTTGTATTAATCTTCATGACGCGCATGTCGGTGCACCGGTTCCACGG	87419

Db	87360	ATCGTCAAAATATCTGTTTAAATCTTCATTCATGACGCGACATGTCGAGTCCACCGGTTCCACGG	874119
QY	87420	GACACGATATATGGTCTTGTTCCTCGTCATCATTCCTCACTCCGGGGTATCGCTTAGACTC	874719
Db	87420	GACACGATATATGGTCTTGTTCCTCGTCATCCATTCCTCACTCCGGGGTATCGCTTAGACTC	874719
QY	87480	CACGGCTCATGATGAACCAACTTTTAAATCATATGCGTCCGCGCATCTCCGATTTCA	875319
Db	87480	CACGGCTCATGATGAACCAACTTTTAAATCATATGCGTCCGCGCATCTCCGCGATTTCA	875319
QY	87540	ATACCTTGACCCGAGCGGCTCACTTAAATATCCGAGCCCCAGAACCCAGCCTTCGGTA	875919
Db	87540	ATACCTTGACCCGAGCGGCTCACTTAAATATCCGAGCCCCAGAACCCAGCCTTCGGTA	875919
QY	87600	ACAAAAGATCTAGATCTGAAGAAGCCCTAATATATGCGCCACGGGAAAACTCTGTA	876519
Db	87600	ACAAAAGATCTAGATCTGAAGAAGCCCTAATATATGCGCCACGGGAAAACTCTGTA	876519
QY	87660	ACAAATGAAAAAATGTTCTCAGAAAAACGAAGAGAGAAACCTGACGACGCAATCTAG	877119
Db	87660	ACAAATGAAAAAATGTTCTCAGAAAAACGAAGAGAGAAACCTGACGACGCAATCTAG	877119
QY	87720	TCAAACCAGAACCTTAAAGGCCGTCACTGACCCATATCTTTCCCTTCCGAGCGAGTGG	877719
Db	87720	TCAAACCAGAACCTTAAAGGCCGTCACTGACCCATATCTTTCCCTTCCGAGCGAGTGG	877719
QY	87780	GTTTCTCAATGCGCGTAGCAAAACGAAGAACGCTACACATATATAGACAGCTGTGAGAGA	878319
Db	87780	GTTTCTCAATGCGCGTAGCAAAACGAAGAACGCTACACATATATAGACAGCTGTGAGAGA	878319
QY	87840	AAACTTTATTTGACAGGGACAGGGCAAAAAGCAAGCTGTGCACGGTATACAGTATGTTCACAG	878919
Db	87840	AAACTTTATTTGACAGGGACAGGGCAAAAAGCAAGCTGTGCACGGTATACAGTATGTTCACAG	878919
QY	87900	GGCCGCATCCCGCGACCCCGCCACAGACACTGTCGCAAAATTTGAATGACAGGGGAT	879519
Db	87900	GGCCGCATCCCGCGACCCCGCCACAGACACTGTCGCAAAATTTGAATGACAGGGGAT	879519
QY	87960	TGTGGACACAGGCTCGCCTTCGGAAGTGGGAAGCCTCTAGGTGGAGAGACGATAGGC	880119
Db	87960	TGTGGACACAGGCTCGCCTTCGGAAGTGGGAAGCCTCTAGGTGGAGAGACGATAGGC	880119
QY	88020	GGCTGGAAATCGGCTTCGGTGGCGGGGGTGGAGTGCACGCACTAGATTTGGGGCAG	880719
Db	88020	GGCTGGAAATCGGCTTCGGTGGCGGGGGTGGAGTGCACGCACTAGATTTGGGGCAG	880719
QY	88080	CGAAAAACGCGGAGAACTCGCGCTGTGTTAATTAATTAATCAACGCGCTCCAGCGAACTTC	881319
Db	88080	CGAAAAACGCGGAGAACTCGCGCTGTGTTAATTAATTAATCAACGCGCTCCAGCGAACTTC	881319
QY	88140	GTTTACCCAGCAGAGAGCTGGAACGTGACCCATATACCGAATGTAAATCCAGACCCGTC	881919
Db	88140	GTTTACCCAGCAGAGAGCTGGAACGTGACCCATATACCGAATGTAAATCCAGACCCGTC	881919
QY	88200	TGCGTAATATCATCAACCCGGGTATGATATCTCCACGACCACTTAGCATCTCGTCTG	882519
Db	88200	TGCGTAATATCATCAACCCGGGTATGATATCTCCACGACCACTTAGCATCTCGTCTG	882519
QY	88260	GTCGAGAAACATATCTCGTGGGGTATAGCGGCAACAGGGCTGTTCGCGCGGAATCCGCG	883119
Db	88260	GTCGAGAAACATATCTCGTGGGGTATAGCGGCAACAGGGCTGTTCGCGCGGAATCCGCG	883119
QY	88320	ACAAACGTGTCCTTGGAGTGTGCTTTGGCGCGGCAACAGCGCAACGCTTGGGGGA	883719
Db	88320	ACAAACGTGTCCTTGGAGTGTGCTTTGGCGCGGCAACAGCGCAACGCTTGGGGGA	883719
QY	88380	CCGACCTCATATTTCCCAACCAACCGCCCATAGTATTAACCAACAGCAGCTAGCATCA	884319
Db	88380	CCGACCTCATATTTCCCAACCAACCGCCCATAGTATTAACCAACAGCAGCTAGCATCA	884319
QY	88440	ACACTGCTCCCGTGGCTCCACGGCGCCTTGATCTCATTCGCGGACGAGATATCCG	884919
Db	88440	ACACTGCTCCCGTGGCTCCACGGCGCCTTGATCTCATTCGCGGACGAGATATCCG	884919

QY 88500 GAATCTGGCGTTACCTCGTTGGCTACGTCCAGAGCATGCCCGGTGGCATCCGCTTC 88559
D 88500 GAATCTGGCGTTACCTCGTTGGCTACGTCCAGAGCATGCCCGGTGGCATCCGCTTC 88559
QY 88560 GTTACAGAGCGGCGAGATGTACAAAGATCGGCACAGCGGAATAAGCGGCACTGTT 88619
D 88560 GTTACAGAGCGGCGAGATGTACAAAGATCGGCACAGCGGAATAAGCGGCACTGTT 88619
QY 88620 AGCGCGCGGCGCGAGGTTCTCCAGTGTACATCTTCGCGGCTGACGTGTGGC 88679
D 88620 AGCGCGCGGCGCGAGGTTCTCCAGTGTACATCTTCGCGGCTGACGTGTGGC 88679
QY 88680 TATAGCGCTGGCCAACCAAGTTCTTACATTCCTGACGCTCAATCGTGTACCGGTCTG 88739
D 88680 TATAGCGCTGGCCAACCAAGTTCTTACATTCCTGACGCTCAATCGTGTACCGGTCTG 88739
QY 88740 CCGTATGCTTTAAATTTGACATATGTACATATCTTTCTCATGCTCAGAGCC 88799
D 88740 CCGTATGCTTTAAATTTGACATATGTACATATCTTTCTCATGCTCAGAGCC 88799
QY 88800 ACCCGCGCTTTAAATGATTCGAAGGTAAACGACAGAGTCTTTCTCATCCAGCCA 88859
D 88800 ACCCGCGCTTTAAATGATTCGAAGGTAAACGACAGAGTCTTTCTCATCCAGCCA 88859
QY 88860 ATGCAATTCAGATGCTTATCATTTATCGCAACATCGAGCAACCTCCCTCAGGCGAGA 88919
D 88860 ATGCAATTCAGATGCTTATCATTTATCGCAACATCGAGCAACCTCCCTCAGGCGAGA 88919
QY 88920 CGGCGGCTTTACGCGGATCGACCCGCGCTCTCCGCAATCTCTGAGGCTCCGCTGC 88979
D 88920 CGGCGGCTTTACGCGGATCGACCCGCGCTCTCCGCAATCTCTGAGGCTCCGCTGC 88979
QY 88980 ATAACTGGCTTAAATCTATCCCCCGCGTGCAGCTGTATTTAGTACACACCTTCG 89039
D 88980 ATAACTGGCTTAAATCTATCCCCCGCGTGCAGCTGTATTTAGTACACACCTTCG 89039
QY 89040 GGCACAGCGCGTAGGCGTGGCAGGAGGACGCCAGCAGCTATTTTCATCTCAGCCG 89099
D 89040 GGCACAGCGCGTAGGCGTGGCAGGAGGACGCCAGCAGCTATTTTCATCTCAGCCG 89099
QY 89100 CTTACTAGCGGAATCTGCGGCTCTACAAATCCACCGACGCCCGGAATGTACACATGAG 89159
D 89100 CTTACTAGCGGAATCTGCGGCTCTACAAATCCACCGACGCCCGGAATGTACACATGAG 89159
QY 89160 TCAATTCATCTGACAGATCACCAAAAGTACAGGAGCTGGGCTTTTACTGAGGCGAG 89219
D 89160 TCAATTCATCTGACAGATCACCAAAAGTACAGGAGCTGGGCTTTTACTGAGGCGAG 89219
QY 89220 GGCAGCCCAAGGTAAAGATGACTGCTGGTGGAGACAGTGTCCCGGGAAACGGGTG 89279
D 89220 GGCAGCCCAAGGTAAAGATGACTGCTGGTGGAGACAGTGTCCCGGGAAACGGGTG 89279
QY 89280 ACCGGCGAGTCTGCGCAGTAGACCCATAACATAGAAATTTGAGATTTGACAGAGATC 89339
D 89280 ACCGGCGAGTCTGCGCAGTAGACCCATAACATAGAAATTTGAGATTTGACAGAGATC 89339
QY 89340 GCACAGCGCGTGTGGTGGTCCCTGCTGCTGCTCCCTGCGCAGCAACCGTGTGGC 89399
D 89340 GCACAGCGCGTGTGGTGGTCCCTGCTGCTGCTCCCTGCGCAGCAACCGTGTGGC 89399
QY 89400 TGGTTCGTTATCCACATATACATCCCGACGTCATTTGCCATGCAAAAACCGCCCTCCAC 89459
D 89400 TGGTTCGTTATCCACATATACATCCCGACGTCATTTGCCATGCAAAAACCGCCCTCCAC 89459
QY 89460 ACCCGTTATATCTCAGACAGGTTTCTCTGCTCCGCGGTAGCGGCGCACTCAACT 89519
D 89460 ACCCGTTATATCTCAGACAGGTTTCTCTGCTCCGCGGTAGCGGCGCACTCAACT 89519
QY 89520 GAGGTTTGGAGCAGCATCTTATAGCGTGTCCATAGAAACCTGCTGAGCCGGTTGG 89579
D 89520 GAGGTTTGGAGCAGCATCTTATAGCGTGTCCATAGAAACCTGCTGAGCCGGTTGG 89579

QY 89580 GGTCTTGGCGCTTATGCAATGTAACCCCTCTACGGTCTTGAGAGTGTGTCCGTACCA 89639
D 89580 GGTCTTGGCGCTTATGCAATGTAACCCCTCTACGGTCTTGAGAGTGTGTCCGTACCA 89639
QY 89640 GCGACCCAAAATTAATAATCTGTAATAGCTAGCGGCCAAAATGAGTATCTGGTGTGAT 89699
D 89640 GCGACCCAAAATTAATAATCTGTAATAGCTAGCGGCCAAAATGAGTATCTGGTGTGAT 89699
QY 89700 GCGGTGTGCAACCGTGCACACCTGCGGCGCCCTGGCATTTACAGGACGCGCGCACCGT 89759
D 89700 GCGGTGTGCAACCGTGCACACCTGCGGCGCCCTGGCATTTACAGGACGCGCGCACCGT 89759
QY 89760 CAGCCTCCGCGGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 89819
D 89760 CAGCCTCCGCGGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 89819
QY 89820 CCGCTCTAATTTAGAGAGGCTCTCCGAATGACATATCTAAGATGACAGCATTAACA 89879
D 89820 CCGCTCTAATTTAGAGAGGCTCTCCGAATGACATATCTAAGATGACAGCATTAACA 89879
QY 89880 GCGGATCCAGCGGCGGTCTCAAGTAAATAATCTTCTCCGCCAAAACGCGTTGTGG 89939
D 89880 GCGGATCCAGCGGCGGTCTCAAGTAAATAATCTTCTCCGCCAAAACGCGTTGTGG 89939
QY 89940 CCGGCGCATGCTCTGTTCAAACCCAGCGTTTCCGAGACACCTTAGCAGTCTTTCC 89999
D 89940 CCGGCGCATGCTCTGTTCAAACCCAGCGTTTCCGAGACACCTTAGCAGTCTTTCC 89999
QY 90000 GGCACCTCGACAGTGTGCTGGCGTCCACATTTCAATTCCTATCCAGGACGTAACGCA 90059
D 90000 GGCACCTCGACAGTGTGCTGGCGTCCACATTTCAATTCCTATCCAGGACGTAACGCA 90059
QY 90060 CCACAGTTCGATTCACATCTACCTGCGGCTCACAATTCGATTCGATTCGATTCGATTCGATTC 90119
D 90060 CCACAGTTCGATTCACATCTACCTGCGGCTCACAATTCGATTCGATTCGATTCGATTCGATTC 90119
QY 90120 GGTGCAACCAACAGTGTGGGAAACGTTGCGTCCAAATTTGAAATTAATCCATC 90179
D 90120 GGTGCAACCAACAGTGTGGGAAACGTTGCGTCCAAATTTGAAATTAATCCATC 90179
QY 90180 TTGCGAGTATGTAATGATGATTTCTATCTGCGGATTTGAACTTGTCCAGCAAACT 90239
D 90180 TTGCGAGTATGTAATGATGATTTCTATCTGCGGATTTGAACTTGTGTCCAGCAAACT 90239
QY 90240 AACTCAAAAGCCCTCACACACTCCCTTAACTGATGATTTATGCTCCACTTATAG 90299
D 90240 AACTCAAAAGCCCTCACACACTCCCTTAACTGATGATTTATGCTCCACTTATAG 90299
QY 90300 GTGCACTGTATGATATGCCCGGTGAAACCTGCACTTCCTATTAATTCGCCAAA 90359
D 90300 GTGCACTGTATGATATGCCCGGTGAAACCTGCACTTCCTATTAATTCGCCAAA 90359
QY 90360 GCGTTTGGGTCGCTCACCTTAATTAATGAGATTAACAGGTTTCAATAGTGTCCGGGT 90419
D 90360 GCGTTTGGGTCGCTCACCTTAATTAATGAGATTAACAGGTTTCAATAGTGTCCGGGT 90419
QY 90420 TTGCGCACTCCCGGACCGGAGAGAGAAAGGTTCAATTTAAAGGGGACCAAGTGC 90479
D 90420 TTGCGCACTCCCGGACCGGAGAGAGAAAGGTTCAATTTAAAGGGGACCAAGTGC 90479
QY 90480 AACTTTATTAAG 90539
D 90480 AACTTTATTAAG 90539
QY 90540 CAAGACTATTTCTTGGGAGGTTCCGGGACAGCTGTAGTTTCTGATTTATTTGTAATTC 90599
D 90540 CAAGACTATTTCTTGGGAGGTTCCGGGACAGCTGTAGTTTCTGATTTATTTGTAATTC 90599
QY 90600 GCATCCAAATGCGCCCAACATATGATTAATAAAGGTTAAACGACACACTGCGGAA 90659
D 90600 GCATCCAAATGCGCCCAACATATGATTAATAAAGGTTAAACGACACACTGCGGAA 90659
QY 90660 CAAATTTATGCTTCTGCGCCCAAGAGAGCTGAGGCTCAGACAGCAGCGGCTGCTAA 90719

```
Db 90660 CAAATTAATGCGTCTGCGCCCAAGAGCGTGTGAGCGCTGACACACAGCGGTCTGTA 90719
Oy 90720 AACATTAACAGAGCGCTAAACGCTTGGACGAAACACAGATCCGAGCAACAAAAGCCC 90779
Db 90720 AACATTAACAGAGCGCTTAAACGCTTGGACGAAACACAGATCCGAGCAACAAAAGCCC 90779
Oy 90780 AACGTGAAGACAAAAAATAGTGTACAAAGTCGAGAGACAGAGCGTGTGAGCCCAAC 90839
Db 90780 AACGTGAAGACAAAAAATAGTGTACAAAGTCGAGAGACAGAGCGTGTGAGCCCAAC 90839
Oy 90840 AGACAGCGTACCCGCGCGCCGCTCCATCAAAACAGTCAAGATAAATGCTCCATCC 90899
Db 90840 AGACAGCGTACCCGCGCGCCGCTCCATCAAAACAGTCAAGATAAATGCTCCATCC 90899
Oy 90900 ACACAGCTCAAGCGCTGCTTATATAGATGTATGATACCGCTAGAGGTAGAGGAA 90959
Db 90900 ACACAGCTCAAGCGCTGCTTATATAGATGTATGATACCGCTAGAGGTAGAGGAA 90959
Oy 90960 AATTGCATGCGGTGCTGCGAGCGCCGCTCATTAAGCGGATGTGACCGCGCTGTAG 91019
Db 90960 AATTGCATGCGGTGCTGCGAGCGCCGCTCATTAAGCGGATGTGACCGCGCTGTAG 91019
Oy 91020 TGAACAAAGCGCACTACTATTAAGGCAACGAGGCGCAAAACACCGGGGCTTAA 91079
Db 91020 TGAACAAAGCGCACTACTATTAAGGCAACGAGGCGCAAAACACCGGGGCTTAA 91079
Oy 91080 AAGGTTCTTAAGAACTAAATAATATACACGAGAAAGCTGCTAAATTCGAATGCTA 91139
Db 91080 AAGGTTCTTAAGAACTAAATAATATACACGAGAAAGCTGCTAAATTCGAATGCTA 91139
Oy 91140 GTATGTGTGGCAATGTGTGGGCGACAAATATACCGATGATTCGCGCAACACAGAG 91199
Db 91140 GTATGTGTGGCAATGTGTGGGCGACAAATATACCGATGATTCGCGCAACACAGAG 91199
Oy 91200 CAGCAGGACAGGCGACGACCCCAAAAATGGAACCGTAAGGAGGTCAAGCGC 91259
Db 91200 CAGCAGGACAGGCGACGACCCCAAAAATGGAACCGTAAGGAGGTCAAGCGC 91259
Oy 91260 GAGGGTGATGCTCATTAAGAACGCGCGTATTAAGAAACCGCAGATGTGACGCTATC 91319
Db 91260 GAGGGTGATGCTCATTAAGAACGCGCGTATTAAGAAACCGCAGATGTGACGCTATC 91319
Oy 91320 CACCTGCGCGGAGACGACGCGCGGTAGCCCAATATACAGATACGAAAGACGCCATG 91379
Db 91320 CACCTGCGCGGAGACGACGCGCGGTAGCCCAATATACAGATACGAAAGACGCCATG 91379
Oy 91380 TAAGCAACCGCGCGCGAGAAATATATGTTCTCAACGCTAATCAAGGGCTTACAA 91439
Db 91380 TAAGCAACCGCGCGCGAGAAATATATGTTCTCAACGCTAATCAAGGGCTTACAA 91439
Oy 91440 ATACAGCGATGATTAATTAACACAGATTAACGAGAAACCGGAGACCGTCCGCTAT 91499
Db 91440 ATACAGCGATGATTAATTAACACAGATTAACGAGAAACCGGAGACCGTCCGCTAT 91499
Oy 91500 AAAAATATAGCCAGGAGGAGGAGCGCTCCGAGGTATACGTCGCTATGCGCGCTTAA 91559
Db 91500 AAAAATATAGCCAGGAGGAGGAGCGCTCCGAGGTATACGTCGCTATGCGCGCTTAA 91559
Oy 91560 ACAACGGGTGAACGTCGCGAGGAGCGTGTGTTTCCCTTCCGAGACTGGGTGAGC 91619
Db 91560 ACAACGGGTGAACGTCGCGAGGAGCGTGTGTTTCCCTTCCGAGACTGGGTGAGC 91619
Oy 91620 TGTGTGTGTTTTCGCTTGCCTGTGTTTTCGCGGTGAGAGCGCTGCGCACTGAT 91679
Db 91620 TGTGTGTGTTTTCGCTTGCCTGTGTTTTCGCGGTGAGAGCGCTGCGCACTGAT 91679
Oy 91680 TGGGCGCGCGCTGTGCGGTGCGAGCGCTGCTCGGCAATGCGGCACTGCTCTTTA 91739
Db 91680 TGGGCGCGCGCTGTGCGGTGCGAGCGCTGCTCGGCAATGCGGCACTGCTCTTTA 91739
Oy 91740 AGTCAGGTGAGCGCTGCTCGAGGAGGAGGAGTCAAGAAACCGCTCGGGATGGGAC 91799
Db 91740 AGTCAGGTGAGCGCTGCTCGAGGAGGAGGAGTCAAGAAACCGCTCGGGATGGGAC 91799
```

```
Db 91740 AGTCAGGTGAGCGCTTCTCGAGGAGGAGGAGGAGTCAAGAAACCGCTCGGGATGGGAC 91799
Oy 91800 CTTCGAGAGATTTGCCCGGAGGAGGATTAATTCGGGTGCGTCCGATCACTTAATAGCA 91859
Db 91800 CTTCGAGAGATTTGCCCGGAGGAGGATTAATTCGGGTGCGTCCGATCACTTAATAGCA 91859
Oy 91860 TGAGCGCCCACTGACGTCAGCAAGGCTATCTGTACAGGCGGACGCCCTCACTTCAGAA 91919
Db 91860 TGAGCGCCCACTGACGTCAGCAAGGCTATCTGTACAGGCGGACGCCCTCACTTCAGAA 91919
Oy 91920 TCTCAATGCGCGTCCAGGAGGAAACAGGCAAAAAAATCCGGAATCTTACATGCGTCA 91979
Db 91920 TCTCAATGCGCGTCCAGGAGGAAACAGGCAAAAAAATCCGGAATCTTACATGCGTCA 91979
Oy 91980 ATGCGGCGCACAGACACTTAATCACTGATGATGTCGAGTGCCTAGAAACACACCCA 92039
Db 91980 ATGCGGCGCACAGACACTTAATCACTGATGATGTCGAGTGCCTAGAAACACACCCA 92039
Oy 92040 GGTCAAGCTTTCTTCTCTAGCGCAAGTCCACTTGGCGTCCGGGTGTGCGGTTTAAAT 92099
Db 92040 GGTCAAGCTTTCTTCTCTAGCGCAAGTCCACTTGGCGTCCGGGTGTGCGGTTTAAAT 92099
Oy 92100 CAATTAATTTTACTAACCCCGTGCAGCTTAACGTCGCAACGTCGACGCGTTGCTTAACG 92159
Db 92100 CAATTAATTTTACTAACCCCGTGCAGCTTAACGTCGCAACGTCGACGCGTTGCTTAACG 92159
Oy 92160 AGACGGTGACCACTGCTTGGCCCTGTGTTTCTGCTGCTTAAGCACCTTAACAAAG 92219
Db 92160 AGACGGTGACCACTGCTTGGCCCTGTGTTTCTGCTGCTTAAGCACCTTAACAAAG 92219
Oy 92220 TCAGGCTCTTAACCGTAAAGAACAGGCAATTCGCGTCCGCGCTGCTTACCGTGTGT 92279
Db 92220 TCAGGCTCTTAACCGTAAAGAACAGGCAATTCGCGTCCGCGCTGCTTACCGTGTGT 92279
Oy 92280 GGAACGAGGAGGTGTGTTGGTTGCTCACGACGCTTGTGACGAGTGTGCTGATTTGT 92339
Db 92280 GGAACGAGGAGGTGTGTTGGTTGCTCACGACGCTTGTGACGAGTGTGCTGATTTGT 92339
Oy 92340 CCGCGTAGGCGATGCTGCTTAACAACTGCGGCTTTCGCGCTCCGATCGTCC 92399
Db 92340 CCGCGTAGGCGATGCTGCTTAACAACTGCGGCTTTCGCGCTCCGATCGTCC 92399
Oy 92400 CCGTGTGTGTAAGACGCAAGCTTCCGCAATTTCAACCTCAACCAACATCCAGGGGT 92459
Db 92400 CCGTGTGTGTAAGACGCAAGCTTCCGCAATTTCAACCTCAACCAACATCCAGGGGT 92459
Oy 92460 GTGTGAAGCTGTTCCCAAGGAGGTGTTTCAAAAGCTAAGCTACCTGCTCCGATGT 92519
Db 92460 GTGTGAAGCTGTTCCCAAGGAGGTGTTTCAAAAGCTAAGCTACCTGCTCCGATGT 92519
Oy 92520 CAGAATATACATCAAGCGGCGCAATGATTTTAAAGCTGAGACGGAAGCGCCGCT 92579
Db 92520 CAGAATATACATCAAGCGGCGCAATGATTTTAAAGCTGAGACGGAAGCGCCGCT 92579
Oy 92580 CCGCGACGCTGAGAGCAAGCTTAAGAGCGGGGCGCTCCGCGCGCTGATCTATTA 92639
Db 92580 CCGCGACGCTGAGAGCAAGCTTAAGAGCGGGGCGCTCCGCGCGCTGATCTATTA 92639
Oy 92640 CGCCTTTCTTAAGATGAGTGCCTTAATGTGTCGTAACCTGCTAATGCTGCCAAGCGAT 92699
Db 92640 CGCCTTTCTTAAGATGAGTGCCTTAATGTGTCGTAACCTGCTAATGCTGCCAAGCGAT 92699
Oy 92700 CGAGCTCAACCTGCGCGCGCTTAATGAACGAGACGAGTGAAGGGAATTAACAC 92759
Db 92700 CGAGCTCAACCTGCGCGCGCTTAATGAACGAGACGAGTGAAGGGAATTAACAC 92759
Oy 92760 CCTAAAGACGAGAGAGAAATGGAACACGACGACAGCGTCAATGTTCAACCTTT 92819
Db 92760 CCTAAAGACGAGAGAGAAATGGAACACGACGACAGCGTCAATGTTCAACCTTT 92819
Oy 92820 TTAATGAGCCCTGCTGCGCGGAAATAGTAACATGAGACATGCGGACTACATCTT 92879
Db 92820 TTAATGAGCCCTGCTGCGCGGAAATAGTAACATGAGACATGCGGACTACATCTT 92879
```

QY 92880 ATGACGATGTGACATATTTCAGAAATTCACGCTCAAAAAAGTTTCACACTCTTGGCACT 92939
|||||
Db 92880 ATGAACGATGTGACATATTTCAGAAATTCACGCTCAAAAAAGTTTCACACTCTTGGCACT 92939
QY 92940 CGTATTACGACAAAGGACACGCGTTTGGGGGGGGGACCGAACAGGGGGGATGTTTAT 92999
|||||
Db 92940 CGTATTACGACAAAGGACACGCGTTTGGGGGGGGGACCGAACAGGGGGGATGTTTAT 92999
QY 93000 TGACCTTTAGAAATCCCTGTGGCGGTGGCTGCAAAAACTGCTGATGTCCTCCGCGTTAC 93059
|||||
Db 93000 TGACCTTTAGAAATCCCTGTGGCGGTGGCTGCAAAAACTGCTGATGTCCTCCGCGTTAC 93059
QY 93060 CATGCTCAGCTCTCGGCTCTTGGAAAGCAATTAACAGAGTCTCTATCTCCAGCGCTTCGG 93119
|||||
Db 93060 CATGCTCAGCTCTCGGCTCTTGGAAAGCAATTAACAGAGTCTCTATCTCCAGCGCTTCGG 93119
QY 93120 AAAGAGCGCTGATATATGCGACGAGGGGATTTGCTCTCGGGAATCATGTTGTTGA 93179
|||||
Db 93120 AAAGAGCGCTGATATATGCGACGAGGGGATTTGCTCTCGGGAATCATGTTGTTGA 93179
QY 93180 CAGCAAGCTGGGGGCGCTGTGTGTAGCAGCTGTCCCTGGAGATGATGCTTACGAC 93239
|||||
Db 93180 CAGCAAGCTGGGGGCGCTGTGTGTAGCAGCTGTCCCTGGAGATGATGCTTACGAC 93239
QY 93240 GCACACCCCGCGCATGATTCGCGGAGAGGCAAAAAAGTCTATAGAGTAAATGAACCTTAT 93299
|||||
Db 93240 GCACACCCCGCGCATGATTCGCGGAGAGGCAAAAAAGTCTATAGAGTAAATGAACCTTAT 93299
QY 93300 AAAGTATATCCCTTCGATTAACAGAAACAGACACCTTCTCGGCCCGCTGTGGCCTT 93359
|||||
Db 93300 AAAGTATATCCCTTCGATTAACAGAAACAGACACCTTCTCGGCCCGCTGTGGCCTT 93359
QY 93360 GGGCACTCGGGAATGAGCGAGTCATCTTCTCGCAGGGTGGCGCTCGACTATTTT 93419
|||||
Db 93360 GGGCACTCGGGAATGAGCGAGTCATCTTCTCGCAGGGTGGCGCTCGACTATTTT 93419
QY 93420 TTTGGCATTAATCATTAAGTCCCGGATTTACCGCAAAAAATTAAGTTCAGTATGTTGGC 93479
|||||
Db 93420 TTTGGCATTAATCATTAAGTCCCGGATTTACCGCAAAAAATTAAGTTCAGTATGTTGGC 93479
QY 93480 ATACACTTTGCCGTGATGTTTTCATGGCTACCTGTTGGCGCTAATAGTGGTCACTC 93539
|||||
Db 93480 ATACACTTTGCCGTGATGTTTTCATGGCTACCTGTTGGCGCTAATAGTGGTCACTC 93539
QY 93540 GTGATGTGTAACCTTTTAACTAGTCTTCGATGTTAAAGTTTAAAGTTTACAGACTCTGCAAT 93599
|||||
Db 93540 GTGATGTGTAACCTTTTAACTAGTCTTCGATGTTAAAGTTTAAAGTTTACAGACTCTGCAAT 93599
QY 93600 ACCCAAAAAATGTGAAGAGAAACTGTAAAACCTCCATCGGTGGGACTCAATAGTGCAC 93659
|||||
Db 93600 ACCCAAAAAATGTGAAGAGAAACTGTAAAACCTCCATCGGTGGGACTCAATAGTGCAC 93659
QY 93660 CTCATGCGAGTCTCTGTCGACGGAAATTTTGACTGGGGAACCATCTGTTCTGCCATGCTC 93719
|||||
Db 93660 CTCATGCGAGTCTCTGTCGACGGAAATTTTGACTGGGGAACCATCTGTTCTGCCATGCTC 93719
QY 93720 CTGGGAGTGTCTAAAAGCAGGGGTGCTCGGCTACAGAAACCGAATCTGGGGCTC 93779
|||||
Db 93720 CTGGGAGTGTCTAAAAGCAGGGGTGCTCGGCTACAGAAACCGAATCTGGGGCTC 93779
QY 93780 CATGGCGGGGTTTACTATTGACAGGCAACATACCTTGGTCCGCTACCGTGGCGCTTT 93839
|||||
Db 93780 CATGGCGGGGTTTACTATTGACAGGCAACATACCTTGGTCCGCTACCGTGGCGCTTT 93839
QY 93840 TGTAGCAGTTAGACTCCGCCCTCTGAAGAGATGTTGTACCCAGACCTATCTAAG 93899
|||||
Db 93840 TGTAGCAGTTAGACTCCGCCCTCTGAAGAGATGTTGTACCCAGACCTATCTAAG 93899
QY 93900 CACTGACGGGCAATTAAGTTTGTCTGTTCTGAAATTCGACAAATTAACAGCATGTTT 93959
|||||
Db 93900 CACTGACGGGCAATTAAGTTTGTCTGTTCTGAAATTCGACAAATTAACAGCATGTTT 93959

QY 93960 AACCTAGCCTGTATCCGGTCAGGAGCAAGTCTGAAATTAATCTCCCGCGGTGCCCTGC 94019
|||||
Db 93960 AACCTAGCCTGTATCCGGTCAGGAGCAAGTCTGAAATTAATCTCCCGCGGTGCCCTGC 94019
QY 94020 TCTCTCTTTAAAAAATTTAAGCGACTGACTCTGCTCTAATAATGAGAGCCCGGACCG 94079
|||||
Db 94020 TCTCTCTTTAAAAAATTTAAGCGACTGACTCTGCTCTAATAATGAGAGCCCGGACCG 94079
QY 94080 GCCCGCTCCAACTGCTTAAATTTGGCAGTAAATCAAGAGCCGTCAAAAAATCTGTATCTG 94139
|||||
Db 94080 GCCCGCTCCAACTGCTTAAATTTGGCAGTAAATCAAGAGCCGTCAAAAAATCTGTATCTG 94139
QY 94140 TCTTACAGGGGTTTCTGAAATGAAGCCAGCTACCTCCGTAACGGCGCACCGTTCCAGG 94199
|||||
Db 94140 TCTTACAGGGGTTTCTGAAATGAAGCCAGCTACCTCCGTAACGGCGCACCGTTCCAGG 94199
QY 94200 TCACCAAGGCTTCACTCTTTAAAAAAGTCACGTTGGCTTCAAGATCTCTTGTGCTG 94259
|||||
Db 94200 TCACCAAGGCTTCACTCTTTAAAAAAGTCACGTTGGCTTCAAGATCTCTTGTGCTG 94259
QY 94260 GTGACCTTCGATCGATATTTGGCAAGAACGATAAATCTTCGCGTACCCCGTAAGC 94319
|||||
Db 94260 GTGACCTTCGATCGATATTTGGCAAGAACGATAAATCTTCGCGTACCCCGTAAGC 94319
QY 94320 TGAAGGTTCCGGCCGTTGGCATCAGCGCCAAAAAAGTGGCTTTGAAATTCATGCTGG 94379
|||||
Db 94320 TGAAGGTTCCGGCCGTTGGCATCAGCGCCAAAAAAGTGGCTTTGAAATTCATGCTGG 94379
QY 94380 GCAATGCTGGCCCCAGCTCTCCCATCTCTCCAAAGGAGGTTGGGACGGCTTAACGCCG 94439
|||||
Db 94380 GCAATGCTGGCCCCAGCTCTCCCATCTCTCCAAAGGAGGTTGGGACGGCTTAACGCCG 94439
QY 94440 TCCACAGTTTGGCAGGAAACACACACCTGAGCAATGAGTCCGCTCCATCCAGAAAC 94499
|||||
Db 94440 TCCACAGTTTGGCAGGAAACACACACCTGAGCAATGAGTCCGCTCCATCCAGAAAC 94499
QY 94460 GAGTCCCTCGCGGAGTAACAACTCATGACTGGTTGGACCCGCGTAAATACATT 94559
|||||
Db 94460 GAGTCCCTCGCGGAGTAACAACTCATGACTGGTTGGACCCGCGTAAATACATT 94559
QY 94560 GCGTGAATAATCTCCACGTCACGTCACGTCGCTCTCGCGCTCAAGTAAGCAAGCCAGT 94619
|||||
Db 94560 GCGTGAATAATCTCCACGTCACGTCACGTCGCTCTCGCGCTCAAGTAAGCAAGCCAGT 94619
QY 94620 TCGGCAAAACAGTCGCGCACTCTTGGAGCCCAATGCGCAATGCTCTCTCTGCGCG 94679
|||||
Db 94620 TCGGCAAAACAGTCGCGCACTCTTGGAGCCCAATGCGCAATGCTCTCTCTGCGCG 94679
QY 94680 CGCCTAACGCTCTCGGTAGGCGCGCTCCGCCCAAAATGCAAGCATTGACAAATGATTA 94739
|||||
Db 94680 CGCCTAACGCTCTCGGTAGGCGCGCTCCGCCCAAAATGCAAGCATTGACAAATGATTA 94739
QY 94740 GCGGCTCCACGGGATCATGAGCAGTTCAAAAACAAATTTTACATCCCTTCCAGGC 94799
|||||
Db 94740 GCGGCTCCACGGGATCATGAGCAGTTCAAAAACAAATTTTACATCCCTTCCAGGC 94799
QY 94800 TCCACACAGACTCTCCCGTGTGGGCTGAGGACACTTTGTGAGCGGCTCTTACGAGG 94859
|||||
Db 94800 TCCACACAGACTCTCCCGTGTGGGCTGAGGACACTTTGTGAGCGGCTCTTACGAGG 94859
QY 94860 TTAACACAGGAACTGACCTCGGCTGTGACAGATTTTCCGACAGAAATTAAGAACAG 94919
|||||
Db 94860 TTAACACAGGAACTGACCTCGGCTGTGACAGATTTTCCGACAGAAATTAAGAACAG 94919
QY 94920 TTTATGGCGCTGCTTGGCTTCAACACATGTTGTTTGTGAGCGGCTCTTACGAGG 94979
|||||
Db 94920 TTTATGGCGCTGCTTGGCTTCAACACATGTTGTTTGTGAGCGGCTCTTACGAGG 94979
QY 94980 ACGTAGGAGTGGCGGCTTAAATGACAGTGTATATAAGGCAATACATCATGATTTTAAC 95039
|||||
Db 94980 ACGTAGGAGTGGCGGCTTAAATGACAGTGTATATAAGGCAATACATCATGATTTTAAC 95039
QY 95040 GGCACAGACTAGAGTGTGTTGCCAGCGGCACATGACTGTGTTGATTCATTCATAATTCG 95099
|||||

Db	95040	GGCAACGAGTAGAGTGTGGCAGCGGCACTAGTCTGTGTATTCATCTCAATTCCG	95099	Db	96120	TTGGCAGATTTTCCCGCAGAGAAAGACTTTCGGTTCATTGTTAAAGAAATAGCTTCC	96179
Qy	95100	GCACCGTAGAGTTTATAGAGATTTTGGCGCCACCTCTGGCGCAAAACAGGTGGCCACTGGCA	95159	Qy	96180	AAGACCCCGGATTTGGAAACAAACTCCGTAATTTTAAACACCGGTAAACAGCGCTTTAA	96239
Db	95100	GCACCGTAGAGTTTATAGAGATTTTGGCGCCACCTCTGGCGCAAAACAGGTGGCCACTGGCA	95159	Db	96180	AAGACCCCGGATTTGGAAACAAACTCCGTAATTTTAAACACCGGTAAACAGCGCTTTAA	96239
Qy	95160	TCGTGGGTTTGTTCGTACAGTCGGAAAAAAGCTCCGGCACACACAGCCCTGAAACAGG	95219	Qy	96240	AGTGAAGCTTTGAAAGATGTTTAAACCGGAAGGACGCTTCAAGTGTGCAACTA	96299
Db	95160	TCGTGGGTTTGTTCGTACAGTCGGAAAAAAGCTCCGGCACACACAGCCCTGAAACAGG	95219	Db	96240	AGTGAAGCTTTGAAAGATGTTTAAACCGGAAGGACGCTTCAAGTGTGCAACTA	96299
Qy	95220	TTGTGACACCGCTCTGATTCCTCGGCATCTTCGGCTCAAAAAATCAAAATCGATGAGA	95279	Qy	96300	CGCCGACGCAAGCCTATTTATATCAGGTCAATTCGAGCTGAAATGATTTGGGCCAA	96359
Db	95220	TTGTGACACCGCTCTGATTCCTCGGCATCTTCGGCTCAAAAAATCAAAATCGATGAGA	95279	Db	96300	CGCCGACGCAAGCCTATTTATATCAGGTCAATTCGAGCTGAAATGATTTGGGCCAA	96359
Qy	95280	TGCCATAGTTCATAGTAGCGCTGGCACCAACAGAGCGGATATGTTATCTGTGAATATC	95339	Qy	96360	TCACGCCCTGTAAAAATCCCTCAATTGGGAGCTATTTCACAATATCTTTACAGACT	96419
Db	95280	TGCCATAGTTCATAGTAGCGCTGGCACCAACAGAGCGGATATGTTATCTGTGAATATC	95339	Db	96360	TCACGCCCTGTAAAAATCCCTCAATTGGGAGCTATTTCACAATATCTTTACAGACT	96419
Qy	95340	CCAAAGTGGGGGTTTATTAATTTTAAACAGCTGGTGATGTTCTTGTTCGGCAAAAGAC	95399	Qy	96420	TAAAAAACCCAAAGTCTTAGCGCGGGCTATTATTTACCTTAATGATGTTAAGCAAACT	96479
Db	95340	CCAAAGTGGGGGTTTATTAATTTTAAACAGCTGGTGATGTTCTTGTTCGGCAAAAGAC	95399	Db	96420	TAAAAAACCCAAAGTCTTAGCGCGGGCTATTATTTACCTTAATGATGTTAAGCAAACT	96479
Qy	95400	GAGACATCTATCCCGACGCTGACTTGTAGCGAGAAAGGGGAGACATTTCCGATGAGAT	95459	Qy	96480	AAATAGAGAGTGGCGGGCAAAAGCTCTGTCGCGCAGGCTGGAGCGCATGATCATCTA	96539
Db	95400	GAGACATCTATCCCGACGCTGACTTGTAGCGAGAAAGGGGAGACATTTCCGATGAGAT	95459	Db	96480	AAATAGAGAGTGGCGGGCAAAAGCTCTGTCGCGCAGGCTGGAGCGCATGATCATCTA	96539
Qy	95460	GCTTTGAGGGTTTGTCTTTCGGTGCGCATGAGACGGCTTTAAATTAACAGCTAGAAAGC	95519	Qy	96540	AATCCACAACATGTCTACTAGAAAGCTAGAGCCCAATATGTGTAAACAAGGGCTCTTGG	96599
Db	95460	GCTTTGAGGGTTTGTCTTTCGGTGCGCATGAGACGGCTTTAAATTAACAGCTAGAAAGC	95519	Db	96540	AATCCACAACATGTCTACTAGAAAGCTAGAGCCCAATATGTGTAAACAAGGGCTCTTGG	96599
Qy	95520	TGACCTCCGCGAAGCCCGGCTGACCTTAATACAGCGCTTGGCGAGACACAATCTGTAC	95579	Qy	96600	CGACTACGTTCCCTTTAAGCCAGACGTCACCTTGTGTACAAACGCTACTGTGGACGTTT	96659
Db	95520	TGACCTCCGCGAAGCCCGGCTGACCTTAATACAGCGCTTGGCGAGACACAATCTGTAC	95579	Db	96600	CGACTACGTTCCCTTTAAGCCAGACGTCACCTTGTGTACAAACGCTACTGTGGACGTTT	96659
Qy	95580	GAGATGTATGTGAAGCGCTTAACCAACAGGTACATCTATCAGTCCGTTTCCGCTCC	95639	Qy	96660	GAACCAAGCGCCGACCGGCGCAAGAACTATGAAGGACCGGTTTCCAACAATCTT	96719
Db	95580	GAGATGTATGTGAAGCGCTTAACCAACAGGTACATCTATCAGTCCGTTTCCGCTCC	95639	Db	96660	GAACCAAGCGCCGACCGGCGCAAGAACTATGAAGGACCGGTTTCCAACAATCTT	96719
Qy	95640	ACCAAGTGTCTGAGGGTCTCCCGCAACACGGAATTTTATACATGACAGCGCCCAAAA	95699	Qy	96720	CAAAATTTGGTATGGCTGCAAGTAGACCGCTCTGCTGGCCGTACCAACACACGCTATTC	96779
Db	95640	ACCAAGTGTCTGAGGGTCTCCCGCAACACGGAATTTTATACATGACAGCGCCCAAAA	95699	Db	96720	CAAAATTTGGTATGGCTGCAAGTAGACCGCTCTGCTGGCCGTACCAACACACGCTATTC	96779
Qy	95700	ACACGCCACCCATTAACATATCTGGGCCACGCTTTCAAAAATGGGTGAAGAACCCCTGGGTT	95759	Qy	96780	TGTTGGTCTGGGGGCAAGTCCGGTCCATCTCTAGACAGTCCGCGCAGCGATGAGCG	96839
Db	95700	ACACGCCACCCATTAACATATCTGGGCCACGCTTTCAAAAATGGGTGAAGAACCCCTGGGTT	95759	Db	96780	TGTTGGTCTGGGGGCAAGTCCGGTCCATCTCTAGACAGTCCGCGCAGCGATGAGCG	96839
Qy	95760	CTCAGCAGTACGTATCGTAAACCTAAGCGCAGACAGTAGCCGCACTTAACGAAATTT	95819	Qy	96840	TGAATTAACATGTCAATGAGGAGACCCAGTGTCACTGTTTAAAGGAAAAACAGTAGGTGC	96899
Db	95760	CTCAGCAGTACGTATCGTAAACCTAAGCGCAGACAGTAGCCGCACTTAACGAAATTT	95819	Db	96840	TGAATTAACATGTCAATGAGGAGACCCAGTGTCACTGTTTAAAGGAAAAACAGTAGGTGC	96899
Qy	95820	GTGTATGCTTGTCTGCTTAAAGTCTGTAAAGACCGTCAAGGGCGCTTCTGTGTTT	95879	Qy	96900	CCCGAGGTTCTGTGCACTCATGCTGTGAGATAAATCAAAAAATCTCCATACGTTTGAAC	96959
Db	95820	GTGTATGCTTGTCTGCTTAAAGTCTGTAAAGACCGTCAAGGGCGCTTCTGTGTTT	95879	Db	96900	CCCGAGGTTCTGTGCACTCATGCTGTGAGATAAATCAAAAAATCTCCATACGTTTGAAC	96959
Qy	95880	GACATTAACCGGGCAACCTCGCTCTTAAGCTTTCCCGGAATACCGCAGATAGCTCCGC	95939	Qy	96960	ATGTAGGGAACAGATTAATAATCATCTTGAATGAGCGCTCCACCCCAATGATGGTGGCGCA	97019
Db	95880	GACATTAACCGGGCAACCTCGCTCTTAAGCTTTCCCGGAATACCGCAGATAGCTCCGC	95939	Db	96960	ATGTAGGGAACAGATTAATAATCATCTTGAATGAGCGCTCCACCCCAATGATGGTGGCGCA	97019
Qy	95940	ACCATTAACGAGCAGCTGTCTCCATTTATCTGTGCCAAAGAGACGGGTAGTGAAGTTG	95999	Qy	97020	CCACATATTTAGAGAGCAGATCAGAACACCCCTTAGAAAATGTCGCGACCGGAGATTAACG	97079
Db	95940	ACCATTAACGAGCAGCTGTCTCCATTTATCTGTGCCAAAGAGACGGGTAGTGAAGTTG	95999	Db	97020	CCACATATTTAGAGAGCAGATCAGAACACCCCTTAGAAAATGTCGCGACCGGAGATTAACG	97079
Qy	96000	GCCCTATGTCCATCCAAAGTGTGCCCTTTAAAGAAATTCACAGATGATTCGGCCATCT	96059	Qy	97080	AAACCCGGTGAAGAGCGGCGGAGTAGACGATCAAACTATCATTCAGCTTGTTCACGT	97139
Db	96000	GCCCTATGTCCATCCAAAGTGTGCCCTTTAAAGAAATTCACAGATGATTCGGCCATCT	96059	Db	97080	AAACCCGGTGAAGAGCGGCGGAGTAGACGATCAAACTATCATTCAGCTTGTTCACGT	97139
Qy	96060	TCAGGGTCAAGGCTTGAAGCTACACCCCGCAATTCCTCCGCGTGGTAACTAGGTTAAAGT	96119	Qy	97140	TTGCGTCCCTGTCTTCAATGCGCTGCTCAATTCCTGCGCACCGGGCTGATTAACGTTGACG	97199
Db	96060	TCAGGGTCAAGGCTTGAAGCTACACCCCGCAATTCCTCCGCGTGGTAACTAGGTTAAAGT	96119	Db	97140	TTGCGTCCCTGTCTTCAATGCGCTGCTCAATTCCTGCGCACCGGGCTGATTAACGTTGACG	97199
Qy	96120	TTGGCAGATTTTGGCGGAGAAAGAGTTTCGGTGTTCATTGTTAAAGAAATAGCTTCC	96179	Qy	97200	AGAACACCGGGGCTTTACAAATTAACCTGCAACCTCTTAACGTGACCGGATGGCTAC	97259
Db	96120	TTGGCAGATTTTGGCGGAGAAAGAGTTTCGGTGTTCATTGTTAAAGAAATAGCTTCC	96179	Db	97200	AGAACACCGGGGCTTTACAAATTAACCTGCAACCTCTTAACGTGACCGGATGGCTAC	97259

QY 97260 AACAGCTAAACTCTGATGAGTTCACCTAAACCACACACACACCTTTAA 97319
D 97260 AACAGCTAAACTCTGATGAGTTCACCTAAACCACACACACACCTTTAA 97319
QY 97320 GCATGCCACCGGTGACCCGGTTTTTAATCTGCAATTCATAATGACACACCCCTGGTTT 97379
D 97320 GCATGCCACCGGTGACCCGGTTTTTAATCTGCAATTCATAATGACACACCCCTGGTTT 97379
QY 97380 CATTATATCAAAAACCCCTGTGTTTTTAAATGAGTCCGACGGCTCCGAGGACAG 97439
D 97380 CATTATATCAAAAACCCCTGTGTTTTTAAATGAGTCCGACGGCTCCGAGGACAG 97439
QY 97380 CATTATATCAAAAACCCCTGTGTTTTTAAATGAGTCCGACGGCTCCGAGGACAG 97439
D 97380 CATTATATCAAAAACCCCTGTGTTTTTAAATGAGTCCGACGGCTCCGAGGACAG 97439
QY 97440 TCATTACAGACACCAAGGACGAGAAACGTCAACAGGACATCTATCCGAGTTGTGATG 97499
D 97440 TCATTACAGACACCAAGGACGAGAAACGTCAACAGGACATCTATCCGAGTTGTGATG 97499
QY 97500 TTCTTAAATACAGCTATTGCAAAAACACACGAGTCCGACGGCTAAAGACACGATTTATC 97559
D 97500 TTCTTAAATACAGCTATTGCAAAAACACACGAGTCCGACGGCTAAAGACACGATTTATC 97559
QY 97560 TGCACAAACGCTGCATTTGGCCATGATTTACAGAAATCATCCATCAGCTAACTTACAGTA 97619
D 97560 TGCACAAACGCTGCATTTGGCCATGATTTACAGAAATCATCCATCAGCTAACTTACAGTA 97619
QY 97620 CGCCCTCGGGGATCCACACACACCAACCAATGGGTATCAGCAATCTACGCTGCTAGAGC 97679
D 97620 CGCCCTCGGGGATCCACACACACCAACCAATGGGTATCAGCAATCTACGCTGCTAGAGC 97679
QY 97680 AAATTTTACACGAAACCCACCGCAATACTGGAACCTAACCTCCGCGAGTCCGATTTTA 97739
D 97680 AAATTTTACACGAAACCCACCGCAATACTGGAACCTAACCTCCGCGAGTCCGATTTTA 97739
QY 97740 TGCACATCGGCGAAGTGGCTCTCCGCTGAGACGTGGCTAAATCCCTATTTGTAATA 97799
D 97740 TGCACATCGGCGAAGTGGCTCTCCGCTGAGACGTGGCTAAATCCCTATTTGTAATA 97799
QY 97800 AACTGCAACGCGGACACACCGCCCTATTTCCACCTGTGCAAGAACTGGCCGCTGTGG 97859
D 97800 AACTGCAACGCGGACACACCGCCCTATTTCCACCTGTGCAAGAACTGGCCGCTGTGG 97859
QY 97860 TTACCGGACACACGAAATTTTGTTCCTTACGACGTCACGTAAGAACTGTAACCA 97919
D 97860 TTACCGGACACACGAAATTTTGTTCCTTACGACGTCACGTAAGAACTGTAACCA 97919
QY 97920 TGCAGATATCAAAAACGCGGCTTGTGAGATATACAGCTTGTGCAAAATCAAAAACA 97979
D 97920 TGCAGATATCAAAAACGCGGCTTGTGAGATATACAGCTTGTGCAAAATCAAAAACA 97979
QY 97980 TAGTGAAGGACACCAATTTTATGCGTTACCGACACAGAACTTACAACTTCCCCG 98039
D 97980 TAGTGAAGGACACCAATTTTATGCGTTACCGACACAGAACTTACAACTTCCCCG 98039
QY 98040 AACTGTTATTCCTGTACGACTTGTGTAATGAGTCCCTGTGCAAAAACGACGATACGGGT 98099
D 98040 AACTGTTATTCCTGTACGACTTGTGTAATGAGTCCCTGTGCAAAAACGACGATACGGGT 98099
QY 98100 GTTCGCGCAACGCAATGAGCAATTTTAAAGAAAGTATCGATTTTATGCGGAGTTGG 98159
D 98100 GTTCGCGCAACGCAATGAGCAATTTTAAAGAAAGTATCGATTTTATGCGGAGTTGG 98159
QY 98160 GGGCGTTCAATGAAAAAACTGTGCGTATGATCAACGTAAGGCTTCCACAGTGAAG 98219
D 98160 GGGCGTTCAATGAAAAAACTGTGCGTATGATCAACGTAAGGCTTCCACAGTGAAG 98219
QY 98220 CCGTTAAGGCGAGGCTGCGAGCTGTGCTATCCAAAGAGGCGTGTGAAGATTTCCGCG 98279
D 98220 CCGTTAAGGCGAGGCTGCGAGCTGTGCTATCCAAAGAGGCGTGTGAAGATTTCCGCG 98279
QY 98280 CAATGATACGATGACACCGCAGAGACGAGCAAGGTAAGTGAAGATTTTACGGAATTTT 98339
D 98280 CAATGATACGATGACACCGCAGAGACGAGCAAGGTAAGTGAAGATTTTACGGAATTTT 98339

QY 98340 TAGAATATGTAACCAATTAACATATACGGGTCTATTTTATACGAGTGTCTTAACAGT 98399
D 98340 TAGAATATGTAACCAATTAACATATACGGGTCTATTTTATACGAGTGTCTTAACAGT 98399
QY 98400 ACAGCCCTACATATTCGCTGCGCAAAATTCAAATATCTTAACCGAGTGCATCCG 98459
D 98400 ACAGCCCTACATATTCGCTGCGCAAAATTCAAATATCTTAACCGAGTGCATCCG 98459
QY 98460 AACGAGGATTCGCGGCTGTGGGCGACTCATTAATCGGGTCTTCCGTTCCGCGGA 98519
D 98460 AACGAGGATTCGCGGCTGTGGGCGACTCATTAATCGGGTCTTCCGTTCCGCGGA 98519
QY 98520 AATTGAACAACGTGCTGGCTTTTAAAGCTTACACCCCGCTGCGCAACGCTTACAAAAA 98579
D 98520 AATTGAACAACGTGCTGGCTTTTAAAGCTTACACCCCGCTGCGCAACGCTTACAAAAA 98579
QY 98580 TCTACAAAGCAATACCGTCTGACTAATGAGTCTTTGTTGCAAAATAGCGCCCAAAAT 98639
D 98580 TCTACAAAGCAATACCGTCTGACTAATGAGTCTTTGTTGCAAAATAGCGCCCAAAAT 98639
QY 98640 CGTGGGTAACATGCGGCTGCGACAGAGCGCCGCTAACCGACATACAGACCGCGAAC 98699
D 98640 CGTGGGTAACATGCGGCTGCGACAGAGCGCCGCTAACCGACATACAGACCGCGAAC 98699
QY 98700 CAGACAGGCTCCGCTGCGCCAGGTTATCGCAAAATATTGCAAGCGCTTCCAAATA 98759
D 98700 CAGACAGGCTCCGCTGCGCCAGGTTATCGCAAAATATTGCAAGCGCTTCCAAATA 98759
QY 98760 GCGGACAGATTTATGACGACACCATGCTCTACACCCGGGATTTGCGCGAGTTCAATTA 98819
D 98760 GCGGACAGATTTATGACGACACCATGCTCTACACCCGGGATTTGCGCGAGTTCAATTA 98819
QY 98820 AAACAAACGTAATCCGATCCCTTAGCAGAGGCTCCGAAACAGCTTCCAAAAAATGAT 98879
D 98820 AAACAAACGTAATCCGATCCCTTAGCAGAGGCTCCGAAACAGCTTCCAAAAAATGAT 98879
QY 98880 CGCTATTTCAAAATAGATGAGTCTATGCTTTCGCGGACAGAGACGCAAGACCTAGCC 98939
D 98880 CGCTATTTCAAAATAGATGAGTCTATGCTTTCGCGGACAGAGACGCAAGACCTAGCC 98939
QY 98940 CTATCAGACGCTGCTGCTGCGCTGCGCTATTTTCAAAATATGAGCATTTTGGAAAGAAC 98999
D 98940 CTATCAGACGCTGCTGCTGCGCTGCGCTATTTTCAAAATATGAGCATTTTGGAAAGAAC 98999
QY 99000 ATTCTCGGAGTCTGTTTACAACTGCTGCACTATCTTACAGAAACATTTAGGTCATAC 99059
D 99000 ATTCTCGGAGTCTGTTTACAACTGCTGCACTATCTTACAGAAACATTTAGGTCATAC 99059
QY 99060 GACAGGTGATACCGGAAGCCACGTCGCCACAAGAAATTTCAATACATGTTGTTACTTTTC 99119
D 99060 GACAGGTGATACCGGAAGCCACGTCGCCACAAGAAATTTCAATACATGTTGTTACTTTTC 99119
QY 99120 AAAACATTTCAATATGACGCGAGCTTCAATTAACATCATGACCTTTGTAGACACCTGA 99179
D 99120 AAAACATTTCAATATGACGCGAGCTTCAATTAACATCATGACCTTTGTAGACACCTGA 99179
QY 99180 AAAAGGCAATCCCGGATATGAGCACTGTCCTTAAGGTCGCGGCTTTTAAATGTA 99239
D 99180 AAAAGGCAATCCCGGATATGAGCACTGTCCTTAAGGTCGCGGCTTTTAAATGTA 99239
QY 99240 AACTACTGTATGATTAACGCTAGACACGTCGATGATTTCCAAACGGAAGAGGCAACCA 99299
D 99240 AACTACTGTATGATTAACGCTAGACACGTCGATGATTTCCAAACGGAAGAGGCAACCA 99299
QY 99300 TCGTGTGAGCATGTTGCTATTTCAATATCAGATTCGCGCTCTGCAAGAGTCTTTACAGG 99359
D 99300 TCGTGTGAGCATGTTGCTATTTCAATATCAGATTCGCGCTCTGCAAGAGTCTTTACAGG 99359
QY 99360 AAGCGTTATTCGCTTAACTCAAAACGTCGGAACGATGAGGACGCGCAATCCGCTGGA 99419
D 99360 AAGCGTTATTCGCTTAACTCAAAACGTCGGAACGATGAGGACGCGCAATCCGCTGGA 99419
QY 99420 TGCACACCTACGCTACATGCAAAAAGATCGCGGACAGCAAGTAATGACACACACACTTC 99479


```
|||||
Db 99420 TGCACACCTTACGTTACATGCAAAAGATGCCGACACGAAATATGACACACATTC 99479
OY 99480 CATCCGTTTTCACGAATATACAGAGGATATTTGACGTGTTTAAAGCGTTTAAACGTC 99539
Db 99480 CATCCGTTTTCACGAATATACAGAGGATATTTGACGTGTTTAAAGCGTTTAAACGTC 99539
OY 99540 TCATGTTACAGTTACGGAGAGCTGCTGCTACTGCTACGCGGATGTTGATTCCTAT 99599
Db 99540 TCATGTTACAGTTACGGAGAGCTGCTGCTACTGCTACGCGGATGTTGATTCCTAT 99599
OY 99600 ATCAACCCCCCTTATACCCGATACGATCGTCAAAAATTTTAACTTATACGCAAA 99659
Db 99600 ATCAACCCCCCTTATACCCGATACGATCGTCAAAAATTTTAACTTATACGCAAA 99659
OY 99660 CGGACACACGACAGACATCTTTAAAGACCTGTCTACAGCCCGCTGAGACAAAGACCTCTAT 99719
Db 99660 CGGACACACGACAGACATCTTTAAAGACCTGTCTACAGCCCGCTGAGACAAAGACCTCTAT 99719
OY 99720 CGGCTGAAAAGGAAGTAGCAGTGCATCTCAAAAAACAGTTGAGTGTCTTCAAAAC 99779
Db 99720 CGGCTGAAAAGGAAGTAGCAGTGCATCTCAAAAAACAGTTGAGTGTCTTCAAAAC 99779
OY 99780 TGTACGACGACTTTGGACCGGCTCCACAACATACCCCACTCTATTAACTTGAT 99839
Db 99780 TGTACGACGACTTTGGACCGGCTCCACAACATACCCCACTCTATTAACTTGAT 99839
OY 99840 ATTCGGGTAAATTAACGAACACAAAGTGTCCGTAGATTGAGACATATATACCTGTGA 99899
Db 99840 ATTCGGGTAAATTAACGAACACAAAGTGTCCGTAGATTGAGACATATATACCTGTGA 99899
OY 99900 CATACACGCGACCCGACGATGCTTAAATTCACCCCGGTTTACACGAGCAGCTAGATC 99959
Db 99900 CATACACGCGACCCGACGATGCTTAAATTCACCCCGGTTTACACGAGCAGCTAGATC 99959
OY 99960 GCATGTTGCAAGATTAACGATGATGATGCCGCAATTTTTCGAAATTTTAAATAGAG 100019
Db 99960 GCATGTTGCAAGATTAACGATGATGATGCCGCAATTTTTCGAAATTTTAAATAGAG 100019
OY 100020 GCGTGGACAGACGACACGAGGCGCACTGCAAGTTGCGACATATACCGCGCTGCACTGCT 100079
Db 100020 GCGTGGACAGACGACACGAGGCGCACTGCAAGTTGCGACATATATACCGCGCTGCACTGCT 100079
OY 100080 TAAAGCACTGCTTATCTACCTCGCACAAAGTTATTTAATAGAGTCCCCGCGAGCG 100139
Db 100080 TAAAGCACTGCTTATCTACCTCGCACAAAGTTATTTAATAGAGTCCCCGCGAGCG 100139
OY 100140 ACACTAACGACCTCGACGATGTTTACGCAAGGCGGCGTGGACTTTATCTAGAGC 100199
Db 100140 ACACTAACGACCTCGACGATGTTTACGCAAGGCGGCGTGGACTTTATCTAGAGC 100199
OY 100200 GGTCCGGAGCGCTGCGCTATAACAATATGCCCACTGCACACATACCCAGCTTATCA 100259
Db 100200 GGTCCGGAGCGCTGCGCTATAACAATATGCCCACTGCACACATACCCAGCTTATCA 100259
OY 100260 AGACCAAGAGTAGAGCCGCGGCACTCTTCAATCTCAGAGATCTTGGACTTAATTTGAC 100319
Db 100260 AGACCAAGAGTAGAGCCGCGGCACTCTTCAATCTCAGAGATCTTGGACTTAATTTGAC 100319
OY 100320 TTGACGCGGCGATCGCGACCTTTCATCGAATCCCTTAAATCGATCTTAACGCAAAAT 100379
Db 100320 TTGACGCGGCGATCGCGACCTTTCATCGAATCCCTTAAATCGATCTTAACGCAAAAT 100379
OY 100380 ACGCCGCGACCGTTCAATCTTCTGTTTATATGCGGACAAACCGGGGCGGTAATTA 100439
Db 100380 ACGCCGCGACCGTTCAATCTTCTGTTTATATGCGGACAAACCGGGGCGGTAATTA 100439
OY 100440 TCAAAAACAAAACGTTTACTGTTGATCCCATGCGTACCCAGCTACCAATATAGTC 100499
Db 100440 TCAAAAACAAAACGTTTACTGTTGATCCCATGCGTACCCAGCTACCAATATAGTC 100499
OY 100500 CGGACGAGTATGTTGCTGTCAGACCGCACGGCATCTAGAGTAGTGCACCGCGAG 100559
|||||
Db 100500 CGGACGAGTATGTTGCTGTCAGACCGCACCGCCATCTAGAGTAGTGCACCGCGAG 100559
OY 100560 ACAGAAATATACACTGGCAGTTTCTATACATTTATGCCAGGAATATGTAATCCAGAGC 100619
Db 100560 ACAGAAATATACACTGGCAGTTTCTATACATTTATGCCAGGAATATGTAATCCAGAGC 100619
OY 100620 ACTACATACCAACGATATATNACTATATAGCTTGGCCAAATATACGGCCCGGCAATAG 100679
Db 100620 ACTACATACCAACGATATATNACTATATAGCTTGGCCAAATATACGGCCCGGCAATAG 100679
OY 100680 ATATATCCACCGGATATAGAGCGGTGACCATATGGAAGACATCCCAAGCCCGCGCATGCG 100739
Db 100680 ATATATCCACCGGATATAGAGCGGTGACCATATGGAAGACATCCCAAGCCCGCGCATGCG 100739
OY 100740 CGGATGTGACGTCAAAATATATCAACTGCGACGCGTGGCGGAACCAACGACGACGT 100799
Db 100740 CGGATGTGACGTCAAAATATATCAACTGCGACGCGTGGCGGAACCAACGACGACGT 100799
OY 100780 CGAGGCGCAACCCCGCACCGGAGCGTATCCGTTTACGGGGCGGGAACCGACGACA 100859
Db 100800 CGAGGCGCAACCCCGCACCGGAGCGTATCCGTTTACGGGGCGGGAACCGACGACA 100859
OY 100860 GCTACCCAGACCCCGGCAACCAACGAGCGGACACAAAACCTTTAACTCCCGCTCCAGCGC 100919
Db 100860 GCTACCCAGACCCCGGCAACCAACGAGCGGAGACACAAAACCTTTAACTCCCGCTCCAGCGC 100919
OY 100920 AAACCGCGTGACACCCCGGATTCCAAACACACTGAGACCGCTACTTCTTTCAG 100979
Db 100920 AAACCGCGTGACACCCCGGATTCCAAACACACTGAGACCGCTACTTCTTTCAG 100979
OY 100980 AACTGCGGATCCAGGGGTGGAAGCAACCTTTCAGCTTACGGATATTCGGAGT 101039
Db 100980 AACTGCGGATCCAGGGGTGGAAGCAACCTTTCAGCTTACGGATATTCGGAGT 101039
OY 101040 CCGAGGAAGCGTGTGCTGACGACGAAGGGGCCCAAGTGGCGCTACACGACGATGGGA 101099
Db 101040 CCGAGGAAGCGTGTGCTGACGACGAAGGGGCCCAAGTGGCGCTACACGACGATGGGA 101099
OY 101100 TATCCGCGAGGTGATCTGAGTGAACGACGATATATCTCTATATTTACCGTGGCGA 101159
Db 101100 TATCCGCGAGGTGATCTGAGTGAACGACGATATATCTCTATATTTACCGTGGCGA 101159
OY 101160 CTCCATGCTTGAAGACGCTTTCGACAGCCCGCAATGAGCCCGGAGTTTATATAGAG 101219
Db 101160 CTCCATGCTTGAAGACGCTTTCGACAGCCCGCAATGAGCCCGGAGTTTATATAGAG 101219
OY 101220 ACGGACAGAGAGACAGGATGGCGGCTTCTAGAAACAGATGCTGAGACGCGGAAACGC 101279
Db 101220 ACGGACAGAGAGACAGGATGGCGGCTTCTAGAAACAGATGCTGAGACGCGGAAACGC 101279
OY 101280 GCTTCTGTGCTTGCAGACGCTTATATAGGACCGACGACTTTCTCTGTTGTAATAAAA 101339
Db 101280 GCTTCTGTGCTTGCAGACGCTTATATAGGACCGACGACTTTCTCTGTTGTAATAAAA 101339
OY 101340 TAGAAGTGTATCAAGTACGAAGGCGCTGACACCTGCGCAAAACATCTGSGCAAC 101399
Db 101340 TAGAAGTGTATCAAGTACGAAGGCGCTGACACCTGCGCAAAACATCTGSGCAAC 101399
OY 101400 AAAAGGGGAGCGCTCCGAGAAAGCGGCGCTCCAGGCGATGAGCAAAATTAATGATTA 101459
Db 101400 AAAAGGGGAGCGCTCCGAGAAAGCGGCGCTCCAGGCGATGAGCAAAATTAATGATTA 101459
OY 101460 ATATCATCTGTAACAGGCTTAATTAAGAGCGCCAGGCGCGGAGCGCTCCGCTGCA 101519
Db 101460 ATATCATCTGTAACAGGCTTAATTAAGAGCGCCAGGCGCGGAGCGCTCCGCTGCA 101519
OY 101520 AAAAGCTCTCAATTTTCACTTCCGTTGGGGAAGAACTCAACTACCAATTAACGAG 101579
Db 101520 AAAAGCTCTCAATTTTCACTTCCGTTGGGGAAGAACTCAACTACCAATTAACGAG 101579
OY 101580 CCAAGCAGGCTCTAGAACTGATGCAACTGATACGCTTACATACGCGTATACAGGAG 101639
Db 101580 CCAAGCAGGCTCTAGAACTGATGCAACTGATACGCTTACATACGCGTATACAGGAG 101639
```

QY	101640	GAAAAATTAACACAGGGGGCGTTTCAAAAAACACCTAAACAATATAAATCAACCGGTGTCTGG	101699
Db	101640	GAAAAATTAACACAGGGGGCGTTTCAAAAAACACCTAAACAATATAAATCAACCGGTGTCTGG	101699
QY	101700	CGTCAATAGGGCCACGCACGCAGATGGGCATAAAAAAACTGGCGTTCGCTTCAACGTGG	101759
Db	101700	CGTCAATAGGGCCACGCACGCAGATGGGCATAAAAAAACTGGCGTTCGCTTCAACGTGG	101759
QY	101760	AAGGCTCACAGATTTTCGTCACGCAGAGCAAAATATACGTCCGGGGCGCTGAAGGAACAGA	101819
Db	101760	AAGGCTCACAGATTTTCGTCACGCAGAGCAAAATATACGTCCGGGGCGCTGAAGGAACAGA	101819
QY	101820	TCGCCAACCCACTGTAGTCCAGGCTTTTAAAGCGGTCTACTCCGGGACGAGGTAAAAATATC	101879
Db	101820	TCGCCAACCCACTGTAGTCCAGGCTTTTAAAGCGGTCTACTCCGGGACGAGGTAAAAATATC	101879
QY	101880	TACGGGATATAAATTCAGAACCTTAATAACAGCATGAGCAGGGCAACAAGAAATTCCAAC	101939
Db	101880	TACGGGATATAAATTCAGAACCTTAATAACAGCATGAGCAGGGCAACAAGAAATTCCAAC	101939
QY	101940	AGGAAGAATCTGTTTTTATGTCGCAATGCTCACAGCCCTGGACAGCTTCCAAACCCCTCCGA	101999
Db	101940	AGGAAGAATCTGTTTTTATGTCGCAATGCTCACAGCCCTGGACAGCTTCCAAACCCCTCCGA	101999
QY	102000	AAAGCGCATTTTCCAAATGCAAGATCTTTCCGCACCGTAATACCGAATGATATGTCGACACC	102059
Db	102000	AAAGCGCATTTTCCAAATGCAAGATCTTTCCGCACCGTAATACCGAATGATATGTCGACACC	102059
QY	102060	TGGGCTGCATTAACCAACAGGTTAAACCGAGGACCGCAACCGCAACCCCTCAACATTAACCTGG	102119
Db	102060	TGGGCTGCATTAACCAACAGGTTAAACCGAGGACCGCAACCGCAACCCCTCAACATTAACCTGG	102119
QY	102120	AGACCCCGCCGACCCAGGAAGAACGCATTAACCAATTTCCAAATCTTTCATCTCATCTGGTG	102179
Db	102120	AGACCCCGCCGACCCAGGAAGAACGCATTAACCAATTTCCAAATCTTTCATCTCATCTGGTG	102179
QY	102180	CAAAATATCATATCCACGTTAAAAAATTCCTTAACGTACCGCAAAAAACGACATGCAATTTAAACG	102239
Db	102180	CAAAATATCATATCCACGTTAAAAAATTCCTTAACGTACCGCAAAAAACGACATGCAATTTAAACG	102239
QY	102240	TAACGCCCATGGCAACGTACAGAGGCTCAAGCTTTGACTCGGAGGCGAGTTAAGCAACA	102299
Db	102240	TAACGCCCATGGCAACGTACAGAGGCTCAAGCTTTGACTCGGAGGCGAGTTAAGCAACA	102299
QY	102300	TCCTTAATTTAGAGTGGCCATACGAACCCGTGCCAACCGGTTCAAGAACTGCCCTCTGTGG	102359
Db	102300	TCCTTAATTTAGAGTGGCCATACGAACCCGTGCCAACCGGTTCAAGAACTGCCCTCTGTGG	102359
QY	102360	CGCGGGCCCAAAAGCAAAAAATGGAAATGCGGTACAAAAATGGAAAAAGAACCAACAGGCTCTGG	102419
Db	102360	CGCGGGCCCAAAAGCAAAAAATGGAAATGCGGTACAAAAATGGAAAAAGAACCAACAGGCTCTGG	102419
QY	102420	ACCAAAATCTGGGAGACCCCGCAAGCGTTACTTGACACAAATAACCGCAATCCGGAGATG	102479
Db	102420	ACCAAAATCTGGGAGACCCCGCAAGCGTTACTTGACACAAATAACCGCAATCCGGAGATG	102479
QY	102480	AGAACCCGGTCCGGCCATGTCTCAATACGATCTGGAGACCTAATTTACAAACGCGAGCGG	102539
Db	102480	AGAACCCGGTCCGGCCATGTCTCAATACGATCTGGAGACCTAATTTACAAACGCGAGCGG	102539
QY	102540	CCCGATATAGGCGATTCGGAACCAACGCGGTTGAAAAAATCTCAAGGCCCGCCATCCACGACC	102599
Db	102540	CCCGATATAGGCGATTCGGAACCAACGCGGTTGAAAAAATCTCAAGGCCCGCCATCCACGACC	102599
QY	102600	TGGCATCATCGGAGTCTGTTCAATAATAATGCTCTTAACCAACAGCGGGCTCGAATTAACATAT	102659
Db	102600	TGGCATCATCGGAGTCTGTTCAATAATAATGCTCTTAACCAACAGCGGGCTCGAATTAACATAT	102659
QY	102660	CAGACAAATCTGGCCAAAGATCGACGGCATCTTGACCAACAACACAGTTTTCTTTCAAAAG	102719
Db	102660	CAGACAAATCTGGCCAAAGATCGACGGCATCTTGACCAACAACACAGTTTTCTTTCAAAAG	102719

QY	102720	CCACTGTTAGCAAAACGCTCCAAACGCTGGGAGCGACGCTATATACGGGAATGCTAGAG	102779
Db	102720	CCACTGTTAGCAAAACGCTCCAAACGCTGGGAGCGAGCTAATACGGGAATGCTAGAG	102779
QY	102780	CGCTAAATAAAGGAGGCCCTTCCCTCCCAACAGCGCGCTCTCGCGGTTCAACCA	102839
Db	102780	CGCTAAATAAAGGAGGCCCTTCCCTCCCAACAGCGCGCTCTCGCGGTTCAACCA	102839
QY	102840	TACTGGGGCAGCGCTCGCTTCAGATCAGAGAGCGTGCACGAAATGTTTCCGGCGTC	102899
Db	102840	TACTGGGGCAGCGCTCGCTTCAGATCAGAGAGCGTGCACGAAATGTTTCCGGCGTC	102899
QY	102900	CCAGGCGCAAAAGGAATCCGCTGGCGATGATCCAGATAGGTGAGCGGATACCGGTC	102959
Db	102900	CCAGGCGCAAAAGGAATCCGCTGGCGATGATCCAGATAGGTGAGCGGATACCGGTC	102959
QY	102960	ACCTAAAGAGACTGAAGCTGTAACTACCAATGGCGTGCAGAAAGCCACAGGGGCA	103019
Db	102960	ACCTAAAGAGACTGAAGCTGTAACTACCAATGGCGTGCAGAAAGCCACAGGGGCA	103019
QY	103020	AACTGTTAATGATATAACCCGTGACCTCAAGAGGCGGAGGTGTTTCAGAGAAAGGTC	103079
Db	103020	AACTGTTAATGATATAACCCGTGACCTCAAGAGGCGGAGGTGTTTCAGAGAAAGGTC	103079
QY	103080	TGGAACAACGSGTGGCAGAGAAACGTGCTAAAGTTTCAACGCTGCAGCTCCAGAGAAATCG	103139
Db	103080	TGGAACAACGSGTGGCAGAGAAACGTGCTAAAGTTTCAACGCTGCAGCTCCAGAGAAATCG	103139
QY	103140	AAGACTTTTTCACGTGGGACCGTACAGCAAAAGGCCGAAATTTGGCAGAGAAACACCTAC	103199
Db	103140	AAGACTTTTTCACGTGGGACCGTACAGCAAAAGGCCGAAATTTGGCAGAGAAACACCTAC	103199
QY	103200	GGAGCGTGATACCCCAATTCAACGGGCCACGAGCACCGCTCGAGGCCACCGCGTTC	103259
Db	103200	GGAGCGTGATACCCCAATTCAACGGGCCACGAGCACCGCTCGAGGCCACCGCGTTC	103259
QY	103260	CCATGACTACACGCGCGACCCCATACCCACGCAAGGCCGTTTCTACGSGCTACCGGG	103319
Db	103260	CCATGACTACACGCGCGACCCCATACCCACGCAAGGCCGTTTCTACGSGCTACCGGG	103319
QY	103320	AAAAGGGAAGGCGGATGGAATAAATTCACAGGCGCTTCACAGATTTCACATTACCC	103379
Db	103320	AAAAGGGAAGGCGGATGGAATAAATTCACAGGCGCTTCACAGATTTCACATTACCC	103379
QY	103380	TCATCGACGCTTCGGATTGGCAGAGAGATGAGATCAGATTACTCGACACGCGCTGTC	103439
Db	103380	TCATCGACGCTTCGGATTGGCAGAGAGATGAGATCAGATTACTCGACAGCGCGCTGTC	103439
QY	103440	TTCTCGTAGCGTTGGACCAAAAGCTGGCGCTTCATGAGAGATCTCAAAACACCTGG	103499
Db	103440	TTCTCGTAGCGTTGGACCAAAAGCTGGCGCTTCATGAGAGATCTCAAAACACCTGG	103499
QY	103500	ACGACATCCTACGAGAAAGTGGCATCTGATTCCAAAGGGCGCGGCTTCAGACCC	103559
Db	103500	ACGACATCCTACGAGAAAGTGGCATCTGATTCCAAAGGGCGCGGCTTCAGACCC	103559
QY	103560	CAGAGTTTGAATGATCGCGGCTTATCAAAACGCGTAAAGCGCTTTTATAAAACATAG	103619
Db	103560	CAGAGTTTGAATGATCGCGGCTTATCAAAACGCGTAAAGCGCTTTTATAAAACATAG	103619
QY	103620	GCTGCGCATGAGTGGCGCAACCTGGCGGCAAGATTCATCACCAATGCCAAACTGTAC	103679
Db	103620	GCTGCGCATGAGTGGCGCAACCTGGCGGCAAGATTCATCACCAATGCCAAACTGTAC	103679
QY	103680	ACGGGATTCATCCGCAACCTTCAACAGGCGCAGGTGGGAACAAAGTTTAAAGACCCG	103739
Db	103680	ACGGGATTCATCCGCAACCTTCAACAGGCGCAGGTGGGAACAAAGTTTAAAGACCCG	103739
QY	103740	CGGCGGAATATGTCGAATACTCTCTGACATGCAAGTGCCTTCAAGCAGCAGGAATCG	103799
Db	103740	CGGCGGAATATGTCGAATACTCTCTGACATGCAAGTGCCTTCAAGCAGCAGGAATCG	103799
QY	103800	CCGTAAAGTCGGAGCGCGCGGCTACAGAGACGCAATTCACCTCGCGGCAACGTCGTGA	103859

Db	103800	CGGTAAAGATCGGAGGCGCGGGGTACAGGAGCGCAATCACTACGCGCGCCAAACGTGTGA	103859
Qy	103860	CTCCCCGAAACCCAACTAGAAAGCCCCAAAGACTATTAACGGCAACTGAACGCCCTAA	103919
Db	103860	CTCCCCGAAACCCAACTAGAAAGCCCCAAAGACTATTAACGGCAACTGAACGCCCTAA	103919
Qy	103920	CCGTGAGGACTCTTCCAGATTTCTTAAAAAGCTCAATCTTTCAACAGAGACGCACTCA	103979
Db	103920	CCGTGAGGACTCTTCCAGATTTCTTAAAAAGCTCAATCTTTCAACAGAGACGCACTCA	103979
Qy	103980	TTGGCTCCAGAGACGGAATTTCAAGCAACTAGAGCCAGCATCTCGCGGCGCGAAGCGC	104039
Db	103980	TTGGCTCCAGAGACGGAATTTCAAGCAACTAGAGCCAGCATCTCGCGGCGCGAAGCGC	104039
Qy	103980	TTGGCTCCAGAGACGGAATTTCAAGCAACTAGAGCCAGCATCTCGCGGCGCGAAGCGC	104039
Db	104040	TCGCGCAATCCACCCGTGACGAGATCGAGGCAAGTGGCAACCGCTATACAGCACTCT	104099
Qy	104040	TCGCGCAATCCACCCGTGACGAGATCGAGGCAAGTGGCAACCGCTATACAGCACTCT	104099
Db	104100	TACCCCGGCGCCCTCGCAATATCATGAGACCGTTGAACTTATCAAAACCTATAGACT	104159
Qy	104100	TACCCCGGCGCCCTCGCAATATCATGAGACCGTTGAACTTATCAAAACCTATAGACT	104159
Db	104160	TTTTAGTTCAACGGTATACGCAAAATCTTGAGCAAGAGCGCTTACGAGACGCCATAG	104219
Qy	104160	TTTTAGTTCAACGGTATACGCAAAATCTTGAGCAAGAGCGCTTACGAGACGCCATAG	104219
Db	104220	CGGAGTTGCGGTGGAATCGCGCAAAATCCGTAATGGTCTACAGTCAACAAACG	104279
Qy	104220	CGGAGTTGCGGTGGAATCGCGCAAAATCCGTAATGGTCTACAGTCAACAAACG	104279
Db	104280	AAAGCAACAGTTAAACGTACTGCTGAGCGAGGTGAAAAACAGAGCACCGTCCGCGAC	104339
Qy	104280	AAAGCAACAGTTAAACGTACTGCTGAGCGAGGTGAAAAACAGAGCACCGTCCGCGAC	104339
Db	104340	GTCTACAGATTTGGAAGCTGTCGCGGAAAAACACGAGACGCTTAAAGGCTGAAGCAGG	104399
Qy	104340	GTCTACAGATTTGGAAGCTGTCGCGGAAAAACACGAGACGCTTAAAGGCTGAAGCAGG	104399
Db	104400	CGCTAGACGAACCTCGCGCCCTCAGGGTAAAGGCGGAAAAACACCGCTAGACGCTGGA	104459
Qy	104400	CGCTAGACGAACCTCGCGCCCTCAGGGTAAAGGCGGAAAAACACCGCTAGACGCTGGA	104459
Db	104460	AAACAAAAGTGAAGGCAATAGATTCCTGCTCGGCCACAGGAGCGGCAAGGCAAAATAT	104519
Qy	104460	AAACAAAAGTGAAGGCAATAGATTCCTGCTCGGCCACAGGAGCGGCAAGGCAAAATAT	104519
Db	104520	CATCGAGACTTGAAGCATCGGACACAGGCGGTTGGACACATCACCGTCCGCAATTAG	104579
Qy	104520	CATCGAGACTTGAAGCATCGGACACAGGCGGTTGGACACATCACCGTCCGCAATTAG	104579
Db	104580	GAAAGCTTCGGAATCAATGCGGGAAGCGCAAAATTTCTCAGAGAGCCAGTCAACCG	104639
Qy	104580	GAAAGCTTCGGAATCAATGCGGGAAGCGCAAAATTTCTCAGAGAGCCAGTCAACCG	104639
Db	104640	AAAGGTTCTGGAGACTAGGCAAAACACTAGAGACTTACAGGCTTAAAGTAACTAAA	104699
Qy	104640	AAAGGTTCTGGAGACTAGGCAAAACACTAGAGACTTACAGGCTTAAAGTAACTAAA	104699
Db	104700	AAAGGTTCTGGAGACTTGAACCAACCCAGCTTAAAGTAACTAAA	104759
Qy	104700	AAAGGTTCTGGAGACTTGAACCAACCCAGCTTAAAGTAACTAAA	104759
Db	104760	CCCAAAACATTAACGAAACGTTCCGCGCGCGCGCGCATGAGTCCGTTGCGCAGATGA	104819
Qy	104760	CCCAAAACATTAACGAAACGTTCCGCGCGCGCGCGCATGAGTCCGTTGCGCAGATGA	104819
Db	104820	CCCAATACACTTACAGTGGCGGAGCGCGCCCACTTAAACAGTGGATTAAGAACGCTAC	104879
Qy	104820	CCCAATACACTTACAGTGGCGGAGCGCGCCCACTTAAACAGTGGATTAAGAACGCTAC	104879
Db	104880	CGACCGTGCATCCGGAACCACTACGTCGCGGCGCAGGAGAGACCCCTCTGCACG	104939
Qy	104880	CGACCGTGCATCCGGAACCACTACGTCGCGGCGCAGGAGAGACCCCTCTGCACG	104939

Db	104880	CGACCGTGCATCCGGAACCACTACGTCGCGGCGCAGGAGAGACCCCTCTGCACG	104939
Qy	104940	GCCAGATCACTACTCAAAAGTCTAGAGGCGTTGTTTCAATATGTTCCACACGCTAA	104999
Db	104940	GCCAGATCACTACTCAAAAGTCTAGAGGCGTTGTTTCAATATGTTCCACACGCTAA	104999
Qy	105000	CCCCGTTTCCGAGCGCCCGGCTGGAATATGCAACCGGCGACCGCGGGGAGAGG	105059
Db	105000	CCCCGTTTCCGAGCGCCCGGCTGGAATATGCAACCGGCGACCGCGGGGAGAGG	105059
Qy	105060	CCGCAAGCTGATGGAACAGACAGTGGCCGACATGCTCAGAGCGTCCAAAGCTTTGCG	105119
Db	105060	CCGCAAGCTGATGGAACAGACAGTGGCCGACATGCTCAGAGCGTCCAAAGCTTTGCG	105119
Qy	105120	ACAGCTAGCAACACACACCGCCGCAACCGGAGCGGCGCATTTAAACATTTCTGG	105179
Db	105120	ACAGCTAGCAACACACACCGCCGCAACCGGAGCGGCGCATTTAAACATTTCTGG	105179
Qy	105180	CGATGTCGTTTACGCAAAATCATGAGGCGGCTAGAGACCGCTGACGCTCCGAAAGT	105239
Db	105180	CGATGTCGTTTACGCAAAATCATGAGGCGGCTAGAGACCGCTGACGCTCCGAAAGT	105239
Qy	105240	TACGAGACACCGCGCTCGATTTTCCAGAAAGATGTTCTAACACCCAGGAAATGACAA	105299
Db	105240	TACGAGACACCGCGCTCGATTTTCCAGAAAGATGTTCTAACACCCAGGAAATGACAA	105299
Qy	105300	CAGTGTACCGCCCATATGAGGCGGCGGCGGCGCAATCTTACGATTTAAATCTTACT	105359
Db	105300	CAGTGTACCGCCCATATGAGGCGGCGGCGGCGGCGCAATCTTACGATTTAAATCTTACT	105359
Qy	105360	CGGAAGCCCTAGACTAATGAGTCTTCTCCGCTAATGTTCCAGGCGGCGCGAC	105419
Db	105360	CGGAAGCCCTAGACTAATGAGTCTTCTCCGCTAATGTTCCAGGCGGCGCGAC	105419
Qy	105420	TAAAGCTAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	105479
Db	105420	TAAAGCTAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	105479
Qy	105480	TTGCCAAACAGAGCAATTCGTAATTTCCGCGCGCAATGCGATAGCAAGCAAGGCGCA	105539
Db	105480	TTGCCAAACAGAGCAATTCGTAATTTCCGCGCGCAATGCGATAGCAAGCAAGGCGCA	105539
Qy	105540	AGAGCTGAGGAGAGAGCGGCTTTGCAAAATGCGGATTAACATCAAGCAAGGCGCA	105599
Db	105540	AGAGCTGAGGAGAGAGCGGCTTTGCAAAATGCGGATTAACATCAAGCAAGGCGCA	105599
Qy	105600	GAGCTGAGGAGAGAGCGGCTTTGCAAAATGCGGATTAACATCAAGCAAGGCGCA	105659
Db	105600	GAGCTGAGGAGAGAGCGGCTTTGCAAAATGCGGATTAACATCAAGCAAGGCGCA	105659
Qy	105660	GCTCCACATTTAAACCCATGACAGCGCGCTCAGAGCAGACGTAAGTCAAGTCAAG	105719
Db	105660	GCTCCACATTTAAACCCATGACAGCGCGCTCAGAGCAGACGTAAGTCAAGTCAAG	105719
Qy	105720	CCCTACACTGACCACTTTGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	105779
Db	105720	CCCTACACTGACCACTTTGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	105779
Qy	105780	AGCACCCGCGTACAGTACGAGAGAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGG	105839
Db	105780	AGCACCCGCGTACAGTACGAGAGAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGG	105839
Qy	105840	CGCGGCTCAGGCTTCAAAACACCGGTAATCCGTTTGAAGGCGGCTCGGAGCAATGG	105899
Db	105840	CGCGGCTCAGGCTTCAAAACACCGGTAATCCGTTTGAAGGCGGCTCGGAGCAATGG	105899
Qy	105900	TGTTTACAGTACCGATTCGAATATTTTGGGCGGCGGCGGCGGCGGCGGCGGCGG	105959
Db	105900	TGTTTACAGTACCGATTCGAATATTTTGGGCGGCGGCGGCGGCGGCGGCGGCGG	105959
Qy	105960	CGCGGCGGATGGGCTCTCTACACCATCTGGAATGGTCCCGGAGCTGCAAGCCCTTCA	106019
Db	105960	CGCGGCGGATGGGCTCTCTACACCATCTGGAATGGTCCCGGAGCTGCAAGCCCTTCA	106019

QY	106020	AAAGCCTGTATTAACGACCCCGCAAAACCCGTGCCCATTGAAAGCTACCCGCATCCCTCC	106079
Db	106020	AAAGCCTGTATTAACGACCCCGCAAAACCCGTGCCCATTGAAAGCTACCCGCATCCCTCC	106079
QY	106080	ACCCGACGACGACGACAGGTCTTCTCTAGACAGGACAGGTGCTATCCCTACCGATTCA	106139
Db	106080	ACCCGACGACGACGACAGGTCTTCTCTAGACAGGACAGGTGCTATCCCTACCGATTCA	106139
QY	106140	CACACACGAAAGCCCGGTGCTGACCTCCCGCTTCTGCTGCTATGACACCCGAAA	106139
Db	106140	CACACACGAAAGCCCGGTGCTGACCTCCCGCTTCTGCTGCTATGACACCCGAAA	106139
QY	106200	ACCTCGTAACGCGCAAGTACTCCAGTGGGGGCGCTCAAAATTTTCGAGAGAGCGCTTTT	106259
Db	106200	ACCTCGTAACGCGCAAGTACTCCAGTGGGGGCGCTCAAAATTTTCGAGAGAGCGCTTTT	106259
QY	106260	ACGTGATGCCCGGACCATACCCCCAGACTGGCCAAAAGCTGTGCGTAACTCAACA	106319
Db	106260	ACGTGATGCCCGGACCATACCCCCAGACTGGCCAAAAGCTGTGCGTAACTCAACA	106319
QY	106320	CGTCGTGAGCGCACTCAGCCACGAGAGATGTAAACCTTACTAGCGCTATCCCGAG	106379
Db	106320	CGTCGTGAGCGCACTCAGCCACGAGAGATGTAAACCTTACTAGCGCTATCCCGAG	106379
QY	106380	AACACGGGACCGTGCAGGAGGAGATATCTTCGACGCGGCTCCGACAAAGTCAACCGG	106439
Db	106380	AACACGGGACCGTGCAGGAGGAGATATCTTCGACGCGGCTCCGACAAAGTCAACCGG	106439
QY	106440	AACAAACCGGCAATCTCTCCGGCATGGGAAAAGGATTAACCGATTAAATACGCAAAAGAAA	106499
Db	106440	AACAAACCGGCAATCTCTCCGGCATGGGAAAAGGATTAACCGATTAAATACGCAAAAGAAA	106499
QY	106500	CGGCCAAAACCTCATTAATTCCTGCGCTCTCTAAAGGGGGAGAGATCCACGGGTGG	106559
Db	106500	CGGCCAAAACCTCATTAATTCCTGCGCTCTCTAAAGGGGGAGAGATCCACGGGTGG	106559
QY	106560	AAACGACGACCCACATTCACAAAGGGCAAGCGTGCAGACACGCAAAACGACAGCTAAACC	106619
Db	106560	AAACGACGACCCACATTCACAAAGGGCAAGCGTGCAGACACGCAAAACGACAGCTAAACC	106619
QY	106620	AGCCCGGTCAAAATCTTCTACACGCGCTCAACGATTAACCGCTACCGCTCAGGCGCT	106679
Db	106620	AGCCCGGTCAAAATCTTCTACACGCGCTCAACGATTAACCGCTACCGCTCAGGCGCT	106679
QY	106680	CATCTTCACGCGGAAAATTCACACGCAAAAGGTGCTGACATTAATTCACAAAGCGTG	106739
Db	106680	CATCTTCACGCGGAAAATTCACACGCAAAAGGTGCTGACATTAATTCACAAAGCGTG	106739
QY	106740	AAACGGCCCATTAATTAACAGCCAGCTCCGGCCAGGTCAACGAAACGAAAGGAAATCTTG	106799
Db	106740	AAACGGCCCATTAATTAACAGCCAGCCCTCCGGCCAGGTCAACGAAACGAAAGGAAATCTTG	106799
QY	106800	GGACGATTAACCCCGAGTGTCTACCGAACCCGCCAAACCGCCGAGGTGAGCCT	106859
Db	106800	GGACGATTAACCCCGAGTGTCTACCGAACCCGCCAAACCGCCGAGGTGAGCCT	106859
QY	106860	CTGCGCAACGAGGGAACCAACGAGTCCGCCAAGTTACGATTAATTCACCCACCGCTA	106919
Db	106860	CTGCGCAACGAGGGAACCAACGAGTCCGCCAAGTTACGATTAATTCACCCACCGCTA	106919
QY	106920	GGGTCTTTATAGGAGCGCGTCCAAACTCTCCGACCCGCTGGAAGAGCAGCGGCCCA	106979
Db	106920	GGGTCTTTATAGGAGCGCGTCCAAACTCTCCGACCCGCTGGAAGAGCAGCGGCCCA	106979
QY	106980	CACCCGACGACATCATGCTGGAATATGATCGGAAAAAATACGCCGAGAGTCCGCTCGCC	107039
Db	106980	CACCCGACGACATCATGCTGGAATATGATCGGAAAAAATACGCCGAGAGTCCGCTCGCC	107039
QY	107040	GCACCCACACCTCTGAAGAGGGGCCAAGGAGCTCAACGCTCAACACGAGGCAC	107099
Db	107040	GCACCCACACCTCTGAAGAGGGGCCAAGGAGCTCAACGCTCAACACGAGGCAC	107099

QY	107100	ACATAACGTCCTCTTAGCCAAAGTCCAAAACACAGTACAGGGCGCGAAATCCGGCC	107159
Db	107100	ACATAACGTCCTCTTAGCCAAAGTCCAAAACACAGTACAGGGCGCGAAATCCGGCC	107159
QY	107160	TTCAAAACAGCACTCTCCAGCGCCCCCAACCAACCGCATTCAAAACCCCGCATTCATACA	107219
Db	107160	TTCAAAACAGCACTCTCCAGCGCCCCCAACCAACCGCATTCAAAACCCCGCATTCATACA	107219
QY	107220	CGCTCCCGAAGAGGAGCGCGGCTGCTTCAGCAGCAATCGAGGTGGAATTCACCCCA	107279
Db	107220	CGCTCCCGAAGAGGAGCGCGGCTGCTTCAGCAGCAATCGAGGTGGAATTCACCCCA	107279
QY	107280	CCGAGGAGGTAAACGATCGCCAAAACACAAAGATGTCTCAAGGGCCCGAAGCGAGC	107339
Db	107280	CCGAGGAGGTAAACGATCGCCAAAACACAAAGATGTCTCAAGGGCCCGAAGCGAGC	107339
QY	107340	ACTCCAGGTGACACCGCCCGCTGCTCACAACCATAGGATTCATCGACTGGAACACCCCC	107399
Db	107340	ACTCCAGGTGACACCGCCCGCTGCTCACAACCATAGGATTCATCGACTGGAACACCCCC	107399
QY	107400	AAATTCCTCAAAATATTAACATCACTACCGCTCCCACTCCGAGAGTCAACCCCAATCCCTC	107459
Db	107400	AAATTCCTCAAAATATTAACATCACTACCGCTCCCACTCCGAGAGTCAACCCCAATCCCTC	107459
QY	107460	CCACTAACATCTGATATACCCCTATCCACAGTCAACATCAACAGAAATACACAGAG	107519
Db	107460	CCACTAACATCTGATATACCCCTATCCACAGTCAACATCAACAGAAATACACAGAG	107519
QY	107520	CCAAAGATGTGTTAAAGCGATTTATTCAAAACGTACGAAGAAACCTTCAAGCGTCTG	107579
Db	107520	CCAAAGATGTGTTAAAGCGATTTATTCAAAACGTACGAAGAAACCTTCAAGCGTCTG	107579
QY	107580	ACGCTCATCGAGGCGATATGCCAAGATAAGTTTATATCTGTAAGCGGCCCATCTCA	107639
Db	107580	ACGCTCATCGAGGCGATATGCCAAGATAAGTTTATATCTGTAAGCGGCCCATCTCA	107639
QY	107640	CTTGCTTTTATTTTGAAGCAGAGCTCTTGCTGCAAGATGAGTTCGCTGAGGTGA	107699
Db	107640	CTTGCTTTTATTTTGAAGCAGAGCTCTTGCTGCAAGATGAGTTCGCTGAGGTGA	107699
QY	107700	TAAAGAGTGGACCTATGCGCAAGAGCGCACGCTCCCGGTCGCGCCAGCGGCGC	107759
Db	107700	TAAAGAGTGGACCTATGCGCAAGAGCGCACGCTCCCGGTCGCGCCAGCGGCGC	107759
QY	107760	GGGGCCCATGAGACCTATCAATGAATGAGGCGCGCTGAGATGCTAAGCTAATTTGA	107819
Db	107760	GGGGCCCATGAGACCTATCAATGAATGAGGCGCGCTGAGATGCTAAGCTAATTTGA	107819
QY	107820	CCCGAGGCTGGAAGGCCAACCGGGCAACGCTCGGGGGCGCCGAGCCGGAACCCGGAACAAAC	107879
Db	107820	CCCGAGGCTGGAAGGCCAACCGGGCAACGCTCGGGGGCGCCGAGCCGGAACCCGGAACAAAC	107879
QY	107880	GCCCGAGATACTGAACTACCGCTTTTCCGCGGAAGGCCCGCGAGGTGCTTTGCG	107939
Db	107880	GCCCGAGATACTGAACTACCGCTTTTCCGCGGAAGGCCCGCGAGGTGCTTTGCG	107939
QY	107940	CAGAATTCATCTCTCTTTTGCATATGATGCTGTAATGATGTTGGCGCTTAAACAC	107999
Db	107940	CAGAATTCATCTCTCTTTTGCATATGATGCTGTAATGATGTTGGCGCTTAAACAC	107999
QY	108000	CAGATATTAAGTTCGCGATGCGCATACTGGGGGGAGACATGTCACCTCGGGGAAGTT	108059
Db	108000	CAGATATTAAGTTCGCGATGCGCATACTGGGGGGAGACATGTCACCTCGGGGAAGTT	108059
QY	108060	GTTTCATCTCGGCAACACGCGGTGATTTGGGTAACTGCTCAAGCGCTCCCTGAACGAT	108119
Db	108060	GTTTCATCTCGGCAACACGCGGTGATTTGGGTAACTGCTCAAGCGCTCCCTGAACGAT	108119
QY	108120	TGGCTCCTTAACCGCAAGAGACATCTTTTAACTTCTATTAACCTTCCACAGAG	108179
Db	108120	TGGCTCCTTAACCGCAAGAGACATCTTTTAACTTCTATTAACCTTCCACAGAG	108179
QY	108180	AGGAGGATATAGACGAGGTCAATTAACAGCTCGGCCACAGCAAAATGCTTAAATAG	108239

Db	108180	AGGACGATATAGACGAGGTCAAATATAAACACTCGCCACACGCAATATCTTATATAG	108239
Qy	108240	CCGGTCGGCAGTCCGGCGACGCCAACAAGGGACGACGACGCTAACAGGAGTTCGGC	108299
Db	108240	CCGGTCGGCAGTCCGGCGACGCCAACAAGGGACGACGACGCTAACAGGAGTTCGGC	108299
Qy	108300	TCTCGTATGGCATGTGGCCGCTGTGTGGGACACGACACCGTAATATAGGATCTCCACA	108359
Db	108300	TCTCGTATGGCATGTGGCCGCTGTGTGGGACACGACACCGTAATATAGGATCTCCACA	108359
Qy	108360	CACGATCTCGAATAGAGATATAACCCGATGCGATCCGCCAATAATAGCAATAT	108419
Db	108360	CACGATCTCGAATAGAGATATAACCCGATGCGATCCGCCAATAATAGCAATAT	108419
Qy	108420	ACGCGCCCGGTGTGACACAGATCGAAMGCTGCTCTTTTGGTCGCGACTGAAAAC	108479
Db	108420	ACGCGCCCGGTGTGACACAGATCGAAMGCTGCTCTTTTGGTCGCGACTGAAAAC	108479
Qy	108480	ACGTTGTGGGGGGAATTTTCGGTTTCAATTTAACCCCGCCGAATTCGAACGTTA	108539
Db	108480	ACGTTGTGGGGGGAATTTTCGGTTTCAATTTAACCCCGCCGAATTCGAACGTTA	108539
Qy	108540	CCGCACTGAGGACACCAACCAACCTCGAGAGTGGACAGGTTCTTCCAGTACGCTCTG	108599
Db	108540	CCGCACTGAGGACACCAACCAACCTCGAGAGTGGACAGGTTCTTCCAGTACGCTCTG	108599
Qy	108600	GCCACCACTGGGACCAACAGGTAGAGATACACGGAACAGTAACGTTATACGCAT	108659
Db	108600	GCCACCACTGGGACCAACAGGTAGAGATACACGGAACAGTAACGTTATACGCAT	108659
Qy	108660	ACTTTTGTACCCAGGTCGCGGGATATCTCCGTCGCTGACATCCCTATGCGCAACACA	108719
Db	108660	ACTTTTGTACCCAGGTCGCGGGATATCTCCGTCGCTGACATCCCTATGCGCAACACA	108719
Qy	108720	ACAGGGGACATGCTACAGAGAGGCCCTTAACGTCAGGCTCTTAGAAGGGCGTTAAAGGG	108779
Db	108720	ACAGGGGACATGCTACAGAGAGGCCCTTAACGTCAGGCTCTTAGAAGGGCGTTAAAGGG	108779
Qy	108780	TTGCGCGACGCGGACGGTGGCGCCAGTTCTCGACACGAGGCGCAGAAAGTCCCGCTCGAA	108839
Db	108780	TTGCGCGACGCGGACGGTGGCGCCAGTTCTCGACACGAGGCGCAGAAAGTCCCGCTCGAA	108839
Qy	108840	GGGCGCGGGAACACTCTCAATTAGGTTACTCCCAACGTCGTGAATGACGGAACGTTTC	108899
Db	108840	GGGCGCGGGAACACTCTCAATTAGGTTACTCCCAACGTCGTGAATGACGGAACGTTTC	108899
Qy	108900	AACGTGATCGAGACACCAACGCGCCCGCTTCCATTCTTCGCAAAAGGGGACGATCTAAC	108959
Db	108900	AACGTGATCGAGACACCAACGCGCCCGCTTCCATTCTTCGCAAAAGGGGACGATCTAAC	108959
Qy	108960	GCGTGTGTGCAAAACAGGTAAACAGGGGAAACCGCTGGCGACGTTAAGGTTTTGTCAC	109019
Db	108960	GCGTGTGTGCAAAACAGGTAAACAGGGGAAACCGCTGGCGACGTTAAGGTTTTGTCAC	109019
Qy	109020	ACGAGACAAACGCGCTCTGAAAGACACAAACAATACCTGAGCAGCGCTCTCGGGA	109079
Db	109020	ACGAGACAAACGCGCTCTGAAAGACACAAACAATACCTGAGCAGCGCTCTCGGGA	109079
Qy	109080	ACGCGCGTTAAACTTAACCTTTCGCTGCGTGGGACAGCCACCGCTGCAAGTATACACTTC	109139
Db	109080	ACGCGCGTTAAACTTAACCTTTCGCTGCGTGGGACAGCCACCGCTGCAAGTATACACTTC	109139
Qy	109140	AGCACCCACGCGTACGCTCTTAACACAGACGCGCGGATATGTGTCAGCCGCGATCTCACG	109199
Db	109140	AGCACCCACGCGTACGCTCTTAACACAGACGCGCGGATATGTGTCAGCCGCGATCTCACG	109199
Qy	109200	TCGCGCGTTTATAGTGGGTATTCGCGGCTCCAGACCGGTAGCAATCTCTTACAGGGCGGTC	109259
Db	109200	TCGCGCGTTTATAGTGGGTATTCGCGGCTCCAGACCGGTAGCAATCTCTTACAGGGCGGTC	109259
Qy	109260	TGAAGAGTGGGGCAGAAATTAACGTGCAGGCCATTTTGGGGTCTGCTCCGACAGCA	109319
Db	109260	TGAAGAGTGGGGCAGAAATTAACGTGCAGGCCATTTTGGGGTCTGCTCCGACAGCA	109319

Db	109267	TCGAAGATGGGGCAGAAATTAACTGACGAAGCCATTTTGGGGGTGCTCCGTCCAGGCA	109312
Qy	109320	CCGAGCCCGTACGTCAACAACACACGTAGCATTCGGGGCATATGTCGATTGAGCCTATA	109379
Db	109320	CCGAGCCCGTACGTCAACAACACACGTAGCATTCGGGGCATATGTCGATTGAGCCTATA	109379
Qy	109380	GAGGCGCGGAGATCTTAAGCCACAGCCGAGAACCTCCAGCAACGATGGGAGGATTAAGAA	109439
Db	109380	GAGGCGCGGAGATCTTAAGCCACAGCCGAGAACCTCCAGCAACGATGGGAGGATTAAGAA	109439
Qy	109440	CCGCGCCCATGACAGGACGCTTCGTTCAAGCCAGTTTAGCAAGCGCCGAGGCGCATC	109489
Db	109440	CCGCGCCCATGACAGGACGCTTCGTTCAAGCCAGTTTAGCAAGCGCCGAGGCGCATC	109489
Qy	109500	CCCCCAATTATACCGATTGAATTGGTTAATTGGTCATCGCCGACCGCTCTCCGGCCCCAT	109558
Db	109500	CCCCCAATTATACCGATTGAATTGGTTAATTGGTCATCGCCGACCGCTCTCCGGCCCCAT	109558
Qy	109560	ATCCTTCAACTCCGACCCCGAAGGGCGGGCCACAGAGCCGCTTCGCTCAAGCACCGAG	109619
Db	109560	ATCCTTCAACTCCGACCCCGAAGGGCGGGCCACAGAGCCGCTTCGCTCAAGCACCGAG	109619
Qy	109620	GCCTGTGAGTGAACCCGTCAGGGCAAAAACCGTCTTAAGAAGGGTTTTTAACCGTTTACG	109679
Db	109620	GCCTGTGAGTGAACCCGTCAGGGCAAAAACCGTCTTAAGAAGGGTTTTTAACCGTTTACG	109679
Qy	109680	GCTCTTTGGAGTACAGACCAAAAACGTAAAAACGTGTGGTGTCCGTTAAAGTAGTGGG	109739
Db	109680	GCTCTTTGGAGTACAGACCAAAAACGTAAAAACGTGTGGTGTCCGTTAAAGTAGTGGG	109739
Qy	109740	GCATATGACATGAGAGCTGTAAACGTTTAGTGTCCGGAGAAAAACAGACGTGCTTTAAA	109799
Db	109740	GCATATGACATGAGAGCTGTAAACGTTTAGTGTCCGGAGAAAAACAGACGTGCTTTAAA	109799
Qy	109800	TTTCAATAAATGCTCTGGGCCAGGGACAGGAGAGTTCCTCTCAAGATATACGCTCCGA	109859
Db	109800	TTTCAATAAATGCTCTGGGCCAGGGACAGGAGAGTTCCTCTCAAGATATACGCTCCGA	109859
Qy	109860	ATTTATAGGCAAGTTTTTTTCCAAACTGGGCAATCGGCGTACGTGCTTACACAAAAACA	109919
Db	109860	ATTTATAGGCAAGTTTTTTTCCAAACTGGGCAATCGGCGTACGTGCTTACACAAAAACA	109919
Qy	109920	TTTCAAGCGGTGGGCAAAACGCTGTGTATTAATAAACAAGGGGCAACGGGTAGGC	109979
Db	109920	TTTCAAGCGGTGGGCAAAACGCTGTGTATTAATAAACAAGGGGCAACGGGTAGGC	109979
Qy	109980	CAGTCTCTACTAGTTTGTGGAGCAAAACTTATACAAACTGAGATGTATAGACGAGCC	110039
Db	109980	CAGTCTCTACTAGTTTGTGGAGCAAAACTTATACAAACTGAGATGTATAGACGAGCC	110039
Qy	110040	GTCGTGACAGGCGCACGGGTGCACACGGGGACCCCGCTTTAGCCTTAACGGGACCCC	110099
Db	110040	GTCGTGACAGGCGCACGGGTGCACACGGGGACCCCGCTTTAGCCTTAACGGGACCCC	110099
Qy	110100	GTCCTGACACCTCTCCAACTCCAGGAGATTTCCAGAGGGTCCAGGTAAAGAGCAACTAA	110159
Db	110100	GTCCTGACACCTCTCCAACTCCAGGAGATTTCCAGAGGGTCCAGGTAAAGAGCAACTAA	110159
Qy	110160	ATCGACACAGCTGTCAACTAAACGTTTTCCGGAACCTCATCGTTATTAAGATCCTTAGGT	110219
Db	110160	ATCGACACAGCTGTCAACTAAACGTTTTCCGGAACCTCATCGTTATTAAGATCCTTAGGT	110219
Qy	110220	GCTGTGCGGTGGTCCCCGTTAAAAACCGGCGTCTGCTAAAGATTTGTGATGACCTGTTT	110279
Db	110220	GCTGTGCGGTGGTCCCCGTTAAAAACCGGCGTCTGCTAAAGATTTGTGATGACCTGTTT	110279
Qy	110280	TACGCGCTTTACCTTGGCGCTCCAGAGACCATGCAAGTGTACAGTGAAGTACCGCTCTG	110339
Db	110280	TACGCGCTTTACCTTGGCGCTCCAGAGACCATGCAAGTGTACAGTGAAGTACCGCTCTG	110339
Qy	110340	AGCAGATGACAGAGAAAGTTTTTAATATCTGACAGTAGATTAAATGCGTTGACCTGGA	110389
Db	110340	AGCAGATGACAGAGAAAGTTTTTAATATCTGACAGTAGATTAAATGCGTTGACCTGGA	110389
Qy	110340	AGCAGATGACAGAGAAAGTTTTTAATATCTGACAGTAGATTAAATGCGTTGACCTGGA	110399
Db	110340	AGCAGATGACAGAGAAAGTTTTTAATATCTGACAGTAGATTAAATGCGTTGACCTGGA	110399

QY	110400	ATATATGGTGGGAAACATATATTTTCATGTCAATCGGGGACAGAGGACTCGAACGCCAATTA	110459
Db	110400	ATATATGGTGGGAAACATATATTTTCATGTCAATCGGGGACAGAGGACTCGAACGCCAATTA	110459
QY	110460	ATCGCACCGGAACATACAGGTGAGACAGAGGTAAAGATCTCTACCGCGGGTACCGGGTAA	110519
Db	110460	ATCGCACCGGAACATACAGGTGAGACAGAGGTAAAGATCTCTACCGCGGGTACCGGGTAA	110519
QY	110520	CACGGGACAGCCACGCCCTTCCAAATATTTTACGCTTTAAAAAGCGGGGCCCTTAAAGTCGT	110579
Db	110520	CACGGGACAGCCACGCCCTTCCAAATATTTTACGCTTTAAAAAGCGGGGCCCTTAAAGTCGT	110579
QY	110580	CCAACTCAGCTTTAAAAAATCTCTTACCCATTATATGTGTCCCGTGGACACTGTGAGACCTCTA	110639
Db	110580	CCAACTCAGCTTTAAAAAATCTCTTACCCATTATATGTGTCCCGTGGACACTGTGAGACCTCTA	110639
QY	110640	TGAGACACTGGGCCCTCTCGCGGGGGACGTGTGAAACAATCTCTCCGCCGGATACCCGGG	110699
Db	110640	TGAGACACTGGGCCCTCTCGCGGGGGACGTGTGAAACAATCTCTCCGCCGGATACCCGGG	110699
QY	110700	ACGGAGCTTTTAAACAGCCCGGTATTATATCCACACTCAGAGACTCTCTAAACCCGCCCTCAT	110759
Db	110700	ACGGAGCTTTTAAACAGCCCGGTATTATATCCACACTCAGAGACTCTCTAAACCCGCCCTCAT	110759
QY	110760	CGTGGAGGGTGTGTAGCCCTCTCGCTTCTACCTCTGTGCGGACATTTCCACCCCGGACTCTT	110819
Db	110760	CGTGGAGGGTGTGTAGCCCTCTCGCTTCTACCTCTGTGCGGACATTTCCACCCCGGACTCTT	110819
QY	110820	TCTTGAAGACTACAGGGCTGGTGTGCGTCACTGCGCTATACGGCCCCCGGATCATGTGACGG	110879
Db	110820	TCTTGAAGACTACAGGGCTGGTGTGCGTCACTGCGCTATACGGCCCCCGGATCATGTGACGG	110879
QY	110880	CTACCCCTATGGTGGCTGCGCACCTTTTGGAACTAAAGCAGCGATCTTCCGCAATGGG	110939
Db	110880	CTACCCCTATGGTGGCTGCGCACCTTTTGGAACTAAAGCAGCGATCTTCCGCAATGGG	110939
QY	110940	TGAAGATATGGGCACTATATACACCGGCCAAAGCATCTCGGAAATCGACATCGTCACTGCACT	110999
Db	110940	TGAAGATATGGGCACTATATACACCGGCCAAAGCATCTCGGAAATCGACATCGTCACTGCACT	110999
QY	111000	TCTTGGCAACCGCGTGTTCGACCCATCGACAGAGAAACAAATATCTCACATCTCATTT	111059
Db	111000	TCTTGGCAACCGCGTGTTCGACCCATCGACAGAGAAACAAATATCTCACATCTCATTT	111059
QY	111060	TAAATTTTTTACAAACCGAGTTTATTAGGGGCATGTTAGAGGACAGCATTTCCGGGATCGT	111119
Db	111060	TAAATTTTTTACAAACCGAGTTTATTAGGGGCATGTTAGAGGACAGCATTTCCGGGATCGT	111119
QY	111120	TCTGTTTAAAAACGTCGTGGCGCGGCACAGAAAGAGACCAACAACCTTACCGTTGGCGT	111179
Db	111120	TCTGTTTAAAAACGTCGTGGCGCGGCACAGAAAGAGACCAACAACCTTACCGTTGGCGT	111179
QY	111180	GTTTGTCCGTTGGCGCGGAAATCAACACCAACCGGGATTAACGCGCTTACCCGAGGACTGG	111239
Db	111180	GTTTGTCCGTTGGCGCGGAAATCAACACCAACCGGGATTAACGCGCTTACCCGAGGACTGG	111239
QY	111240	AAGAGGCGTTCAATCTCAACGAAAGCGCGGAGAAAAGCCACGCTCTCGGCGTCTTTTCGG	111299
Db	111240	AAGAGGCGTTCAATCTCAACGAAAGCGCGGAGAAAAGCCACGCTCTCGGCGTCTTTTCGG	111299
QY	111300	CAAGCTGGGGAGAAATCCAGCTTCTTGGTCTCGGACACAAACAGAGAGATATACCATTTAC	111359
Db	111300	CAAGCTGGGGAGAAATCCAGCTTCTTGGTCTCGGACACAAACAGAGAGATATACCATTTAC	111359
QY	111360	AACCTCTCGGCTTCCCAACCCGAGAAAGTGTGACCAATCAAGAGGCGCCCTGCGTGTATGC	111419
Db	111360	AACCTCTCGGCTTCCCAACCCGAGAAAGTGTGACCAATCAAGAGGCGCCCTGCGTGTATGC	111419
QY	111420	ACCCAGCGTCAACCTTAAAAACAAAAAACACACGCGATCATATGCGTTTATGCGAGT	111479
Db	111420	ACCCAGCGTCAACCTTAAAAACAAAAAACACACGCGATCATATGCGTTTATGCGAGT	111479

[illegible]

|||||
Db 112560 TATCTCTAAAAACCTTTGGCCAGATCCTTTACCTATTTTAAAGTCGATGCCGATGAGA 112619
QY 112620 GACTCGACCTCTGGGGGCTGTTTCCACACTAGAGACCTACACCGGGGGAAACAGTCTGC 112679
Db 112620 GACTCGACCTCTGGGGGCTGTTTCCACACTAGAGACCTACACCGGGGGAAACAGTCTGC 112679
QY 112680 GACTCATTTAGCAACCTTCCAAATTTATGACATTAAGGCTGATCAACCAACGCT 112739
Db 112680 GACTCATTTAGCAACCTTCCAAATTTATGACATTAAGGCTGATCAACCAACGCT 112739
QY 112740 ACATTAATGAAGTTTAAACCTCGCCGACCGGACACCGACCGTGGAGGTTCTGTCAACA 112799
Db 112740 ACATTAATGAAGTTTAAACCTCGCCGACCGGACACCGTGGAGGTTCTGTCAACA 112799
QY 112800 GCATTTGGCAGGCGCGGCGACACCTGAGCTGACCGACGAGTTTCGAGAAATTCAAA 112859
Db 112800 GCATTTGGCAGGCGCGGCGACACCTGAGCTGACCGACGAGTTTCGAGAAATTCAAA 112859
QY 112860 GGGGCAAGCCATCATTAACCTCCAGGGGCTATTGTAACTTCCCTAGACGGAACAGA 112919
Db 112860 GGGGCAAGCCATCATTAACCTCCAGGGGCTATTGTAACTTCCCTAGACGGAACAGA 112919
QY 112920 TGTAACTCACTTAAATGTTAACTTTGTTTGAACATATTCACCAATTAACCAAC 112979
Db 112920 TGTAACTCACTTAAATGTTAACTTTGTTTGAACATATTCACCAATTAACCAAC 112979
QY 112980 TTATGTTTACACAAATTTGAAGAGCGTTTCAATTTTACCATTAACCAATTAACCAAC 113039
Db 112980 TTATGTTTACACAAATTTGAAGAGCGTTTCAATTTTACCATTAACCAATTAACCAAC 113039
QY 113040 TAACTAAATCTAATAGCGATTTGCGATGGGATCCCTAGAGCAATGACGTGGCGG 113099
Db 113040 TAACTAAATCTAATAGCGATTTGCGATGGGATCCCTAGAGCAATGACGTGGCGG 113099
QY 113040 TAACTAAATCTAATAGCGATTTGCGATGGGATCCCTAGAGCAATGACGTGGCGG 113099
Db 113100 GTATTAATGAGCGGAGCGAGCTTAACTGCTCCACGAAATGCGAACTCCGCGTTT 113159
QY 113100 GTATTAATGAGCGGAGCGAGCTTAACTGCTCCACGAAATGCGAACTCCGCGTTT 113159
Db 113100 GTATTAATGAGCGGAGCGAGCTTAACTGCTCCACGAAATGCGAACTCCGCGTTT 113159
QY 113160 AGGACCATTCGACGCGGTTAAATTAATGCGAGTAATGCGAAAGGGCGTACATCGCAGTA 113219
Db 113160 AGGACCATTCGACGCGGTTAAATTAATGCGAGTAATGCGAAAGGGCGTACATCGCAGTA 113219
QY 113220 GTGATTTTACGATGTCACACCTTCCGGGTTTACCGGCAACAAAGCGGCTACC 113279
Db 113220 GTGATTTTACGATGTCACACCTTCCGGGTTTACCGGCAACAAAGCGGCTACC 113279
QY 113280 AGGACCATTAATGCGCGGCTTTATGCGCAAAAGTACAAAGGAGCGGCTTACGCT 113339
Db 113280 AGGACCATTAATGCGCGGCTTTATGCGCAAAAGTACAAAGGAGCGGCTTACGCT 113339
QY 113340 TCACGAAACAACCTGTTGATCGCAAAATAGTGTGTGTGACCGCAAACTGCCAA 113399
Db 113340 TCACGAAACAACCTGTTGATCGCAAAATAGTGTGTGTGACCGCAAACTGCCAA 113399
QY 113400 ATCTTAATTAATGATGACATAGCTCTCAAAATCTAAGAGAACTTCCAAAACATCGGC 113459
Db 113400 ATCTTAATTAATGATGACATAGCTCTCAAAATCTAAGAGAACTTCCAAAACATCGGC 113459
QY 113460 AATTAACAACCCCTTGCAGTTAATGACATCGTAAGAGAGCGAATCCAAAGAACGCGC 113519
Db 113460 AATTAACAACCCCTTGCAGTTAATGACATCGTAAGAGAGCGAATCCAAAGAACGCGC 113519
QY 113520 CGATCTTAAGACACGCGGACGCTTTGGGTTCCGGGGGCGTTACGATGGAAGTTCAAT 113579
Db 113520 CGATCTTAAGACACGCGGACGCTTTGGGTTCCGGGGGCGTTACGATGGAAGTTCAAT 113579
QY 113580 CACCAAGTATCCCATTAACCTGTTACAAAAGCGTAAAGATTAATCGGTTTACATTAACAA 113639
Db 113580 CACCAAGTATCCCATTAACCTGTTACAAAAGCGTAAAGATTAATCGGTTTACATTAACAA 113639
QY 113640 TAAAAAATGATGAGCACTTACATTCGACATACAAAGGAGGCCAAACACCCCAA 113699
Db 113640 TAAAAAATGATGAGCACTTACATTCGACATACAAAGGAGGCCAAACACCCCAA 113699

Db 113640 TAAAAAATGAGCACTTACATTCGACATACAAAGGAGGCCAAACACCCCAA 113699
QY 113700 CGCAAAAACAACCTGAGACCTGCTGTTTGGGTCCTTCCACGTCGATGAGATTTCTGCT 113759
Db 113700 CGCAAAAACAACCTGAGACCTGCTGTTTGGGTCCTTCCACGTCGATGAGATTTCTGCT 113759
QY 113760 GACCGTGTGCTTAACGCGTTACAGTGTGTTTATGCGTACGTAACACACCAATCT 113819
Db 113760 GACCGTGTGCTTAACGCGTTACAGTGTGTTTATGCGTACGTAACACACCAATCT 113819
QY 113820 AGAATGCTAACAGTGCACCGCGCTTAAAGCGGCTTGTGCAACTACTGCTGACAGTA 113879
Db 113820 AGAATGCTAACAGTGCACCGCGCTTAAAGCGGCTTGTGCAACTACTGCTGACAGTA 113879
QY 113880 CTACTCTTAATTTTAAACAAGTACATACCACTGCAATTAATGCACTAAACCACTTTA 113939
Db 113880 CTACTCTTAATTTTAAACAAGTACATACCACTGCAATTAATGCACTAAACCACTTTA 113939
QY 113940 GTCTTTTATGTCAGTCCGCGCTTAAAGCGGCTTAAAGCGGCTTGTGCAACTACTGCTGACAGTA 113999
Db 113940 GTCTTTTATGTCAGTCCGCTTAAAGCGGCTTAAAGCGGCTTGTGCAACTACTGCTGACAGTA 113999
QY 114000 GGGCTGCGGTTACCGGTTGTTTGGGGCAAAACAGGCTCGGGGGAAAAAGAGCAACA 114059
Db 114000 GGGCTGCGGTTACCGGTTGTTTGGGGCAAAACAGGCTCGGGGGAAAAAGAGCAACA 114059
QY 114060 TATGTCAGTAAACAACCTCAAGTCTTAAATTCACCCACTCGTAAACAAAAACAT 114119
Db 114060 TATGTCAGTAAACAACCTCAAGTCTTAAATTCACCCACTCGTAAACAAAAACAT 114119
QY 114120 CGCAGTTAAGGTATGATGACCAACATTAACACACAAAGTTTAAACACAGCTCGCT 114179
Db 114120 CGCAGTTAAGGTATGATGACCAACATTAACACACAAAGTTTAAACACAGCTCGCT 114179
QY 114180 AAGTAACCCCATTTGCGACGCGTGGCGTGAAGTGTGTTTAAATTAACATTTGCGCT 114239
Db 114180 AAGTAACCCCATTTGCGACGCGTGGCGTGAAGTGTGTTTAAATTAACATTTGCGCT 114239
QY 114240 TTTACACACCGAGCACTAATCTCAGAGGCGGTTAAAGAGCGATATACATATTCCTTAA 114299
Db 114240 TTTACACACCGAGCACTAATCTCAGAGGCGGTTAAAGAGCGATATACATATTCCTTAA 114299
QY 114300 ACACGGGAACCGCGCTGACCGGCTTCCCAATTCACACACGCGGCTCAAAAGCCTAGT 114359
Db 114300 ACACGGGAACCGCGCTGACCGGCTTCCCAATTCACACACGCGGCTCAAAAGCCTAGT 114359
QY 114360 GTTAATTAATCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 114419
Db 114360 GTTAATTAATCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 114419
QY 114420 GGTACCTAGACCTTCCCTATACCTTCAAAAACAGCGGTTATTTGACCAACGCTT 114479
Db 114420 GGTACCTAGACCTTCCCTATACCTTCAAAAACAGCGGTTATTTGACCAACGCTT 114479
QY 114480 AAGTAACAACCCCTAGCAATTAATCCGCTTATCAAAATGGAATAATTAAGGCTTGCGCT 114539
Db 114480 AAGTAACAACCCCTAGCAATTAATCCGCTTATCAAAATGGAATAATTAAGGCTTGCGCT 114539
QY 114540 TAAATCTGCTAAACGCAAGGCACTTAATTTTCCAGTTTGGAGCTCGGAACCTTACCGC 114599
Db 114540 TAAATCTGCTAAACGCAAGGCACTTAATTTTCCAGTTTGGAGCTCGGAACCTTACCGC 114599
QY 114600 TAAAGTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 114659
Db 114600 TAAAGTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 114659
QY 114660 TACAGCTAAAGTTAATTAACGCGGCTTTGGGCAAGCAATCAGTGTGTGTCGCAACCCG 114719
Db 114660 TACAGCTAAAGTTAATTAACGCGGCTTTGGGCAAGCAATCAGTGTGTGTCGCAACCCG 114719
QY 114720 TTAATTTAAACAACAAGGAGCGGAGCTTAAACAAGGAGCTAATCTGATCGGGCGCTG 114779
Db 114720 TTAATTTAAACAACAAGGAGCGGAGCTTAAACAAGGAGCTAATCTGATCGGGCGCTG 114779

QY	114780	TTGAAGAAGTTG	GTGTTGTC	CAATGCAT	TATAGGCAATCT	ATAAAGCAAAATCC	TGCTCGGTAAC	114839
Db	114780	TTGAAGAAGTTG	GTGTTGTC	CAATGCAT	TATAGGCAATCT	ATAAAGCAAAATCC	TGCTCGGTAAC	114839
QY	114840	ACGGAATATGCTT	AGTTAGTTCC	CTACAGCATC	CAACAAATTTG	AAACCAATTAAC	CGTAACGGG	114839
Db	114840	ACGGAATATGCTT	AGTTAGTTCC	CTACAGCATC	CAACAAATTTG	AAACCAATTAAC	CGTAACGGG	114839
QY	114900	CGTGGGGTTG	GTGTTGTC	GTAANAATCT	TGTTGTC	CAACTGTTC	ATATGAGGCGGATTTGTAATG	114959
Db	114900	CGTGGGGTTG	GTGTTGTC	GTAANAATCT	TGTTGTC	CAACTGTTC	ATATGAGGCGGATTTGTAATG	114959
QY	114960	TGTTGCTTTG	GTGTC	CAACGGTGTG	GGGGTGC	CAAGTCCCCCGGTTG	CAAGTCCCCCGGT	115019
Db	114960	TGTTGCTTTG	GTGTC	CAACGGTGTG	GGGGTGC	CAAGTCCCCCGGTTG	CAAGTCCCCCGGT	115019
QY	115020	GGGGTGC	AGTCCCCCGGGT	GTGCAAGTCCCCCGGGT	GTGCAAGTCCCCCGGGT	GTGCAAGTCCCCCGGGT	GTGCAAGTCCCCCGGGT	115079
Db	115020	GGGGTGC	AGTCCCCCGGGT	GTGCAAGTCCCCCGGGT	GTGCAAGTCCCCCGGGT	GTGCAAGTCCCCCGGGT	GTGCAAGTCCCCCGGGT	115079
QY	115080	GTGCAAGTCCCCCGGGT	GTGCAAGTCCCCCGGGT	GTGCAAGTCCCCCGGGT	GTGCAAGTCCCCCGGGT	GTGCAAGTCCCCCGGGT	GTGCAAGTCCCCCGGGT	115139
Db	115080	GTGCAAGTCCCCCGGGT	GTGCAAGTCCCCCGGGT	GTGCAAGTCCCCCGGGT	GTGCAAGTCCCCCGGGT	GTGCAAGTCCCCCGGGT	GTGCAAGTCCCCCGGGT	115139
QY	115140	CAAGTCCCCCGGGT	GTGCAAGTCCCCCGGGT	GTGCAAGTCCCCCGGGT	GTGCAAGTCCCCCGGGT	GTGCAAGTCCCCCGGGT	GTGCAAGTCCCCCGGGT	115199
Db	115140	CAAGTCCCCCGGGT	GTGCAAGTCCCCCGGGT	GTGCAAGTCCCCCGGGT	GTGCAAGTCCCCCGGGT	GTGCAAGTCCCCCGGGT	GTGCAAGTCCCCCGGGT	115199
QY	115200	GTCCCCCGGGT	GTGCAAGTCCCCCGGGT	GTGCAAGTCCCCCGGGT	GTGCAAGTCCCCCGGGT	GTGCAAGTCCCCCGGGT	GTGCAAGTCCCCCGGGT	115259
Db	115200	GTCCCCCGGGT	GTGCAAGTCCCCCGGGT	GTGCAAGTCCCCCGGGT	GTGCAAGTCCCCCGGGT	GTGCAAGTCCCCCGGGT	GTGCAAGTCCCCCGGGT	115259
QY	115260	CCCCGGTGGGGT	GTGCAAGTCCCCCGGGT	GTGCAAGTCCCCCGGGT	GTGCAAGTCCCCCGGGT	GTGCAAGTCCCCCGGGT	GTGCAAGTCCCCCGGGT	115319
Db	115260	CCCCGGTGGGGT	GTGCAAGTCCCCCGGGT	GTGCAAGTCCCCCGGGT	GTGCAAGTCCCCCGGGT	GTGCAAGTCCCCCGGGT	GTGCAAGTCCCCCGGGT	115319
QY	115320	CGGTGGGGT	GTGCAAGTCCCCCGGGT	GTGCAAGTCCCCCGGGT	GTGCAAGTCCCCCGGGT	GTGCAAGTCCCCCGGGT	GTGCAAGTCCCCCGGGT	115379
Db	115320	CGGTGGGGT	GTGCAAGTCCCCCGGGT	GTGCAAGTCCCCCGGGT	GTGCAAGTCCCCCGGGT	GTGCAAGTCCCCCGGGT	GTGCAAGTCCCCCGGGT	115379
QY	115380	TGGGAGCGGCT	TCGGGTTGGG	GTGCTCCGGGTTGGGGG	GTGCTCCGGGTTGGGGG	GTGCTCCGGGTTGGGGG	GTGCTCCGGGTTGGGGG	115439
Db	115380	TGGGAGCGGCT	TCGGGTTGGG	GTGCTCCGGGTTGGGGG	GTGCTCCGGGTTGGGGG	GTGCTCCGGGTTGGGGG	GTGCTCCGGGTTGGGGG	115439
QY	115440	CGGGTGGGGG	GTGCTCCGGGTTGGG	GTGCTCCGGGTTGGGGG	GTGCTCCGGGTTGGGGG	GTGCTCCGGGTTGGGGG	GTGCTCCGGGTTGGGGG	115499
Db	115440	CGGGTGGGGG	GTGCTCCGGGTTGGG	GTGCTCCGGGTTGGGGG	GTGCTCCGGGTTGGGGG	GTGCTCCGGGTTGGGGG	GTGCTCCGGGTTGGGGG	115499
QY	115500	GCTCCGGGTTGGGGG	GTGCTCCGGGTTGGG	GTGCTCCGGGTTGGGGG	GTGCTCCGGGTTGGGGG	GTGCTCCGGGTTGGGGG	GTGCTCCGGGTTGGGGG	115559
Db	115500	GCTCCGGGTTGGGGG	GTGCTCCGGGTTGGG	GTGCTCCGGGTTGGGGG	GTGCTCCGGGTTGGGGG	GTGCTCCGGGTTGGGGG	GTGCTCCGGGTTGGGGG	115559
QY	115560	GTTGGGCTCCGGGTTGGGGG	GTGCTCCGGGTTGGG	GTGCTCCGGGTTGGGGG	GTGCTCCGGGTTGGGGG	GTGCTCCGGGTTGGGGG	GTGCTCCGGGTTGGGGG	115619
Db	115560	GTTGGGCTCCGGGTTGGGGG	GTGCTCCGGGTTGGG	GTGCTCCGGGTTGGGGG	GTGCTCCGGGTTGGGGG	GTGCTCCGGGTTGGGGG	GTGCTCCGGGTTGGGGG	115619
QY	115620	CCGGGTTGGGCTCCGGGTTGGGGG	GTGCTCCGGGTTGGG	GTGCTCCGGGTTGGGGG	GTGCTCCGGGTTGGGGG	GTGCTCCGGGTTGGGGG	GTGCTCCGGGTTGGGGG	115679
Db	115620	CCGGGTTGGGCTCCGGGTTGGGGG	GTGCTCCGGGTTGGG	GTGCTCCGGGTTGGGGG	GTGCTCCGGGTTGGGGG	GTGCTCCGGGTTGGGGG	GTGCTCCGGGTTGGGGG	115679
QY	115680	GCTTCGGGTTGGGCTCCGGGTTGGGGG	GTGCTCCGGGTTGGG	GTGCTCCGGGTTGGGGG	GTGCTCCGGGTTGGGGG	GTGCTCCGGGTTGGGGG	GTGCTCCGGGTTGGGGG	115739
Db	115680	GCTTCGGGTTGGGCTCCGGGTTGGGGG	GTGCTCCGGGTTGGG	GTGCTCCGGGTTGGGGG	GTGCTCCGGGTTGGGGG	GTGCTCCGGGTTGGGGG	GTGCTCCGGGTTGGGGG	115739
QY	115740	GCTTCGGGTTGGGCTCCGGGTTGGGGG	GTGCTCCGGGTTGGG	GTGCTCCGGGTTGGGGG	GTGCTCCGGGTTGGGGG	GTGCTCCGGGTTGGGGG	GTGCTCCGGGTTGGGGG	115799
Db	115740	GCTTCGGGTTGGGCTCCGGGTTGGGGG	GTGCTCCGGGTTGGG	GTGCTCCGGGTTGGGGG	GTGCTCCGGGTTGGGGG	GTGCTCCGGGTTGGGGG	GTGCTCCGGGTTGGGGG	115799
QY	115800	GCGGGCTCGGCTCCGGGTTGGGCTCCGGGTTGGGGG	GTGCTCCGGGTTGGG	GTGCTCCGGGTTGGGGG	GTGCTCCGGGTTGGGGG	GTGCTCCGGGTTGGGGG	GTGCTCCGGGTTGGGGG	115859
Db	115800	GCGGGCTCGGCTCCGGGTTGGGCTCCGGGTTGGGGG	GTGCTCCGGGTTGGG	GTGCTCCGGGTTGGGGG	GTGCTCCGGGTTGGGGG	GTGCTCCGGGTTGGGGG	GTGCTCCGGGTTGGGGG	11585

QY	115860	1GGGGGGGGGCTCGGCTCCGGGGTGGCTCCGGGTGGGGGGGGGCTGGCTCCGGGGTGGCTC	115919
Db	115860	TGGGGGGGGGCTCGGCTCCGGGGTGGCTCCGGGTGGGGGGGGGCTGGCTCCGGGGTGGCTC	115919
QY	115920	CGGGGGGGGGGGCTCGGCTCCGGGGTGGCTCCGGGTGGGGGGGGGCTGGCTCCGGGGTGG	115979
Db	115920	CGGGTGGGGGGGGCTCGGCTCCGGGGTGGCTCCGGGTGGGGGGGGGCTGGCTCCGGGGTGG	115979
QY	115980	GCTCGGGGTGGGGGGGGCTCGGCTCCGGGGTGGCTCCGGGTGGGGGGGGGCTCGGCTCCGG	116039
Db	115980	GCTCGGGGTGGGGGGGGCTCGGCTCCGGGGTGGCTCCGGGTGGGGGGGGGCTCGGCTCCGG	116039
QY	116040	GGTGGGCTCCGGGTGGGGGGGGCTGGCTCCGGGGTGGCTCCGGGTGGGGGGGGGCTCGGCT	116099
Db	116040	GGTGGGCTCCGGGTGGGGGGGGCTGGCTCCGGGGTGGCTCCGGGTGGGGGGGGGCTCGGCT	116099
QY	116100	CGGGGGTGGGCTCGGGGTGGGGGGGGGCTCGGCTCCGGGGTGGCTCCGGGTGGGGGGGGGCTC	116159
Db	116100	CGGGGGTGGGCTCGGGGTGGGGGGGGGCTCGGCTCCGGGGTGGCTCCGGGTGGGGGGGGGCTC	116159
QY	116160	GGGCTCCGGGGTGGGCTCGGGGTGGGGGGGGGCTCGGCTCCGGGGTGGCTCCGGGTGGGGGGG	116219
Db	116160	GGGCTCCGGGGTGGGCTCGGGGTGGGGGGGGGCTCGGCTCCGGGGTGGCTCCGGGTGGGGGGG	116219
QY	116220	GCTCGGCTCCGGGGTGGCTCCGGGTGGGGGGGGGCTCGGCTCCGGGGTGGCTCCGGGTGGG	116279
Db	116220	GCTCGGCTCCGGGGTGGCTCCGGGTGGGGGGGGGCTCGGCTCCGGGGTGGCTCCGGGTGGG	116279
QY	116280	GGGGGCTCGGGTCCGGGGTGGCTCCGGGTGGGGGGGGGCTCGGCTCCGGGGTGGCTCCGGG	116339
Db	116280	GGGGGCTCGGGTCCGGGGTGGCTCCGGGTGGGGGGGGGCTCGGCTCCGGGGTGGCTCCGGG	116339
QY	116340	TGGGGGGGGGCTCGGCTCCGGGGTGGCTCCGGGTGGGGGGGGGCTCGGCTCCGGGGTGGCTC	116399
Db	116340	TGGGGGGGGGCTCGGCTCCGGGGTGGCTCCGGGTGGGGGGGGGCTCGGCTCCGGGGTGGCTC	116399
QY	116400	CGGGTGGGGGGGCTCGGCTCCGGGTGGCTCCGGGTGGGGGGGGGCTCGGCTCCGGGTGGG	116459
Db	116400	CGGGTGGGGGGGCTCGGCTCCGGGTGGCTCCGGGTGGGGGGGGGCTCGGCTCCGGGTGGG	116459
QY	116460	TCCCGAAGCTAGCCGACAGAGGGTGGCACTCCGTCGCAAGGCTCTGGGGCTCTTTTAT	116519
Db	116460	TCCCGAAGCTAGCCGACAGAGGGTGGCACTCCGTCGCAAGGCTCTGGGGCTCTTTTAT	116519
QY	116520	AGCGCTAATGCCCTCCCAATAGGTTACTATGTTAGTTAGTTAGTTAGTTAGTTAGTTAGTTAG	116579
Db	116520	AGCGCTAATGCCCTCCCAATAGGTTACTATGTTAGTTAGTTAGTTAGTTAGTTAGTTAGTTAG	116579
QY	116580	AAATGAATCACCAGAATAGCGGCCACGCGCAGCTCCAAACCGCCTCCAAACCGTGCAG	116639
Db	116580	AAATGAATCACCAGAATAGCGGCCACGCGCAGCTCCAAACCGCCTCCAAACCGTGCAG	116639
QY	116640	CGCGGTATTTGCAATTTGCTTCCGACAGATACGGGGCGCAGCATGGTGGCGGGAGGCT	116699
Db	116640	CGCGGTATTTGCAATTTGCTTCCGACAGATACGGGGCGCAGCATGGTGGCGGGAGGCT	116699
QY	116700	GGCAATTTGGCAATTTTCCACACATTTCCAAAGCGGACGCAAGGGTCCAGAGCTACCGGGGAT	116759
Db	116700	GGCAATTTGGCAATTTTCCACACATTTCCAAAGCGGACGCAAGGGTCCAGAGCTACCGGGGAT	116759
QY	116760	TCCCCAAACATCATTCAGCGCATAGAGGTTGTGGCTGAGCTATCTGGGGATTCCC	116819
Db	116760	TCCCCAAACATCATTCAGCGCATAGAGGTTGTGGCTGAGCTATCTGGGGATTCCC	116819
QY	116820	AAACCCGAGACCCACTAGATGCTATTCAGTGGGACATGCAAGGCTGGGTCTCTCCAGGACA	116879
Db	116820	AAACCCGAGACCCACTAGATGCTATTCAGTGGGACATGCAAGGCTGGGTCTCTCCAGGACA	116879
QY	116880	GGTGCTCCGTGTGGTAAAGGAGTTCCCTAATTTAAATATTAATTAATTAATTAATTAAC	116939
Db	116880	GGTGCTCCGTGTGTGGTAAAGGAGTTCCCTAATTTAAATATTAATTAATTAATTAATTAAC	116939
QY	116940	CAGGCTAAGCTGTATTAATGAGGACAGGCTGCCAGCTAGGTAACCTGGGGAAACCCCT	116999

D	116940	CGGGCTAAGCTGTAATTAATGAGGACAGGCTGCGACCACTAGTACTGGGGAAACCCCT	116959	D	118020	GAACATTTTTCATTAACCCCACTGACCCCGGCGCCCAAAATG6GGCCCATGCTGC	118079
Q	117000	AACGGGATGTAATTAATTAACCTATATAAATTCACCCCTGTAGGGGATCCCACT	117059	Q	118080	GGCGGCGCCCAACCGCTCCCATATTTCCACAGGTTTGTCTATG6GACACGAGGTCCTGTG	118139
D	117000	AACGGGATGTAATTAATTAACCTATATAAATTCACCCCTGTAGGGGATCCCACT	117059	D	118080	GGCGGCGCCCAACCGCTCCCATATTTCCACAGGTTTGTCTATG6GACACGAGGTCCTGTG	118139
Q	117060	GTAAGCTGAATTAATGCGGATACAGGCTAGTGTGTAATGCGTACCAAGGCTGAGTG	117119	Q	118140	GTCATATGTTTCAATGATACCTCGGATGACCCCGGCGACGTTTGGCCACCATGTCCTCA	118199
D	117060	GTAAGCTGAATTAATGCGGATACAGGCTAGTGTGTAATGCGTACCAAGGCTGAGTG	117119	D	118140	GTCATATGTTTCAATGATACCTCGGATGACCCCGGCGACGTTTGGCCACCATGTCCTCA	118199
Q	117120	ACTCATACCATGAGGATTAATACCAAGGATACAGGCTAGGTTGCTAACGGGTCACG	117179	Q	118200	ATTCGCCCAATGATACATGTTTGGGACCCCGGCGGACCCCGGCGGCAAAAGCGCGC	118259
D	117120	ACTCATACCATGAGGATTAATACCAAGGATACAGGCTAGGTTGCTAACGGGTCACG	117179	D	118200	ATTCGCCCAATGATACATGTTTGGGACCCCGGCGGACCCCGGCGGCAAAAGCGCGC	118259
Q	117180	GCTGAGTACTCATACCATGAGGATTAATACCAAGGATACAGGCTAGGTTGCTGTAAT	117239	Q	118260	CCATGGGCAACCGGACGCGACCATGTCACATCTTTCAGTACCCCGGCGGACCCCGCGG	118319
D	117180	GCTGAGTACTCATACCATGAGGATTAATACCAAGGATACAGGCTAGGTTGCTGTAAT	117239	D	118260	CCATGGGCAACCGGACGCGACCATGTCACATCTTTCAGTACCCCGGCGGACCCCGCGG	118319
Q	117240	GGGTACACGCTGAGTACATACCATGAGGATTAATACCAAGGATACAGGCTAGG	117299	Q	118320	GGGCGACCGCGGCGCTGGGGGATATGTTCTGATGACCGCGCTTACGTTTGACAGG	118379
D	117240	GGGTACACGCTGAGTACATACCATGAGGATTAATACCAAGGATACAGGCTAGG	117299	D	118320	GGGCGACCGCGGCGCTGGGGGATATGTTCTGATGACCGCGCTTACGTTTGACAGG	118379
Q	117300	TTGCGTAATGGGATACAGGCTGAGTACCATACCATGAGGATTAATACCAAGGATAC	117359	Q	118380	GTCACGCGAACAATATTCCTCCCGGCTCCGAGCCCGGCGGCGGACCCGAGTGGG	118439
D	117300	TTGCGTAATGGGATACAGGCTGAGTACCATACCATGAGGATTAATACCAAGGATAC	117359	D	118380	GTCACGCGAACAATATTCCTCCCGGCTCCGAGCCCGGCGGCGGACCCGAGTGGG	118439
Q	117360	GGCTGAGGTTGCGTAATTAACCTATATAAATTTACCTGTGGGGGAATCCCGCTT	117419	Q	118440	TTATTAAGTTACGTTAGGATTAATTTAATTCATACATACCCCTTAATGTCGCGTGG	118499
D	117360	GGCTGAGGTTGCGTAATTAACCTATATAAATTTACCTGTGGGGGAATCCCGCTT	117419	D	118440	TTATTAAGTTACGTTAGGATTAATTTAATTCATACATACCCCTTAATGTCGCGTGG	118499
Q	117420	TGTACTGAATTAATATAGGAATACAGGCTGTAGATCGGTATGGAACACAGGCTGTAG	117479	Q	118500	CCGCGGCGACCTGACGCGCGGCGGTGTGACCCATGACCCGATCGGTGGCGCGGCG	118559
D	117420	TGTACTGAATTAATATAGGAATACAGGCTGTAGATCGGTATGGAACACAGGCTGTAG	117479	D	118500	CCGCGGCGACCTGACGCGCGGCGGTGTGACCCATGACCCGATCGGTGGCGCGGCG	118559
Q	117480	GACTAGCTGAGTACTCATACCATGAGGATTAATACCAAGGATTAATATAGATA	117539	Q	118560	AGAGCGCGGCGGCAAAAGTGTGATCGCGGCTGTGACCCACCCCTGTGGAGAAACCCCT	118619
D	117480	GACTAGCTGAGTACTCATACCATGAGGATTAATACCAAGGATTAATATAGATA	117539	D	118560	AGAGCGCGGCGGCAAAAGTGTGATCGCGGCTGTGACCCACCCCTGTGGAGAAACCCCT	118619
Q	117540	TATATATATATAGGAATCTGTAAACAAACCACTCGGATGGCTGCTGTTTGGG	117599	Q	118620	CGGTTCCGTTGTCCTGCTGCGGCTCCTGCGCCCTGCGCCACCGGCGGAGTCTTGTG	118679
D	117540	TATATATATATAGGAATCTGTAAACAAACCACTCGGATGGCTGCTGTTTGGG	117599	D	118620	CGGTTCCGTTGTCCTGCTGCGGCTCCTGCGCCCTGCGCCACCGGCGGAGTCTTGTG	118679
Q	117600	CCAACACGAGGAGATTCCTGATGACAGGCGGACATGAGGTTTGGGACAT	117659	Q	118680	AGCATTTCCCGGTCAGAAATGACAGGAGGCGCGGCAACGATCGAGCGGGTGGCGG	118739
D	117600	CCAACACGAGGAGATTCCTGATGACAGGCGGACATGAGGTTTGGGACAT	117659	D	118680	AGCATTTCCCGGTCAGAAATGACAGGAGGCGCGGCAACGATCGAGCGGGTGGCGG	118739
Q	117660	TTTGATTTGACAGACGCGCGGCAATCGACCGAGACATCGGCGAGCAAGCAAAAGACA	117719	Q	118740	GTCGTTGAACGAGGAGGCGCGCTGTCGCTGAGTGTGCGCGGTGGGCGGTATGAC	118799
D	117660	TTTGATTTGACAGACGCGCGGCAATCGACCGAGACATCGGCGAGCAAGCAAAAGACA	117719	D	118740	GTCGTTGAACGAGGAGGCGCGCTGTCGCTGAGTGTGCGCGGTGGGCGGTATGAC	118799
Q	117720	GACGCGCGGCGGACCAATGCGCGCGGCTGATTGATGACGCGCTTGGCGGCA	117779	Q	118800	CCCCGCAACGAGAGGCGCGCTGCGGCGGAAATTTCCGAGAAACGCGCGCGCTTGG	118859
D	117720	GACGCGCGGCGGACCAATGCGCGCGGCTGATTGATGACGCGCTTGGCGGCA	117779	D	118800	CCCCGCAACGAGAGGCGCGCTGCGGCGGAAATTTCCGAGAAACGCGCGCGCTTGG	118859
Q	117780	TGGGAAACGTCCTGCGCGCGGCTATCCCTGCTGCTTAAGGATTAACGCGCTTAA	117839	Q	118860	CGGCGCGCTCCTCCCGCAAGACCCCAATTTGTTTAAAGTTTAAAGTTC	118919
D	117780	TGGGAAACGTCCTGCGCGCGGCTATCCCTGCTGCTTAAGGATTAACGCGCTTAA	117839	D	118860	CGGCGCGCTCCTCCCGCAAGACCCCAATTTGTTTAAAGTTTAAAGTTC	118919
Q	117840	CATCGCTGCGGCGGTCACCGCGCGCAACCCCGCGCGCTTGGCGTACCTCGGC	117899	Q	118920	CGCTGCTTGTGGACGCGGCTTAAGCTTGCACCTGTGGGAGATCCCGCGTGGCA	118979
D	117840	CATCGCTGCGGCGGTCACCGCGCGCAACCCCGCGCGCTTGGCGTACCTCGGC	117899	D	118920	CGCTGCTTGTGGACGCGGCTTAAGCTTGCACCTGTGGGAGATCCCGCGTGGCA	118979
Q	117900	GGGACCGCGCGCTCATGCGCACCATGTCGATGGGACCGCGCGCAACATTAATTC	117959	Q	118980	TCGCGCGCTCCTCGCTGCGGTCGAGCGTCCGAGCGTCCACCTGTTGGTTGTCAT	119039
D	117900	GGGACCGCGCGCTCATGCGCACCATGTCGATGGGACCGCGCGCAACATTAATTC	117959	D	118980	TCGCGCGCTCCTCGCTGCGGTCGAGCGTCCGAGCGTCCACCTGTTGGTTGTCAT	119039
Q	117960	GCTGACCGCGGACGACCCCGCGCAAGAGCGCGCATGGGTACCGCGCGACATC	118019	Q	119040	CCCATGTGGCATCCCGCATTTATTCGCCGACGAGCAACATPAACGTACGCTGT	119099
D	117960	GCTGACCGCGGACGACCCCGCGCAAGAGCGCGCATGGGTACCGCGCGACATC	118019	D	119040	CCCATGTGGCATCCCGCATTTATTCGCCGACGAGCAACATPAACGTACGCTGT	119099
Q	118020	GAACATTTTTCATTAACCCCACTGACCCCGGCGCCCAAAATG6GGCCCATGCTGC	118079	Q	119100	TGTAGAAATTAATGCTTTTATTTTATTTTGTAAACCGGCAACCGGATACGTCCTG	119159
D	118020	GAACATTTTTCATTAACCCCACTGACCCCGGCGCCCAAAATG6GGCCCATGCTGC	118079	D	119100	TGTAGAAATTAATGCTTTTATTTTATTTTGTAAACCGGCAACCGGATACGTCCTG	119159

OY	119160	CCTTTACACGGTGTGTTGTACACAGCCCTCTTGTGGCGCCGACACCGGCGCTTAACCGGG	119219
Db	119160	CCTTTACACCGCTGTGTTGTGTACACAGCCCTCTTGTGGCGCCGACACCGGCGCTTAACCGGG	119219
OY	119220	TGCGTTGGCGGACACAGACCTTGGCCACGTCGGGCGCTTGAGAGAGGGCGCTTGACGAGGCTACT	119279
Db	119220	TGCGTTGGCGGCGACAGACCTTGGCCACGTCGGGCGCTTGAGAGAGGGCGCTTGACGAGGCTACT	119279
OY	119280	TAAACCATGTAGTTTGAGGGGCTGACACAGGGCGCCCTTTCATATTTGGGAGAGCCACCG	119339
Db	119280	TAAACCATGTAGTTTGAGGGGCTGACACAGGGCGCCCTTTCATATTTGGGAGAGCCACCG	119339
OY	119340	AAAAAAGTGGGTGACTGCTGCTGCGCTTGACACCAAGCTGGTGGCCGTTAGAAAACTTA	119399
Db	119340	AAAAAAGTGGGTGACTGCTGCTGCGCTTGACACCAAGCTGGTGGCCGTTAGAAAACTTA	119399
OY	119400	ATTTTTCACGTCCTCTTTCGAGAGCTGGGGGTCATGAGAGCATCAGGTGTTGTATGG	119459
Db	119400	ATTTTTCACGTCCTCTTTCGAGAGCTGGGGGTCATGAGAGCATCAGGTGTTGTATGG	119459
OY	119460	ACTAAAGTACTGGGGCTGAGACCGGACGCTCTCGATTAATTAATCCACGCTTAGTAAAA	119519
Db	119460	ACTAAAGTACTGGGGCTGAGACCGGACGCTCTCGATTAATTAATCCACGCTTAGTAAAA	119519
OY	119520	AAAGGTGAGACACAGTCCAAATCGCCCAACGAAAAACAGCGCTCCAGCACAACCGGAG	119579
Db	119520	AAAGGTGAGACACAGTCCAAATCGCCCAACGAAAAACAGCGCTCCAGCACAACCGGAG	119579
OY	119580	GGGAATACCGGGTTCCTCCAGTTGAGGGGACAGCCCGTTTGGAAAAACCCCTCGGGGCTATC	119639
Db	119580	GGGAATACCGGGTTCCTCCAGTTGAGGGGACAGCCCGTTTGGAAAAACCCCTCGGGGCTATC	119639
OY	119640	GTCGACGACCGCGGCGGTCAAAAAGACACAGCAGCGGCTCTCTGTGCTGACCTCTAGGTG	119699
Db	119640	GTCGACGACCGCGGCGGTCAAAAAGACACAGCAGCGGCTCTCTGTGCTGACCTCTAGGTG	119699
OY	119700	GCGACCGAAGTCTCACTAACCGCTTATGCGGGAACATGGGTCCGGTTCGGCGCTCGCCGAC	119759
Db	119700	GCGACCGAAGTCTCACTAACCGCTTATGCGGGAACATGGGTCCGGTTCGGCGCTCGCCGAC	119759
OY	119760	ACCCCTCTCTACCTACCTACGACGAGCGCTTGATTAATCAGAC	119800
Db	119760	ACCCCTCTCTACCTACCTACGACGAGCGCTTGATTAATCAGAC	119800
RESULT 2			
LOCUS	AF210726	130733 bp	DNA linear
DEFINITION	Macaca mulatta rhadinovirus 26-95 long unique region L-DNA, complete sequence.		
ACCESSION	AF210726		
VERSION	AF210726.1		
KEYWORDS	GI:7329990		
SOURCE			
ORGANISM	Macaca mulatta rhadinovirus 26-95		
REFERENCE	1 (bases 1 to 130733)		
AUTHORS	Alexander, L., Denekamp, L., Knapp, A., Auerbach, M.R., Damania, B. and Desrosiers, R.C.		
TITLE	The primary sequence of rhesus monkey rhadinovirus isolate 26-95: sequence similarities to Kaposi's sarcoma-associated herpesvirus and rhesus monkey rhadinovirus isolate 17577		
JOURNAL	J. Virol. 74 (7), 3388-3398 (2000)		
MEDLINE	20173730		
PUBMED	10708456		
REFERENCE	2 (bases 1 to 130733)		
AUTHORS	Alexander, L., Denekamp, L.M., Knapp, A., Auerbach, M., Czajak, S., Damania, B. and Desrosiers, R.C.		
TITLE	Direct Submission		
JOURNAL	Submitted (02-Dec-1999) Microbiology, New England Regional Primate Research Center, One Pinehill Dr, Southborough, MA 01772, USA		

FEATURES

source location/Qualifiers

1. .130703

/organism="Macaca mulatta rhadinovirus 26-95"

/mol_type="genomic DNA"

/isolate="Macaca mulatta rhadinovirus isolate 26-95"

/db_xref="taxon:119193"

513. .1784

/gene="R1"

513. .1784

/gene="R1"

CDS

codon_start=1

/product="ORF01"

/protein_id="AAFS9980.1"

/db_xref="GI:7329991"

/translation="MEVLVLEMLQPSVELLPAKLISVPTMCPRHGQDTYLLTACGTSTADQSTQWTFRRNNITLMRGSNFGRLVSYTPNATISDRACQTKTTRNNINIDFRVSSRITLQRCSSXYGTAYANNTRVLRCYSGSNVTLRNVFHLNGTAVNGTIRNHFVLTETGGTGYCSAFTIGNEKFSYOTINFFNFSFPEKNDIPNESHKNGQIOOTQASVQHNPVYVSPVPSITIGLVTGATISLMCMCLFTTRCNENSSSNASQSTYQPSHNONSNTWCSHHHTYRNAHOBESIELLNQHTSETDSCCOLVLEKVAIVADGQENTWVEWQYDHNVENIETQTSYEDVNEHDYSDTINPNPNYSGILLEEDVEFYNELENQYHLLIENDLNDNNYHNLNMLNIEQYDWLE"

complement(1852. .2418)

/gene="ORF02"

complement(1852. .2418)

/gene="ORF02"

/codon_start=1

/product="DHER"

/protein_id="AAFS9981.1"

/db_xref="GI:7329992"

/translation="MDIAYNCIYAVDQLQIGKNGTTPMYRLREMMYFQKMTSTPSVVEGNVIMGKRTWFSIPEKRRPLVNRINITILSELPEPHGAFHLKRTLDLDAFNFRQYKLEQLNTVWVIGKSYVESYLNKCPKLXYTRIMESFDDVFPSSINTFETWMLSELGDKDNEFNQIKYKFOYEKNFK"

2595. .3782

/gene="ORF04"

2595. .3782

/gene="ORF04"

/codon_start=1

/product="complement binding protein"

/protein_id="AAFS9982.1"

/db_xref="GI:7329993"

/translation="MEWIPITLFCICVILVDSKGSNVTCLRPFPREVRWKAQNE NYAGTAVVELICRPFYKLOANVVECLSGWTTTPAECRRKCSNPEDILNGEVIITDSNNAKFGSNIYKNTGTGLLGAIVRCLLKYDSNLVMDPAATCEIECKKQPDIEGKAYVPOEENYLETJTFTECNKFSILGNTTTCMNGTSSSPVCCQITGCAPNIDGHILVGGSSRYKHGOSVITGCGDEGTLINCHKKCTOEYSLMNPPLPLCPVINTDPTESEVPSGCTKQEMPTPEBNRSHSESTTTTPTCTOCTSTSPBPKYNPETHCP TTPGAGISKOTTTNRPSKAPSQNPPIAPMSKMRHVVLVFAVASLLFVLALVCC FLK"

4213. .7611

/gene="ORF06"

4213. .7611

/gene="ORF06"

/codon_start=1

/product="ssDBP"

/protein_id="AAFS9983.1"

/db_xref="GI:7329994"

/translation="MAKGNAGQLEDNOCGRAPIGACGVYVASKDPFPAEASTIGNRSGSGVSTLPIILYGLVTHEPPLVIAKAKVDTTLVAVKTCFHEVIVFHNLSLFRPVDGTGNECLCEEARLFGYTGQLEKRPHSINMPLBCPOLPDKDEFLGVVYEGFKRILMRGCLIPAVPQTOVOVLAGROAFVPLDEDLAPHGIMRPFYKHQVSALYDSLFTSIAOLRLKDYTAIVIAHAKOFMODHKIAKIVQAKGSTPLPTTDSHMLIVDSVVELALISYGCMLFECPOACCELLANDSMPIPGCDSPEARVVALRMSAEQAVHVAQLFAANSVLYLTVOKQAPRGQKGVNYSNFFLQGLGFLNEATIKENGSEAFKGVSNALDGSSEFTPHLAYAASFSPHLAKLCYVMOFLQHNKSTIQOATNMVHYVGT AANSSEDTLGHGNTPATCLNTLFLYRLKDRPVAYTPQRPDYVYVYAGTFNDLEILG NFASFRRREDGPNADDEHPKTYTQWLCQYTEKLSAIGTEDHDNHNLTNIOSEFLR VFKDITSDVGEVWKFEVNSKNNFNREHVKSVNHLIOFCNVYMOAPAVFLINLYY KSLIMTIDICLIPYCMITYEODNPAMGLPSEWKLKMHQGTLMTPKAKCIDRGVLTGE LKTYHRMFCDFEDTDAGSGNLAAPFEMQVRIARAMNVFKSITIKRKLIFSNRAGE AVDSGEFLKTRDTYVVAAPYPMKFLNLSLRLEPDKTATYLMNHISQNTPTVYLK DVPDGLAEILVSYKTNLSLAFEEETINVDVDPDSLMSYARIKLGCALIRACQIQIOPAT

gene
CDS
7636..9696
/gene="ORF07"
/codon_start=1
/product="transport protein"
/protein_id="AAF59984.1"
/db_xref="GI:7329995"
/translation="MARELAALYAOALSALAVDLVLEADPSIDGARRSLKTKKTOEN
LNRDLPLREONSVESTSLSEVHELANIDKLGELERSLRORSREHETLHLR
PECHYHSTVFQFGGGLIDVMNCILINDELLCKRGSVFCIGANEAELGKRVLE
LSTLRGISPIHPDLVYVSPVOCRLREIIEVNOGSSLLAVIADHCHGLCKRAE
PIHGLEPTELSQLKVRKSDATQHGVSADQLRESLAIODHNIFFKRSASIME
LSNLIYMAAGOTGIOTGTENESQMARLTTHADMEHREALLTPKLSATHFYDCRRP
PLESLFCGGLENSIDDTINALSRDCVTFEQANTVMRKONELFTRLNSILRQSA
GSOQKATPSEPPRTTVAATAADSVIKDAQYREQYKKVARGFKRLCELOTOGAVL
ANALCMRWGVAEASSELVNHFLRRFVALPPEARCRSDIILFENSKYKNSLYS
ORLSREHVEITLQFYGLITGPTROSDFPGPANYLAOCFEAAGMLPHHMLVSEM
IMPOLOPKMIDOTENRFYOLPEGDLNAVOKSACMFIRELYSVALLYNTWEKTRIF
SLAREKLSINIDVGLNSGLYLTLYEQDAPLVLSQNTGMIFKDLALYHHLQSDC
HDDN"
5683..12172
/gene="ORF08"
9683..12172
/gene="ORF08"
/codon_start=1
/product="ORF08"
/protein_id="AAF59985.1"
/db_xref="GI:7329996"
/translation="MAITNRRLRLAMVLIATGAVENYTPKGAATTAKPTPG
SPTPEPBRPAEAFKFRYCSATGELFRENLEKTEGTEDEKTLQEGILMKKNIV
PHIEVRRYRKATSVTVYRGWTEAVYKQVIRPVQYETNHDDTYTQCSSSRVN
VNGIYNTTDRFTNQTVPLOPVEGLTDNIQTESQVPLTTPGMFGIYRRTVNC
ELVDMIASAEPSYFVIALGDTVEVSPCHDSTCSVAEKENLGVAFALNVTIVD
FATRPPTETREAFADSGEYVSWKAEDPSACALTLKTPRAIOTHEASVHEVAN
DVTATFETPLSEVANETGYSCLDVIOIKTLNDITIKLSDTIVTNGSAQYVTEGFL
LMLQPLPLSLDEMRKNGTTPAPPATSTVSRRVRSNTNEOATNDAALFOFAY
DKLRASINKVLEELSRAMCREQVSDTYVYELSKINPNSVMAITGPRASQVDAI
SVTDCVAYDOASVSHKSLRTSPGMCYSRPVTPRPLNSTLTFPGQLGPRREIITLD
NOVEACKETCEHTFASVNTYIKDYVVKIKINISEIISLGLFIALNSLENDIRV
IELYSRAEKLSGVSVDIETMREYNYTQRLAGLEDIDNDINRRLAEDLSEIV
ADLQVGRVTVNVAASVITLFGSIVSGFINFTKSPGGMLMLIVAVVLYIFALNR
TNAIADPILMAYPDIDKMOFGKVDQEOIKNIIAGMHQLOQEBRRRLDEQORAPS
LEFRASDGLKRRFRGYKPLENEAQEYEMSK"
12290..15334
/gene="ORF09"
12290..15334
/gene="ORF09"
/codon_start=1
/product="polymerase"
/protein_id="AAF59986.1"
/db_xref="GI:7329997"
/translation="MDFNPYVIGPRGPRPHSHRGTDAPAPACAGAVOPPDVCRLLIPA
CLRTPGAGGMIPVITPPTTYFENGARDVLANRSMWTAADRPVAPDDQDSITF
HAYDVETTYAADRCAEVSRFODIPSGVTLKLGREDTSCVNVFROOYVEYA
KVPAGINTVHILQALKNTAGAACGFSRRNRKILITDYDAHEPVAITETLSSEML
STLSRLVACCGCEVFESNVDAVRVLDHGFTTPEVSCARTPLAARDARTALEFD
CSMEDLSYOADSRSDMPYRIYAFDIECTGEGFPATDGDVAVIDISCVFATRRGAP
NPENILFSVGTCDLIPDNDVLEDFSEYDMLVSFMMIDFEDKVLGNISFDFLYL
ITRASQVYNLRINETYKIKTGSIEFHEVRGGGFMGSVSKITAGIYVINDMYOVR
EKLISDYKLDITVAROCGLGKKEVDYSIDIPILFRSGGGRKAVSYCVMSVPMOGL
LKMEIHYEISEIKLAKIOARVYLTDQOLRVPSCLLEAARREPIIVPPEBQSG
YOGATVNPISGFYDEPVYVYDPSLITIOAHNLCTSTHGHDLHHPNLTDDY
ETVLSGSPVHFVKHKRESLSGLLITVLEKRRRIKRTLAACDPSLTKTILDKOLA
IKVTNNAYGFTGVAAGSLPLCINIAETVTLRGRMLLEMSKSYEALITBEDLRTLRG
VTARHGAFFRVYVGTDSLFTACDYSAEVSAFGCDLAARTADLPPIKLEMEKT
FKCLLTKRRYIGVILNDKVMGVDLIRTKACFVQERCAIIDLVLHDEYVAAA
RLCKRPPHAYEBGLPAGFTIKIYEVLAASVLDLNSVVPLEQLFSTELSRPVQDK

gene
CDS
15429..16679
/gene="ORF10"
15429..16679
/gene="ORF10"
/codon_start=1
/product="ORF10"
/protein_id="AAF59987.1"
/db_xref="GI:7329998"
/translation="MLVNELSVLDMEVTFHRGRFSFVNLRILOTENGHGAYARVL
PSLDIOLHOFARGLVTRKLELPPRSDCVALLAPLDGSDADARVAPGFILDSRP
LTVWYNASGRHTIRCLFLKPIDEBRATTVYFGENGARSSEGTKPTCATSLECGP
LKVSEASQTSPSHSFVAFFPANSVACSLRLQVRFPSDDAHRDARISPVYVFSN
SGANVCASVHTLSPSRCKTAQMETIYAPGDNAIVLGOSPLVPTHGGRVLDGYA
DAEKTLOPSEKRVOLIFQOGAARGLAIVGVAPPELFTVTPALLISGCTHL
LFENNGPTTTRKRLTVLAAPCPVVRLLSSADPARDLVASPDGALISINFTIPVG
PFGVYSACRQVLSLRONGVHERNNH"
16688..17917
/gene="ORF11"
16688..17917
/gene="ORF11"
/codon_start=1
/product="ORF11"
/protein_id="AAF59988.1"
/db_xref="GI:7329999"
/translation="MGTPVRFPRFGEOMQTSLVNDNGTPRYSSLVMAATITHGYLTLVNR
SELCTERSPCPLPACPSIGRLVGRFRFPASVAILDGRGTATVYAFGRHNPDLIDV
PAVERADRDELTVRHAPQDTRVRSRYGLKVFAYIVTVRRPVGFLHPDRVIALTD

Query Match	78.1%;	Score 31222;	DB 1;	Length 130733;
Best Local Similarity	99.8%;	Pred. No. 0;		
Matches 35132;	Conservative	0;	Mismatches 53;	Indels 11; Gaps 10;
QY 79800	TCCCCACGGGTCGTCAACAGATGAGCGCCCAACACGAGAAAGCCGTGATGCAGATAG	79859		
DB 77786	TCCCCACGGGTCGTCAACAGATGAGCGCCCAACACGAGAAACCCGTGATGCAGATAG	77845		
QY 79860	CGGACAGGGCGTTTCCCGGGGACGCAACCGCGCCCTTGACTATGTCTCGCTAC	79919		
DB 77846	CGGACAGGGCGTTTCCCGGGGACGCAACCGCGCCCTTGACTATGTCTCGCTAC	77905		
QY 79920	GTCTTACCGGAGGGCGGTTCGGGTGACAGCCCTCGGGGCGGGCGGTATGATGTA	79979		
DB 77906	GTCTTACCGGAGGGCGGTTCGGGTGACAGCCCTCGGGGCGGGCGGTATGATGTA	77965		
QY 79980	GGTACCGGGGAGCGGTTACGAGTAGCCCGAGCAGTGTCTTACCGTGTATGAGATAC	80039		
DB 77966	GGTACCGGGGAGCGGTTACGAGTAGCCCGAGCAGTGTCTTACCGTGTATGAGATAC	78025		
QY 80040	CCTGCCCGGCTGTGTGGGGCCCTTGCGCTTAACATCCGAACCTCAAGCCCGCATTC	80099		
DB 78026	CCTGCCCGGCTGTGTGGGGCCCTTGCGCTTAACATCCGAACCTCAAGCCCGCATTC	78085		
QY 80100	TGCGGCTACCCAGAGGGCCGAGGGGACACACTGGATTAACATCTGTATCGAGCGCA	80159		
DB 78086	TGCGGCTACCCAGAGGGCCGAGGGGACACACTGGATTAACATCTGTATCGAGCGCA	78145		
QY 80160	CCTGAAGACCAAGTTTGAAGAAAGAAAACCTCGTCTCAAAACGTCTTTTCTATGAA	80219		
DB 78146	CCTGAAGACCAAGTTTGAAGAAAGAAAACCTCGTCTCAAAACGTCTTTTCTATGAA	78205		
QY 80220	ATAGGACCTTTTCTTATCGACCCCAATAGCGCGCTTGCGCTGAGCCACGCTAGACCT	80279		
DB 78206	ATAGGACCTTTTCTTATCGACCCCAATAGCGCGCTTGCGCTGAGCCACGCTAGACCT	78265		
QY 80280	CCCGGACGAAGGGGAGTCTTCTGTGAGTAGAGTCCCTGATCATCTTCCCATCCCG	80339		
DB 78266	CCCGGACGAAGGGGAGTCTTCTGTGAGTAGAGTCCCTGATCATCTTCCCATCCCG	78325		
QY 80340	AAGTAATCAATCCCAAGACACGAGGCGTATGCTCCGACGACGACCTGTGTTTTC	80399		
DB 78326	AAGTAATCAATCCCAAGACACGAGGCGTATGCTCCGACGACGACCTGTGTTTTC	78385		

OY	80400	GTCGTCGCCCAAAAGCATGCCGAATACGTTGCCGAATGACGATCAATTC	80405
Db	78386	GTGCGTCGCCCAAAAGCATGCCGAATACGTTGCCGAATGACGATCAATTC	78445
OY	80460	TCCAAAGCCCATGGCGGACGAGACACCGCTCGAGGTGGGGCCGAGTAAGCATGGCTGT	80519
Db	78446	TCGAAGTCCCATGGCGGACGAGACACCGCTCGAGGTGGGGCCGAGTAAGCATGGCTGT	78505
OY	80520	ATAATGCCAGGTGTATACTCACCGCTTTCAGTTTCGTGTAAATTAACAAACCTCGGCCAT	80579
Db	78506	ATAATGCCAGGTGTATACTCACCGCTTTCAGTTTCGTGTAAATTAACAAACCTCGGCCAT	78565
OY	80580	GCGGCTACGCGCGCTGGGCGCAGATGTGTGCAGCGCTCACAAAAGATCCCATCGGCGCA	80639
Db	78566	GCGGCTACGCGCGCTGGGCGCAGATGTGTGCAGCGCTCACAAAAGATCCCATCGGCGCA	78625
OY	80640	ACTAATTCCTCCAGCGCCGACAGTAGTGGCTACCGGTTCACTTCACACGAGCAGCGCA	80699
Db	78626	ACTAATTCCTCCAGCGCCGACAGTAGTGGCTACCGGTTCACTTCACACGAGCAGCGCA	78685
OY	80700	CCCCATCATCTTTCACCGCTGTGTTCCGCGCTCGGATCGTCCATTTGATCTGGTCCGAGAT	80759
Db	78686	CCCCATCATCTTTCACCGCTGTGTTCCGCGCGTCCGAGTCGTTCATTTGATCTGGTCCGAGAT	78745
OY	80760	CGCCCACTACTGCCCGGTCATCGGATTTGGCTCGTCCCTCTCTGTGATCTTCATCT	80819
Db	78746	CGCCCACTACTGCCCGGTCATCGGATTTGGCTCTCTCTCTGTGATCTTCATCT	78805
OY	80820	GGATTAAGACAGTGGGTGGCCAGCCCTGTGATGTTACATGCTGCCGGGGTAAAAACAACCT	80879
Db	78806	GGATTAAGACAGTGGGTGGGTGCACCTCTGTGATGTTACATGCTGCCGGGGTAAAAACAACCT	78865
OY	80880	CTGTACCGCATACAGACAGAGTTTGCACACGTAACGATGTCATTTGGCGATGGCGCAT	80939
Db	78866	CTGTACCGCATACAGACAGAGTTTGCACACGTAACGATGTCATTTGGCGATGGCGCAT	78925
OY	80940	CGAGCGGATTCGGCGCAGCTGGACCGAAGACACAGGGCGATTCGTGCATTAATCTCTAAGTG	80999
Db	78926	CGAGCGGATTCGGCGCAGCTGGACCGAAGACACAGGGCGATTCGTGCATTAATCTCTAAGTG	78985
OY	81000	GTTCGTCCTCCAGGGTTCCGGGACCTTTCGAAGACCTTAGATTAATTCACATATCAATAAA	81059
Db	78986	GTTCGTCCTCCAGGGTTCCGGGACCTTTCGAAGACCTTAGATTAATTCACATATCAATAAA	79045
OY	81060	CTTGACGSGGTTCCCTGGATGCGAGTCCCTAATCTCTGTCATTTGTTAGTAAGCACCT	81119
Db	79046	CTTGACGSGGTTCCCTGGATGCGAGTCCCTAATCTCTGTCATTTGTTAGTAAGCACCT	79105
OY	81120	TCATTTCCCGGTTCTCCAGGTTCTTTCACGCAAAATGCAATATTCGTAAGGGTAATCAACA	81179
Db	79106	TCATTTCCCGGTTCTCCAGGTTCTTTCACGCAAAATGCAATATTCGTAAGGGTAATCAACA	79165
OY	81180	CACCTTCCTGGACATTTTGTGATTAACCTTTCGATCTCTGTGGCAAACTACAGTCAA	81239
Db	79166	CACCTTCCTGGACATTTTGTGATTAACCTTTCGATCTCTGTGGCAAACTACAGTCAA	79225
OY	81240	CGACCCCGGTGACGTTAAAAACAAGTCCCTCATCTTGGAAACACACGCGTGGCCAG	81299
Db	79226	CGACCCCGGTGACGTTAAAAACAAGTCCCTCATCTTGGAAACACACGCGTGGCCAG	79285
OY	81300	CGAGAGAGGGGACATGGTGCAGCTGCACACCCGTAATTCACACATGAACACGTTGAGAGCCAA	81359
Db	79286	CGAGAGAGGGGACATGGTGCAGCTGCACACCCGTAATTCACACATGAACACGTTGAGAGCCAA	79345
OY	81360	CGGTCCTCCAAAAATAGAAAGTTTAATTTGATGTGCCCTCGGACGCCATGCTGGCGCA	81419
Db	79346	CGGTCCTCCAAAAATAGAAAGTTTAATTTGATGTGCCCTCGGACGCCATGCTGGCGCA	79405
OY	81420	CAGCGTTGTTTGTGTCATTCGACCTCGAAGCCAAATACGTTGGGTTAAAAACCGGTCTTC	81479
Db	79406	CAGCGTTGTTTGTGTCATTCGACCTCGAAGCCAAATACGTTGGGTTAAAAACCGGTCTTC	79465

QY	81480	TTTCAAGTCACAGACCCACCCCTCGTGTATTTGGACACTGATTAACCAAGCACT	81533
Db	79466	TTTTCACGTCCACACCACCCCTCGTGTATTTGAACCACTGATTAACCAAGCACT	79525
QY	81540	GAGTTTCGTGGACACATCAGATTACATTGCAACTTTCACACCGGTTCCGGACAA	81599
Db	79526	GAGTTTCGTGGACACATCAGATTACATTGCAACTTTCACACCGGTTCCGGACAA	79585
QY	81600	GGCGAAGCTATATCGAGCACCCCGGTGCGCCATAGGCTTATTAATTAATTAAGCT	81659
Db	79586	GGCGAAGCTATATATGAGGACACCCCGGTGCGCCATAGGCTTATTAATTAATTAAGCT	79645
QY	81660	CTCGTATACCTTTTGTGTGTCTCATGTGCTACAGATCTCATTTTCTCGAATCTGCCAT	81719
Db	79646	CTCGTATACCTTTTGTGTGTCTCATGTGCTACAGATCTCATTTTCTCGAATCTGCCAT	79705
QY	81720	AGTGGAGGGTTTTCGCGCTACATATCCCTCGCATGTGTGGAGTGCATCAAAAACCT	81779
Db	79706	AGTGGAGGGTTTTCGCGCTACATATCCCTCGCATGTGTGGAGTGCATCAAAAACCT	79765
QY	81780	TCTCGCATTTCCATCAGGACCGCATCTGCACTTACTTGTTCACGGGACCCGGACACGG	81839
Db	79766	TCTCGCATTTCCATCAGGACCGCATCTGCACTTACTTGTTCACGGGACCCGGACACGG	79825
QY	81840	TCTTTTCTCATCTTCGCCAACCAATCCGCGGTACTCGCCGATTCGACCGGGACACA	81899
Db	79826	TCTTTTCTCATCTTCGCCAACCAATCCGCGGTACTCGCCGATTCGACCGGGACACA	79885
QY	81900	GCCAGAGCCCTGATTCAGATCCAGAGCCCGCCATTCGCGGTATTGGAGACTTGACGATC	81959
Db	79886	GCCAGAGCCCTGATTCAGATCCAGAGCCCGCCATTCGCGGTATTGGAGACTTGACGATC	79945
QY	81960	AGCTCTCAAGACAAATGAAACCCCTTGCCTTCACGGCACGATTCATTAATGTATCTAAAT	82019
Db	79946	AGCTCTCAAGACAAATGAAACCCCTTGCCTTCACGGCACGATTCATTAATGTATCTAAAT	80005
QY	82020	GACGAGATCATGTGCCCTTAACATATGGCTAAGACTACTCAAACTGTGCTAGGGAGAA	82079
Db	80006	GACGAGATCATGTGCCCTTAACATATGGCTAAGACTACTCAAACTGTGCTAGGGAGAA	80065
QY	82080	GTGACAAACACCTGGCACTCAATTAATTTTGGAGTCGGGACATTCACCCGTGCTTC	82139
Db	80066	GTGACAAACACCTGGCACTCAATTAATTTTGGAGTCGGGACATTCACCCGTGCTTC	80125
QY	82140	TGCTTATTAATTAACCCCATCGCCACCATATTCAGAGAAACAAACACTCCAGATACAAAC	82199
Db	80126	TGCTTATTAATTAACCCCATCGCCACCATATTCAGAGAAACAAACACTCCAGATACAAAC	80183
QY	82200	ACTTATTTACAGATGAGAGGGCTCACGGGCTCACAAACCGGTTGGCGGACAGGTA	82259
Db	80184	ACTTATTTACAGATGAGAGGGCTCACGGGCTCACAAACCGGTTGGCGGACAGGTA	80242
QY	82260	CATTAAACATTAGCGGCGGACAAAGCGCGGCGACAGACATCGTGGCCACAGCTAAATTA	82319
Db	80242	CATTAAACATTAGCGGCGGACAAAGCGCGGCGACAGACATCGTGGCCACAGCTAAATTA	80302
QY	82320	AGCGGTACAGTCTTTTGGCACTCGCGCTTGGGTTGAGTACGCGCCCAAAATTAAGTTAA	82379
Db	80303	AGCGGTACAGTCTTTTGGCACTCGCGCTTGGGTTGAGTACGCGCCCAAAATTAAGTTAA	80362
QY	82380	ACACAAAGCTTTGGAAGCGCGCTCCGTCGCGAGATGTTCTGGCCATGGCTGTCAATTA	82439
Db	80363	ACACAAAGCTTTGGAAGCGCGCTCCGTCGCGAGATGTTCTGGCCATGGCTGTCAATTA	80422
QY	82440	TCAACCAAGTTAAATGACAGACGCGTTGGGGACAGACGACACGCAACCGCCCGGTA	82499
Db	80423	TCAACCAAGTTAAATGACAGACGCGTTGGGGACAGACGACACGCAACCGCCCGGTA	80482
QY	82500	GATTGCAGCTTTCCTTTGAAGCAAGCGCAGAGGATGCCCAACCATTTAATGTAAATGCCG	82559
Db	80483	GATTGCAGCTTTCCTTTGAAGCAAGCGCAGAGGATGCCCAACCATTTAATGTAAATGCCG	80542
QY	82560	GAGGGGTGGCCCAAAACGCCACCCGCGCAAAAGATCTTTATTCAGAGAGCGCAACGCC	82619


```
Db 80543 GAGGGTGGCCCAACGCCAACCCGCCAAAAAGTCTTTATCCAGGAAGCGCAACGCC 80602
Oy 82620 TCGGCTGAAAGCTTCTCTAAGTGGCTTGGAAATCTCGGAACAGAGTGCCTGCTCGGATC 82679
Db 80603 TCGGCTGAAAGCTTCTCTAAGTGGCTTGGAAATCTCGGAACAGAGTGCCTGCTCGGATC 80662
Oy 82680 GGTGGCGGCATATGTGCTTGGAGGCGACGTTGCGACAATGGAGCACACAGGATGCCG 82739
Db 80663 GGTGGCGGCATATGTGCTTGGAGGCGACGTTGCGACAATGGAGGCGACAGGATGCCG 80722
Oy 82740 TTGGAGGATTCAGTCCACCTTCCACACTGTGTCCCAATATAGTAAACAATATAGCT 82799
Db 80723 TTGGAGGATTCAGTCCACCTTCCACACTGTGTCCCAATATAGTAAACAATATAGCT 80782
Oy 82800 AACATCCAAACACTGTTACACCCCGGCTCCACGCGACAGTGTACCGGAACACGCGGCCA 82859
Db 80783 AACATCCAAACACTGTTACACCCCGGCTCCACGCGACAGTGTACCGGAACACGCGGCCA 80842
Oy 82860 AACGGAACAACTTATTCACGGCTCTCTGGCGAACCCCGCTAACATAGCAGTAGTCCG 82919
Db 80843 AACGGAACAACTTATTCACGGCTCTCTGGCGAACCCCGCTAACATAGCAGTAGTCCG 80902
Oy 82920 GAGGCGTGTATCGAACAGACACAGCCTCAGGTAATGTAAAGGGGAATGATTCGG 82979
Db 80903 GAGGCGTGTATCGAACAGACACAGCCTCAGGTAATGTAAAGGGGAATGATTCGG 80962
Oy 82980 CATCTGTCCGGAATATGAGATCGAAGGTTGCTTATAGTACACGTCACACAGGTTTGA 83039
Db 80963 CATCTGTCCGGAATATGAGATCGAAGGTTGCTTATAGTACACGTCACACAGGTTTGA 81022
Oy 83040 CATCTGTCCGGAATATGAGATCGAAGGTTTGGATTTGGATTCCTTATAGGCTTATTCCTCGCA 83099
Db 81023 CATCTGTCCGGAATATGAGATCGAAGGTTTGGATTTGGATTCCTTATAGGCTTATTCCTCGCA 81082
Oy 83100 GCGCGGTGCAAGATGCGCTGATGACAGTATGATCAATATAAATGTTTTTTCGCGCTCC 83159
Db 81083 GCGCGGTGCAAGATGCGCTGATGACAGTATGATCAATATAAATGTTTTTTCGCGCTCC 81142
Oy 83160 TCGACTCTCTGCTCCCTCTGTCTGTGATTCACAGGATGCGGATTAAGTTCTTTCCTCG 83219
Db 81143 TCGACTCTCTGCTCCCTCTGTCTGTGATTCACAGGATGCGGATTAAGTTCTTTCCTCG 81202
Oy 83220 TCAACCCACCGAATTCGGGATGAGACAGCTGTCTGACATTTCCACCGACCATCTCTGA 83279
Db 81203 TCAACCCACCGAATTCGGGATGAGACAGCTGTCTGACATTTCCACCGACCATCTCTGA 81262
Oy 83280 AAGCTGATGTTTGGTCACTGACGCGCGCTCCATATCTCGCGCGGTGACAGGCA 83339
Db 81263 AAGCTGATGTTTGGTCACTGACGCGCGCTCCATATCTCGCGCGGTGACAGGCA 81322
Oy 83340 TCGCAAAACCTTGTCCAAAGTTACCTCTGACAAAGACACTGCAACCCACAGACACTACGCG 83399
Db 81323 TCGCAAAACCTTGTCCAAAGTTACCTCTGACAAAGACACTGCAACCCACAGACACTACGCG 81382
Oy 83400 TCGCAAAAGGGAATGTGCTGTAGTCTGCTGGAGACAGTACCTTACGCTATTTTATCT 83459
Db 81383 TCGCAAAAGGGAATGTGCTGTAGTCTGCTGGAGACAGTACCTTACGCTATTTTATCT 81442
Oy 83460 GTCTGTCACTCTCTGGGCGGGAAGTTTGTGTTATGAGCACACGCGGAAGATTCATGT 83519
Db 81443 GTCTGTCACTCTCTGGGCGGGAAGTTTGTGTTATGAGCACACGCGGAAGATTCATGT 81502
Oy 83520 GTCTGTCACTCTCTGGGCGGGAAGTTTGTGTTATGAGCACACGCGGAAGATTCATGT 83579
Db 81503 GTCTGTCACTCTCTGGGCGGGAAGTTTGTGTTATGAGCACACGCGGAAGATTCATGT 81562
Oy 83580 GGGGCAACAGGCTGTGTGAGATACAGTGTGCGCGCTTGGACGCGCGATGCTCTCG 83639
Db 81563 GGGGCAACAGGCTGTGTGAGATACAGTGTGCGCGCTTGGACGCGCGATGCTCTCG 81622
Oy 83640 GTCCCGAGAGCGGCGCAAGCTTCTCATGAAACCATGAAATTAATTTCTGTGTAG 83699
|||||
Db 81623 GTCCCGAGAGCGGCGCAAGCTTCTCATGAAACCATGAAATTAATTTCTGTGTAG 81682
Oy 83700 AGAGAACATGACCTCTCTGTGGATATATACCATATACAGTGTACCGCGCGGTACA 83759
Db 81683 AGAGAACATGACCTCTCTGTGGATATATACCATATACAGTGTACCGCGCGGTACA 81742
Oy 83760 GCGTTTCCCTGTTCCTATATGAGAGTACACCTCCGTTTCGTTCCGCTTACGTAGTATGC 83819
Db 81743 GCGTTTCCCTGTTCCTATATGAGAGTACACCTCCGTTTCGTTCCGCTTACGTAGTATGC 81802
Oy 83820 CCGTTTATACGAGACACATCTGTTTATTTGCTATCTGTTCTGCGGTACGTTT 83879
Db 81803 CCGTTTATACGAGACACATCTGTTTATTTATTTGCTATCTGTTCTGCGGTACGTTT 81862
Oy 83880 CACGATCTGAGATGGAACACAGACAGTAAACCGGTGCATAGAAACACAGATGACCG 83939
Db 81863 CACGATCTGAGATGGAACACAGACAGTAAACCGGTGCATAGAAACACAGATGACCG 81922
Oy 83940 GATGGGGAACCGGCGCGGATGCAACGAAACCTCTCCGATCTTGGAGCGTGTATCCA 83999
Db 81923 GATGGGGAACCGGCGCGGATGCAACGAAACCTCTCCGATCTTGGAGCGTGTATCCA 81982
Oy 84000 GTGCCGAACGCGCAAAATATAACACCTGAAATCTCAACCGCAAAACGCGCAATTTGAT 84059
Db 81983 GTGCCGAACGCGCAAAATATAACACCTGAAATCTCAACCGCAAAACGCGCAATTTGAT 82042
Oy 84060 GAGGACGCGCGCTCTTGGACCCGAGACAGATGTGCTGCGGCTGATCTTCGTCG 84119
Db 82043 GAGGACGCGCGCTCTTGGACCCGAGACAGATGTGCTGCGGCTGATCTTCGTCG 82102
Oy 84120 GAGGACCAACGTGGGCAAGGGGGGCGAGGCGCATCCCGCTAACCCGATGCCAG 84179
Db 82103 GAGGACCAACGTGGGCAAGGGGGGCGAGGCGCATCCCGCTAACCCGATGCCAG 82162
Oy 84180 ACACCTGCTCAAAATATTTATATATCCCTTACAGAGTTCATCAAGATACAGCATAC 84239
Db 82163 ACACCTGCTCAAAATATTTATATATCCCTTACAGAGTTCATCAAGATACAGCATAC 82222
Oy 84240 ATCCAGATTCATCAAAAGTTTATCCCGGAAGCGGTCCAGCGCGCACGCTGTCGCA 84299
Db 82223 ATCCAGATTCATCAAAAGTTTATCCCGGAAGCGGTCCAGCGCGCACGCTGTCGCA 82282
Oy 84300 CGACCCCATGCTCCACTTCTTGAATCCAGCATTCCTCCCTCAACCCCTCAAAATTCGT 84359
Db 82283 CGACCCCATGCTCCACTTCTTGAATCCAGCATTCCTCCCTCAACCCCTCAAAATTCGT 82342
Oy 84360 TCTTACACTCTAGCAGAGTTTCCATCTAGGCCCAACCTGACAGCTCTCTCCACGAGTAG 84419
Db 82343 TCTTACACTCTAGCAGAGTTTCCATCTAGGCCCAACCTGACAGCTCTCTCCACGAGTAG 82402
Oy 84420 CGACAAAGGCTGAGTTCCAGCTGCCCTTCTTCCAGACAGCTTAAGCTTTTTC- 84478
Db 82403 CGACAAAGGCTGAGTTCCAGCTGCCCTTCTTCCAGACAGCTTAAGCTTTTTC- 82462
Oy 84479 CCTCATCGCACCAAGTTAGTGTGAATAGTTTTCGTTGAGATGTTGAAGGTCACG 84538
Db 82463 CCTCATCGCACCAAGTTAGTGTGAATAGTTTTCGTTGAGATGTTGAAGGTCACG 82522
Oy 84539 ATCTAGATGAGCTGTAGTGAATCTGATTCGATTCGACATGACAGCTTACATTA 84598
Db 82523 ATCTAGATGAGCTGTAGTGAATCTGATTCGATTCGACATGACAGCTTACATTA 82582
Oy 84599 GCGCGGATACGAGTACTTTTCCCTGTATGATATTTGAGAGGCTCTATCTCTCAAAAC 84658
Db 82583 GCGCGGATACGAGTACTTTTCCCTGTATGATATTTGAGAGGCTCTATCTCTCAAAAC 82642
Oy 84659 GTGCACTGGCTTAAAGACACCTCTATTTGCGCACTTCCATTTTAAACCATAT 84718
Db 82643 GTGCACTGGCTTAAAGACACCTCTATTTTCCCACTTCCATTTTAAACCATAT 82702
Oy 84719 GTTCTGTGCTCAGCTTTTTCAGCTACCTGCAACGACAGGTTGATGCCGAGTTTC 84778
Db 82703 GTTCTGTGCTCAGCTTTTTCAGCTACCTGCAACGACAGGTTGATGCCGAGTTTC 82762
```

QY	84779	GCTCTCCAGTGCCTTGACAAACACTGGCCAGATTTAAAGATGANGCAAAAGCATAG	84838
Db	82763	GCTCTCCAGTGCCTTGACAAACACTGGCCAGATTTAAAGATGANGCAAAAGCATAG	82822
QY	84839	CTTTCGATTTAGTACCGGAGTGAAGTGGGACATTTAGAAAGTGTGGCCACACAT	84898
Db	82823	CTTTCGATTTAGTACCGGAGTGAAGTGGGACATTTAGAAAGTGTGGCCACACAT	82882
QY	84899	TCAGTGTGACTAAAGCCCGACCAATATGGACAGTACATTCCTCTATCACAACTA	84958
Db	82883	TCAGTGTGACTAAAGCCCGACCAATATGGACAGTACATTCCTCTATCACAACTA	82942
QY	84959	GTACAGAAAAACGAACACACCGGAGGTGACATTTTCCAGGTTAGAGAAATTTATTA	85018
Db	82943	GTACAGAAAAACGAACACACCGGAGGTGACATTTTCCAGGTTAGAGAAATTTATTA	83002
QY	85019	GCGGCGAATCATCTTAACAAACAGCAATGTTTATTCAAAGTCCGTATAGATTTCGT	85078
Db	83003	GCGGCGAATCATCTTAACAAACAGCAATGTTTATTCAAAGTCCGTATAGATTTCGT	83062
QY	85079	TTGATTAACAATTAATAGATGTGAGCCCTTCGAAAGATTTTCGCTCCGCCAGGAGAA	85138
Db	83063	TTGATTAACAATTAATAGATGTGAGCCCTTCGAAAGATTTTCGCTCCGCCAGGAGAA	83122
QY	85139	ACCCGAAACCCAGAGTTTAACAAAGCCCGGGGGGACCCGTGTCCGGCCGGAGGGGA	85198
Db	83123	ACCCGAAACCCAGAGTTTAACAAAGCCCGGGGGGACCCGTGTCCGGCCGGAGGGGA	83182
QY	85199	CCTGGCCATATCAAGCAAAATACGATCAGTGTCAAAATGCCACACGTCATCCCGGTGA	85258
Db	83183	CCTGGCCATATCAAGCAAAATACGATCAGTGTCAAAATGCCACACGTCATCCCGGTGA	83242
QY	85259	GGCAGATGTGGCAAACTGTACGGTCCACGGTATTTCCCTGAAACACACAGTTAGGACC	85318
Db	83243	GGCAGATGTGGCAAACTGTACGGTCCACGGTATTTCCCTGAAACACACAGTTAGGACC	83302
QY	85319	CCCGGTAATCGTGAACAAATTTCCCGCTGCTGCTGCTGCAAGAAATTTATTCATCAGAG	85378
Db	83303	CCCGGTAATCGTGAACAAATTTCCCGCTGCTGCTGCTGCTGCAAGAAATTTATTCATCAGAG	83362
QY	85379	CCATTTCAAAAGCGTCTCGAGTCTCTGCACACAGACGACTCACTGCTGTGTATCGG	85438
Db	83363	CCATTTCAAAAGCGTCTCGAGTCTCTGCACACAGACGACTCACTGCTGTGTATCGG	83422
QY	85439	AGGAACACAGCCCTGGAAGGGTCCATCCAAACACACAGTGTGTCCCGCTTATTTGT	85498
Db	83423	AGGAACACAGCCCTGGAAGGGTCCATCCAAACACACAGTGTGTCCCGCTTATTTGT	83482
QY	85499	TGGTTTGAAGATAGCCGATTCCTCGCCGGTGGTCAACAGTCAAGCTCAGCTGCATTTG	85558
Db	83483	TGGTTTGAAGATAGCCGATTCCTCGCCGGTGGTCAACAGCTCAGCTGCATTTG	83542
QY	85559	CCCATAGTAATTAATCTTTATATGATGATGTGACCCCATAGATCGCCGGAGATGGCGAGC	85618
Db	83543	CCCATAGTAATTAATCTTTATATGATGATGTGACCCCATAGATCGCCGGAGATGGCGAGC	83602
QY	85619	ACAGGCCATTAAGTCTGGCGCCAGAGGGCCCGAAGAATAGCTCTCATCTGTCTCTCGC	85678
Db	83603	ACAGGCCATTAAGTCTGGCGCCAGAGGGCCCGAAGAATAGCTCTCATCTGTCTCTCGC	83662
QY	85679	GTCGTGTCATCTTGATGATACCTTCGCGATACGTCCTCTTGATGACATTAAGAGGGTCC	85738
Db	83663	GTCGTGTCATCTTGATGATACCTTCGCGATACGTCCTCTCTTGATGACATTAAGAGGGTCC	83722
QY	85739	CGAAAGGGCGTGAAGCATTCGCGCCCGAGCATGGCAAAACCGCATTTTGGCACTCAAG	85798
Db	83723	CGAAAGGGCGTGAAGCATTCGCGCCCGAGCATGGCAAAACCGCATTTTGGCACTCAAG	83782
QY	85799	GCGGAGCCCGACACGGCCGGACACACCGGACAGACATCTTCTCGGATGAAGCAACCT	85858
Db	83783	GCGGAGCCCGACACGGCCGGACACACCGGACAGACATCTTCTCGGATGAAGCAACCT	83842

QY	85859	CTTTCGATTTAGTACCGGAGTGAAGTGGGACATTTAGAAAGTGTGGCCACACAT	85918
Db	83843	CTTTCGATTTAGTACCGGAGTGAAGTGGGACATTTAGAAAGTGTGGCCACACAT	83902
QY	85919	CTTTCGATTTAGTACCGGAGTGAAGTGGGACATTTAGAAAGTGTGGCCACACAT	85978
Db	83903	CTTTCGATTTAGTACCGGAGTGAAGTGGGACATTTAGAAAGTGTGGCCACACAT	83962
QY	85979	AGAGGCGAGTGGGATGTGTCTTAACACAGATAGAGCATATAGTGTGGCCGTGGGTTG	86038
Db	83963	AGAGGCGAGTGGGATGTGTCTTAACACAGATAGAGCATATAGTGTGGCCGTGGGTTG	84022
QY	86039	ATATATATTAATTTGGGAAACGACGGTGTGTAGTGCACACACAGCTGTCTTTGCTC	86098
Db	84023	ATATATATTAATTTGGGAAACGACGGTGTGTAGTGCACACACAGCTGTCTTTGCTC	84082
QY	86099	GTCGCGCAAAACAGCCCGGGGACAGACACATATGCGTTTGAACGTGACCATTCCT	86158
Db	84083	GTCGCGCAAAACAGCCCGGGGACAGACACATATGCGTTTGAACGTGACCATTCCT	84142
QY	86159	GAGGCCATATCCATTAACGAGATGGCCCTTCTCGATTCGCCAGCGCCATATTCATGTC	86218
Db	84143	GAGGCCATATCCATTAACGAGATGGCCCTTCTCGATTCGCCAGCGCCATATTCATGTC	84202
QY	86219	GGCAAGCTTTAAACCCCATGTAAAGTTTCAATTCAATTTAAATGACAACTCCGCCCA	86278
Db	84203	GGCAAGCTTTAAACCCCATGTAAAGTTTCAATTCAATTTAAATGACAACTCCGCCCA	84262
QY	86279	TGCTGTGACAAACATTAAGAAATGGGACACAGTGTGC - CTTTGGCGCTCTGTGATG	86337
Db	84263	TGCTGTGACAAACATTAAGAAATGGGACACAGTGTGTGCGCTTGTGATG	84322
QY	86338	AACCCCGCGGTAACTTACTTCTCCCATACGATGTCGAGGGATGATACAGATGTCTT	86397
Db	84323	AACCCCGCGGTAACTTACTTCTCCCATACGATGTCGAGGGATGATACAGATGTCTT	84382
QY	86398	CCCGTGTTCGGAACACCGGACCGGCTCCAGAGCGTCCGTCGCTCCCGGCTCATAT	86458
Db	84383	CCCGTGTTCGGAACACCGGACCGGCTCCAGAGCGTCCGTCGCTCCCGGCTCATAT	84442
QY	86458	CCCGGCGACCGTGTGTGATCATCATCTGACATCTCATCTCATCTGACAGATAGCAATTC	86517
Db	84443	CCCGGCGACCGTGTGTGATCATCATCTGACATCTCATCTCATCTGACAGATAGCAATTC	84502
QY	86518	AGGGCAATGGGACATCCCATGTATTTTGGAGTGTGATGAGAGGGGACATGAATATCCAC	86577
Db	84503	AGGGCAATGGGACATCCCATGTATTTTGGAGTGTGATGAGAGGGGACATGAATATCCAC	84562
QY	86578	GCACGTGACACGGCGGGACATCTCTCGAGTGGGAGTGTGCGCCAGTCCGCAATTA	86637
Db	84563	GCACGTGACACGGCGGGACATCTCTCGAGTGGGAGTGTGCGCCAGTCCGCAATTA	84622
QY	86638	TGCAAGAGATCGAAGCCTTGAGAGGGCTGCGAAGCCGACGCTCATAGTAATTTTCAGAA	86697
Db	84623	TGCAAGAGATCGAAGCCTTGAGAGGGCTGCGAAGCCGACGCTCATAGTAATTTTCAGAA	84682
QY	86698	TAGTTGTCAATTCGCTCATGTGTGCGCTTCTCCAGGTTTTCACACAGATTCGACATCC	86758
Db	84683	TAGTTGTCAATTCGCTCATGTGTGCGCTTCTCCAGGTTTTCACACAGATTCGACATCC	84742
QY	86758	GTCATTAACACAGATTCAAACCTCTCTGCAATGTTTTCGAGAGGCCGCAAAATCTGCGCTG	86817
Db	84743	GTCATTAACACAGATTCAAACCTCTCTGCAATGTTTTCGAGAGGCCGCAAAATCTGCGCTG	84802
QY	86818	GCAAACTCGCAGGGAATCAACTGAGACAGAGCGCAGAGAAACAGTCAATGGATTTATCGCA	86877
Db	84803	GCAAACTCGCAGGGAATCAACTGAGACAGAGCGCAGAGAAACAGTCAATGGATTTATCGCA	84862
QY	86878	CAACACAGGTGTCGGGAGCTTTGGGATACAGAAAGCCACATATACGACACCCGAGCGG	86937
Db	84863	CAACACAGGTGTCGGGAGCTTTGGGATACAGAAAGCCACATATACGACACCCGAGCGG	84922
QY	86938	GCTCGCAAAATTTGAATCTCGAGCTTCTCTCCAAAGTAAAAAAAGGATACCTCAACAGCC	86997


```
|||||
Db 84923 GCTCGAATTTTGAACCTCGACGTTCTCTCCAAAGTAAAAAGATACCTCAACAGCC 84982
86998 CCTACACAGGTTGGCGACAGAGAGTCTGAGTCTGTTGGATTTCCGTTTATAAACGAG 87057
84983 CCTAGACAGGTTGGCGAGAGAGTCTGAGTCTGTTGGATTTCCGTTTATAAACGAG 85042
87058 ACTTCAGTGGGCGCTTAGCCCTCGGCCCGCTGTCTCTCGAAAAACATCTCTGACG 87117
85043 ACTTCAGTGGGCGCTTAGCCCTCGGCCCGCTGTCTCTCGAAAAACATCTCTGACG 85102
87118 CAAGTCCCATGGAACAGTATGCAACGATGTGTGGGATGAGGTATACAGATCGCAG 87177
85103 CAAGTCCCATGGAACAGTATGCAACGATGTGTGGGATGAGGTATACAGATCGCAG 85162
87178 CCCACCGTAACCTCAAGAAAGCAATTGAAGAGTCTGTATCTTTCCCAAGAGAGCCCGC 87237
85163 CCCACCGTAACCTCAAGAAAGCAATTGAAGAGTCTGTATCTTTCCCAAGAGAGCCCGC 85222
87238 GCGTTGCTGGGCGGTGTCAGTCCCTCAAAATACGTGTGATCTCACTGATATACATC 87297
85223 GCGTTGCTGGGCGGTGTCAGTCCCTCAAAATACGTGTGATCTCACTGATATACATC 85282
87298 CTAATTTCTTAATTTCTGGGATGTGAACCGGTTTGACACAGCCAGCGCTGAGCA 87357
85283 CTAATTTCTTAATTTCTGGGATGTGAACCGGTTTGACACAGCCAGCGCTGAGCA 85342
87358 AAATGCTCAATATCTTGTATATCTTCATCGACGCGACTGTGGTGACCGGGTTCCAC 87417
85343 AAATGCTCAATATCTTGTATATCTTCATCGACGCGACTGTGGTGACCGGGTTCCAC 85402
87418 GGGACAGATATAGTGTCTGTCGTCGTCATCCATTCACGCGGGGATAGGCTTAGAC 87477
85403 GGGACAGATATAGTGTCTGTCGTCGTCATCCATTCACGCGGGGATAGGCTTAGAC 85462
87478 TCCACGCGCTCGATGACCAACCTTTTAATCATATGCGCTCCGCACTCGGATAT 87537
85463 TCCACGCGCTCGATGACCAACCTTTTAATCATATGCGCTCCGCACTCGGATAT 85522
87538 CAATACCTCTGACGAGCGGCTCAATTAATACGAGCGCCAGAACCCAGCGCTCCG 87597
85523 CAATACCTCTGACGAGCGGCTCAATTAATACGAGCGCCAGAACCCAGCGCTCCG 85582
87598 TAACAAAAGATAGATCTGAAGAAGCCTAATATATAGCCGAGGGAACCTCG 87657
85583 TAACAAAAGATAGATCTGAAGAAGCCTAATATATAGCCGAGGGAACCTCG 85642
87658 TAACAAATGAAAAAATGTTCTCAGAAAAAGAGAGAGAAACAGACGCAATCT 87717
85643 TAACAAATGAAAAAATGTTCTCAGAAAAAGAGAGAAACAGACGCAATCT 85702
87718 AGTCAAAACAGACCTAAAGGCGTCACTGACCCATATCTTCCCTCCGAGGAGTG 87777
85703 AGTCAAAACAGACCTAAAGGCGTCACTGACCCATATCTTCCCTCCGAGGAGTG 85762
87778 CGGTTTCCACATGCGCGTGAAGAAAGCAAGCTACATATATAGACAGTGTGAAG 87837
85763 CGGTTTCCACATGCGCGTGAAGAAAGCAAGCTACATATATAGACAGTGTGAAG 85822
87838 GAAACTTATTTGACGAGGACAGGCAAAAGCAAGTGTGCAAGGTAACAGTATGTGAC 87897
85823 GAAACTTATTTGACGAGGACAGGCAAAAGCAAGTGTGCAAGGTAACAGTATGTGAC 85882
87898 TGGGCGGATCCCGCAGCGCCGACAGACACTGTGCCAAATTTGAATGACAGGGG 87957
85883 TGGGCGGATCCCGCAGCGCCGACAGACACTGTGCCAAATTTGAATGACAGGGG 85942
87958 ATTGGGACACAGGCTCGCTTCCGAGTGGAGAGCGCTCCTAGTGAAGAGACGATAG 88017
85943 ATTGGGACACAGGCTCGCTTCCGAGTGGAGAGCGCTCCTAGTGAAGAGACGATAG 86002
88018 GCGGCTGAATGCGGTTCCGTTGGGGGGGCTGACCGCACTGAGATATTTGGGCG 88077
|||||

Db 86003 GCGGCTGAATGCGGTTCCGTTGGGGGGGCTGACACCGCACTGAGATTTGGGCG 86062
88078 AGCGAAAACAGCGAGAACTCGCGGTTGTTAATATATCCACCGGCTCAGCAACCT 88137
86063 AGCGAAAACAGCGAGAACTCGCGGTTGTTAATATATCCACCGGCTCAGCAACCT 86122
88138 CCGTTACCCAGAGAGAGGCTGGAACGTGACCATATATACGAATGTAATCCACAGCG 88197
86123 CCGTTACCCAGAGAGAGGCTGGAACGTGACCATATATACGAATGTAATCCACAGCG 86182
88198 TCTGGTAAATATATCAACCGCGGTATGATCTCTTCCAGGACCTTTAGATGCTGTC 88257
86183 TCTGGTAAATATATCAACCGCGGTATGATCTCTTCCAGGACCTTTAGATGCTGTC 86242
88258 TGGTGAAGAAACATATCTGTGGGTATGCGGCAACAGGCGCTGTCCGCGGAATGCC 88317
86243 TGGTGAAGAAACATATCTGTGGGTATGCGGCAACAGGCGCTGTCCGCGGAATGCC 86302
88318 GCACAAACGTGTCTTGAAGTGTGCTGCTTGGCGCGGCAAGCGCGCTTGGGCG 88377
86303 GCACAAACGTGTCTTGAAGTGTGCTGCTTGGCGCGGCAAGCGCGCTTGGGCG 86362
88378 GACCCGACCTCCATGTTCCCAACACGCGCCATAGTAAATAAACACAGCGCTAGCATC 88437
86363 GACCCGACCTCCATGTTCCCAACACGCGCCATAGTAAATAAACACAGCGCTAGCATC 86422
88438 CAACACGTCTCCCGCTCGCTCCACAGCGCGCTTGTATCTCATCCGCGACGAGATAC 88497
86423 CAACACGTCTCCCGCTCGCTCCACAGCGCGCTTGTATCTCATCCGCGACGAGATAC 86482
88498 CGGAATGCGGCGTTACGTCGTTGCTGACGTGTCAGAGAGATGCGCGCGGTGCACTCG 88557
86483 CGGAATGCGGCGTTACGTCGTTGCTGACGTGTCAGAGAGATGCGCGCGGTGCACTCG 86542
88558 TCGTTACAGAGCGGCGCAAGATGTAACAAAGATCGGCAACAGCGGATTAACGCGCACTG 88617
86543 TCGTTACAGAGCGGCGCAAGATGTAACAAAGATCGGCAACAGCGGATTAACGCGCACTG 86602
88618 TTAGCGCGCGCGCGGACAGGTTCTCTCAGTGAATACATCTTCAAGCGCTGACTGTG 88677
86603 TTAGCGCGCGCGCGGACAGGTTCTCTCAGTGAATACATCTTCAAGCGCTGACTGTG 86662
88678 CGTATAGGCGTGGCAACAGTCTTACATTCCTGAGCGTCAATCGTGTACCGGTC 88737
86663 CGTATAGGCGTGGCAACAGTCTTACATTCCTGAGCGTCAATCGTGTGTACCGGTC 86722
88738 TGCCGTAATGCTTTAAATTTGCAATAGTCCAGATCATGTTCTCTCATCGTCAAGAG 88797
86723 TGCCGTAATGCTTTAAATTTGCAATAGTCCAGATCATGTTCTCTCATCGTCAAGAG 86782
88798 CCACCGCGCGCTTTAAATGATTCAGAGGTAACGAGACAGAGTCTTTTCTCATCGACG 88857
86783 CCACCGCGCGCTTTAAATGATTCAGAGGTAACGAGACAGAGTCTTTTCTCATCGACG 86842
88858 CAATGCATTCAGAGTGTCTATCATTCATGCAACAAATGAGCAACATGCGCTCGAGGCA 88917
86843 CAATGCATTCAGAGTGTCTATCATTCATGCAACAAATGAGCAACATGCGCTCGAGGCA 86902
88918 GACGCGCGGTTTACCGGATGACCGCTCGCTTCCGCACTCTGAGAGGTCGCGTC 88977
86903 GACGCGCGGTTTACCGGATGACCGCTCGCTTCCGCACTCTGAGAGGTCGCGTC 86962
88978 GCATAACTGCTTAAAAATCTATCCCGCGCGGACACTGTACTTACAGTCAACCTT 89037
86963 GCATAACTGCTTAAAAATCTATCCCGCGGTCACCTGACTTACAGTCAACCTT 87022
89038 CCGGACACGCGGTTAGGCTGAGAGGACGCGACAGCAGCAGTATTTTCAATCTAGGCG 89097
87023 CCGGACACGCGGTTAGGCTGAGAGGACGCGACAGCAGCAGTATTTTCAATCTAGGCG 87082
89098 CGCCTACTAGAGGAAATCTGGGGTCTACAAATCCACGAGCGCGGCAATGTACCATG 89157
87083 CGCCTACTAGAGGAAATCTGGGGTCTACAAATCCACGAGCGCGGCAATGTACCATG 87142
|||||
```

OY	89158	AGTCATTTCTCTGTGACATATCCAAATGACAGGACCTGGGGCTTTTATCTGGACC	89217
Db	87143	AGTCATTTCTCTGTGACATATCCAAATGACAGGACCTGGGGCTTTTATCTGGACC	87202
OY	89218	AGGGCGACCCCCAAAGTAAGATGACTCGTTGGTGGGACAAGTGTCCCGGGAACGGG	89277
Db	87203	AGGGCGACCCCCAAAGTAAGATGACTCGTTGGTGGGACAACAGTGTCCCGGGAACGGG	87262
OY	89278	TGACCCGGGCGAGTCTGGCGAGTAGACCCATTAACATAGAAGATTGAGATTGACAGAGA	89337
Db	87263	TGACCCGGGCGAGTCTGGCGAGTAGACCCATTAACATAGAAGATTGAGATTGACAGAGA	87322
OY	89338	TTCGACAGCCCGTTGTGGCGGTGTCCCGTCTGGTGTCTCCCTGGGCAACCGTGTG	89397
Db	87323	TTCGACAGCCCGTTGTGGCGGTGTCCCGTCTGGTGTCTCCCTGGGCAACCGTGTG	87382
OY	89398	CTGTGTTCTGTATTTCACATATCATTCGCCAGCTCATTTGGCATCAAAAAGACCCCTCTGC	89457
Db	87383	CTGTGTTCTGTATTTCACATATCATTCGCCAGCTCATTTGGCATCAAAAAGACCCCTCTGC	87442
OY	89458	ACACCCGTTTATATCTCACACAGGTTTCTCTGTGCTCCGGCGTTAGCGGCCATCCAA	89517
Db	87443	ACACCCGTTTATATCTCACACAGGTTTCTCTGTGCTCCGGCGTTAGCGGCCATCCAA	87502
OY	89518	CTGAGGTTTGGAAAGCCACATCTTTATAGCGTGTGCCATAGAAAACACTGTGACCCGGTTT	89577
Db	87503	CTGAGGTTTGGAAAGCCACATCTTTATAGCGTGTGCCATAGAAAACACTGTGACCCGGTTT	87562
OY	89578	GGGGTCTTTGGCGCTTATGCAATCGTACCCCTCTACGCTCTGTGGAGAGTGTATCCGCTAC	89637
Db	87563	GGGGTCTTTGGCGCTTATGCAATCGTACCCCTCTACGCTCTGTGGAGAGTGTATCCGCTAC	87622
OY	89638	CAGCGACCCAAATTAATAAACTGTATAGCTAGCCGCAAAATGAGTATGTGTTGG	89697
Db	87623	CAGCGACCCAAATTAATAAACTGTATAGCTAGCCGCAAAATGAGTATGTGTTGG	87682
OY	89698	ATGGGGGTGGTGCAAACGTTGCGCAACCTGGCGCGCCCTGGCATATAGCGACCGGGCGGACCC	89757
Db	87683	ATGGGGGTGGTGCAAACGTTGCGCAACCTGGCGCGCCCTGGCATATAGCGACCGGGCGGACCC	87742
OY	89758	GTCAGCCTCCCGCGGAGCGGGAGAGGAGGAGGGCGTCCCTGGCTCAAGCCCATGAGACGA	89817
Db	87743	GTCAGCCTCCCGCGGAGCGGGAGAGGAGGAGGGCGTCCCTGGCTCAAGCCCATGAGACGA	87802
OY	89818	GGCGCGCTCTTAAGTAAATTTAAGACGCTCTCCGATGACTATCTAAGATCGAGGATTAACA	89877
Db	87803	GGCGCGCTCTTAAGTAAATTTAAGACGCTCTCCGATGACTATCTAAGATCGAGGATTAACA	87862
OY	89878	CAGGGATTCACAGCGGGGCTCTCAAGTAATAAAATCTTTCTCCGCCAAAAGCGTGTCT	89937
Db	87863	CAGGGATTCACAGCGGGGCTCTCAAGTAATAAAATCTTTCTCCGCCAAAAGCGTGTCT	87922
OY	89938	TGCCCGGGGCATTCGTCCTGTTCAAAACCGAGGTTTCCGCAAGACCCCTTAGCAGTCTTTT	89997
Db	87923	TGCCCGGGGCATTCGTCCTGTTCAAAACCGAGGTTTCCGCAAGACCCCTTAGCAGTCTTTT	87982
OY	89998	CCGGCACTCGGACACGTTGTGTGGCGTCCACATTCAGATCCCTATCCAGGCAGTACGC	90057
Db	87983	CCGGCACTCGGACACGTTGTGTGGCGTCCACATTCAGATCCCTATCCAGGCAGTACGC	88042
OY	90058	AACCAACAGTTGCAATGCGACATCACTACCTCGGTCCCATATGATATCTTAACCTCTCTTTTC	90117
Db	88043	AACCAACAGTTGCAATGCGACATCACTACCTCGGTCCCATATGATATCTTAACCTCTCTTTTC	88102
OY	90118	CTCGTCCACACACACAAAGTGTTCGGGAAACGTTTCGGTCTCCCAATTTGGAATATATCA	90177
Db	88103	CTCGTCCACACACACAAAGTGTTCGGGAAACGTTTCGGTCTCCCAATTTGGAATATATCA	88162
OY	90178	TCTTTGCAAGTGATTTGATGTGATTTCTATCTCGGTCAATTTGGAACCTTGTCACAGAAA	90237
Db	88163	TCTTTGCAAGTGATTTGATGTGATTTCTATCTCGGTCAATTTGGAACCTTGTCACAGAAA	88222

QY	90238	CTAAGCTAAAGGCCCTCACACGCTCCCTTAAAGTACGTACGATATTTTATGTCACCTTTATA	90297
Db	88223	CTTAAGCTAAAAAGCCCTCACACGCTCCCTTAAAGTACGATATTTTATGTCACCTTTATA	88282
QY	90298	GGGAGCGACGTCAGTATATAGCCCGCTGAAAAAGCTGCACTTCCTCATTAATTAATCCCA	90357
Db	88283	GGGAGCGACGTCAGTATATAGCCCGCTGAAAAAGCTGCACTTCCTCATTAATTAATCCCA	88342
QY	90358	AAGCGTTTCGGGTGCGCTCACCTTAAGCTAACTAAGTACGAGATTACAGCGTTCTAATGTGCCGG	90417
Db	88343	AAGCGTTTCGGGTGCGCTCACCTTAAGCTAACTAAGTACGAGATTACAGCGTTCTAATGTGCCGG	88402
QY	90418	GTTTCGGCACTCCCCCAGCGGCGACAGAAAGCAAGCAAGTTCATTTAAAGGCGACCAAGC	90477
Db	88463	GTTTCGGCACTCCCCCAGCGGCGACAGAAAGCAAGCAAGTTCATTTAAAGGCGACCAAGC	88522
QY	90478	TCAACTTTATTTAAGAGGAAAAAACAACCGCCATCAGAAAGTTTCCGAGGACACACAC	90537
Db	88463	TCAACTTTATTTAAGAGGAAAAAACAACCGCCATCAGAAAGTTTCCGAGGACACACAC	88522
QY	90538	CCCAAGACATTTCTTGCGCAGTTCGCGGCGACGCTAGTATTTTCTGATTTATTTGTAA	90597
Db	88523	CCCAAGACATTTCTTGCGCAGTTCGCGGCGACGCTAGTATTTTCTGATTTATTTGTAA	88582
QY	90598	TTCGATCTCAATTCGCCCCAACAATAGTCATTAATAAAAAACCGTAAACACACACTCTGGTG	90657
Db	88583	TTCGATCTCAATTCGCCCCAACAATAGTCATTAATAAAAAACCGTAAACACACACTCTGGTG	88642
QY	90658	AACAATTTATGCGTCTCGGCCCAAGAGTGCTGTAAGGCTGACGACGACACGCGTGCT	90717
Db	88643	AACAATTTATGCGTCTCGGCCCAAGAGTGCTGCTAGGCTGACGACGACGCGTGCT	88702
QY	90718	AAAACATTAACCAAGGCGTTAAACGTTTGAACCGAACAACGAGTCCGAGCGACAAAAAAGC	90777
Db	88703	AAAACATTAACCAAGGCGTTAAACGTTTGAACCGAACAACGAGTCCGAGCGACAAAAAAGC	88762
QY	90778	CCAACGTGGAAGACAAAAAATAGTGTACAAGTCCGAGACGACAGAGGCGTCTGACGGCA	90837
Db	88763	CCAACGTGGAAGACAAAAAATAGTGTACAAGTCCGAGAGCGACAGAGGCGTCTGACGGCA	88822
QY	90838	ACAGACAGCGGACCGCGGCGCGCCCTCCATATCAAAAAAGTCCAGTGCAAGATTAAGTCCAT	90897
Db	88823	ACAGACAGCGGTACCGCGGCGCGCCCTCCATATCAAAAAAGTCCAGTGCAAGATTAAGTCCAT	88882
QY	90898	CCACACACGTCAGACGCGCTTATAGAGTATGTATGATACCGCCTAGAGGTGAGCGAA	90957
Db	88883	CCACACACGTCAGACGCGCTTATAGAGTATGTATGATGATACCGCCTAGAGGTGAGCGAA	88942
QY	90958	AAAAATTCATGCGGTGCTGCTGACAGCGCGCTCATTAAGCGGATGTACCGCAGCGCTCTG	91017
Db	88943	AAAAATTCATGCGGTGCTGCTGACAGCGCGCTCATTAAGCGGATGTACCGCAGCGCTCTG	89002
QY	91018	AGTGAACAAAGCGCAGCTACTATTAAGAGGCGCACAGGCGGACGAAAAACACGCGGGGCTTAA	91077
Db	89003	AGTGAACAAAGCGCAGCTACTATTAAGAGGCGCACAGGCGGACGAAAAACACGCGGGGCTTAA	89062
QY	91078	AAAAAGTTCCTTAAGAACTAAAAAATATATACCCGAGAACGTCGTAAAAATCCAAGTTCG	91137
Db	89063	AAAAAGTTCCTTAAGAACTAAAAAATATATACCCGAGAACGTCGTAAAAATCCAAGTTCG	89122
QY	91138	TAGTATCTGTGGGCAATCGTGGGGCAAAATATATCAACGTCATTCGCGCGCAACACACAG	91197
Db	89123	TAGTATCTGTGGGCAATCGTGGGGCAAAATATATCAACGTCATTCGCGCGCAACACACAG	89182
QY	91198	AGCGACAGGGAACAGGCGACGACCCCAAAAAATGGAACGTAAGAACCATGGAAGGTCAACG	91257
Db	89183	AGCGACAGGGAACAGGCGACGACCCCAAAAAATGGAACGTAAGAACCATGGAAGGTCAACG	89242
QY	91258	CCGAGGGTGGATGCGATAGAAACCGCGGGTAATTAAGAAAGCGCGAGATGTGACCGGTACA	91317
Db	89243	CCGAGGGTGGATGCGATAGAAACCGCGGGTAATTAAGAAAGCGCGAGATGTGACCGGTACA	89302
QY	91318	TTCACGTCGCGGACGAGCGACGCGCGGTAGCCCAATATATACAGATATGCAAAAAAGCAGCCCA	91377

```
|||||
Db 89303 TTCACCTGCGCGAGAGCGAGCGCGGTACCCCAATATACAGAAATGCAAAAAGCAGCCCA 89362
OY 91378 TGTAAAGCCAAACCCGCCCCAGAGAGATATATGTTCTCAACGCTATACAGGGGCTCTACA 91437
Db 89363 TGTAAAGCCAAACCCGCCCCAGAGAGATATATGTTCTCAACGCTATACAGGGGCTCTACA 89422
OY 91438 AATATCAGGAGTGTATTAATTAACACAGATTAACAGGGGAAAGCCGAGCCTCCCGCTC 91497
Db 89423 AATATCAGGAGTGTATTAATTAACACAGATTAATGAGGAAAGCCGAGCCTCCCGCTC 89482
OY 91498 ATAAAGATAGCCAGGAGGAGCGCTCCGAGGTACGTGCTCCATGGCGGGGGTTTA 91557
Db 89483 ATAAAGATAGCCAGGAGGAGCGCTCCGAGGTACGTGCTCCATGGCGGGGGTTTA 89542
OY 91558 AAACAAAGGTTGAACGTGCGCGAGGAGGCTTGTTGTTTCTTTCCGCGAGCTGGGTGA 91617
Db 89543 AAACAAAGGTTGAACGTGCGCGAGGAGGCTTGTTGTTTCTTTCCGCGAGCTGGGTGA 89602
OY 91618 GCTGCTGTGTTTTCGCTTGCGGTGTTTTCGCGTGCAGAGCCGCTGTCGCAATGA 91677
Db 89603 GCTGCTGTGTTTTCGCTTGCGGTGTTTTCGCGTGCAGAGCCGCTGTCGCAATGA 89662
OY 91678 TTTGGCGGCCCGCTGCTGCGGTGCGACCGCTCCTCGGCAATTGGAGCGCACTGCTTT 91737
Db 89663 TTTGGCGGCCCGCTGCTGCGGTGCGACCGCTCCTCGGCAATTGGAGCGCACTGCTTT 89722
OY 91738 TAAGTCCAGGTGAGCGGTCTTCGAGAGGAGCGGAGCTCAGAACCCCTCCGGATCGGC 91797
Db 89723 TAAGTCCAGGTGAGCGGTCTTCGAGAGGAGCGGAGCTCAGAACCCCTCCGGATCGGC 89782
OY 91798 ACCTTCGAGAGATGCCCCGGAGCGGCAATTATCCGCGTCCGCGATCTACCTTAAATG 91857
Db 89783 ACCTTCGAGAGATGCCCCGGAGCGGCAATTATCCGCGTCCGCGATCTACCTTAAATG 89842
OY 91858 CATGACGCGCCAACTGAGCTGCGAGGATATCTGTCAGCGGAGCGGCGCTCAACTTCAG 91917
Db 89843 CATGACGCGCCAACTGAGCTGCGAGGATATCTGTCAGCGGAGCGGCGCTCAACTTCAG 89902
OY 91918 AATTCATTTGGCGTCCGAGCGGAAACAGGCAAAAAATCCGGAATCTTACATGCGTT 91977
Db 89903 AATTCATTTGGCGTCCGAGCGGAAACAGGCAAAAAATCCGGAATCTTACATGCGTT 89962
OY 91978 CAATCGCGGCCACACAGACTCTAAACTCAGATGAGTCTGAGGTGCGTGAACCAACACC 92037
Db 89963 CAATCGCGGCCACACAGACTCTAAACTCAGATGAGTCTGAGGTGCGTGAACCAACACC 90022
OY 92038 CACGTCCAGGTTTCTTCCTCTAGGCGCAAGTCCACTTGGCGTCCGGGGTGGGTTTAA 92097
Db 90023 CACGTCCAGGTTTCTTCCTCTAGGCGCAAGTCCACTTGGCGTCCGGGGTGGGTTTAA 90082
OY 92098 ATCAATTAATTTTACTAACCCGCTGACGCTAAACGCTGCACTGCCAGCGTTTCCCTTAA 92157
Db 90083 ATCAATTAATTTTACTAACCCGCTGACGCTAAACGCTGCACTGCCAGCGTTTCCCTTAA 90142
OY 92158 CGAGACGCTGACACCTGCTTGCGCTTGCTGCTGCTTACGCACTTAAACACAA 92217
Db 90143 CGAGACGCTGACACCTGCTTGCGCTTGCTGCTGCTTACGCACTTAAACACAA 90202
OY 92218 AGTCAGCGCTTAACGCTAAGAACAGGAGATTCGCCGTCGCCGGCTGCTGTAAGCTGTC 92277
Db 90203 AGTCAGCGCTTAACGCTAAGAACAGGAGATTCGCCGTCGCCGGCTGCTGTAAGCTGTC 90262
OY 92278 GTGGAACAGAGGTAGGTGGTTCGTCCAGCAGCGCTTGTGTCAGCGTCTGTGTGAT 92337
Db 90263 GTGGAACAGAGGTAGGTGGTTCGTCCAGCAGCGCTTGTGTCAGCGTCTGTGTGAT 90322
OY 92338 GTCCCGGTAGCGAGTGTGCTCTTAACAACTCGCGGCTTCTCTCCGCGTCCGACTGCTC 92397
Db 90323 GTCCCGGTAGCGAGTGTGCTCTTAACAACTCGCGGCTTCTCTCCGCGTCCGACTGCTC 90382
OY 92398 CCGGTGTGTAGAACGCGCAGTTCATTTCCGCAATGTTAACTCCAAACATCTCAGGCT 92457
|||||

Db 90383 CCGGTGTGTAGAACGCGCAGCTTCATTTCCCAATGTTAACTCCAAACATCTCAGGCT 90442
OY 92458 GTGTGTGAACGCTGTTCCCAAGGAGGAGTGTGTTGAAAAGCTAAAGCTATCCTGCTGCAT 92517
Db 90443 GTGTGTGAACGCTGTTCCCAAGGAGGAGTGTGTTGAAAAGCTAAAGCTATCCTGCTGCAT 90502
OY 92518 GTGAGATATATACCATCAGCGCGCCAGATGCTATTTTAAAGCTGAGACCGAAGACCCGCG 92577
Db 90503 GTGAGATATATACCATCAGCGCGCCAGATGCTATTTTAAAGCTGAGACCGAAGACCCGCG 90562
OY 92578 GTCCCGCAGCGTGGAGAGCAGCTTAAGGAGCGGGGGCCCTGACCTGACGCTGATCTGAT 92637
Db 90563 GTCCCGCAGCGTGGAGAGCAGCTTAAGGAGCGGGGGCCCTGACCTGACGCTGATCTGAT 90622
OY 92638 AACGCTTCTTAAAGATGCCCTTATATGTGTGCTGAACCCGCTCAATGCTCCAAAGCGC 92697
Db 90623 AACGCTTCTTAAAGATGCCCTTATATGTGTGCTGAACCCGCTCAATGCTCCAAAGCGC 90682
OY 92698 ATCGACGTCCACCTTGCGCGCGCTAATGAACGAGACAGGCAATGCTAAGGCGAAATTAAC 92757
Db 90683 ATCGACGTCCACCTTGCGCGCGCTAATGAACGAGACAGGCAATGCTAAGGCGAAATTAAC 90742
OY 92758 ACCCTAAAGAGAGAGAGATGGCAAAACAGACAGACACAGCGCTCAATGTTCAACT 92817
Db 90743 ACCCTAAAGAGAGAGAGATGGCAAAACAGACAGACACAGCGTTCAATGTTCAACT 90802
OY 92818 TTTAATAGAGCCTCTGCCCCGGAATAGTAACATGGGACACATGGGGACTACAGATCA 92877
Db 90803 TTTAATAGAGCCTCTGCCCCGGAATAGTAACATGGGACACATGGGGACTACAGATCA 90862
OY 92878 TTATGAGGAGATGTACATATTCAGAAATTTATACGCTCAAAAAGTTTCACTCTTGGA 92937
Db 90863 TTATGAGGAGATGTACATATTCAGAAATTTATACGCTCAAAAAGTTTCACTCTTGGA 90922
OY 92938 CTGCTATACGACAAAGGAGACACGCTTTGGGGGGCGGACCGCAAGAGGGCGTATGTT 92997
Db 90923 CTGCTATACGACAAAGGAGACACGCTTTGGGGGGCGGACCGCAAGAGGGCGTATGTT 90982
OY 92998 ATTGACTTTAGATTCCTGTCGCGCTGCGCTGCAAAAAGCTGCTGATGCTCCGACGTT 93057
Db 90983 ATTGACTTTAGATTCCTGTCGCGCTGCGCTGCAAAAAGCTGCTGATGCTCCGACGTT 91042
OY 93058 ACCATGCTACGCTTCGCGCTTGGAGACGAATTAACAGAGTCTATCTCCAGCGCTTCG 93117
Db 91043 ACCATGCTACGCTTCGCGCTTGGAGACGAATTAACAGAGTCTATCTCCAGCGCTTCG 91102
OY 93118 CGAAAGAGCGCTGATGATGTCGACGAGGAGGGGATGCTCCGAGATCAATGCTGTTG 93177
Db 91103 CGAAAGAGCGCTGATGATGTCGACGAGGAGGGGACTGCTCCGGAGATCAATGCTGTTG 91162
OY 93178 TACAGCAAGCTTGCGGCCCTGCGTGTAGCAGCTGCTCCGAGATGATGCTTACGC 93237
Db 91163 TACAGCAAGCTTGCGGCCCTGCGTGTAGCAGCTGCTCCGAGATGATGCTTACGC 91222
OY 93238 AGGCACACCCCGCGCATGATTTCCGGGAAGCGCAAAAGTCTATAGATTAATATACCT 93297
Db 91223 AGGCACACCCCGCGCATGATTTCCGGGAAGCGCAAAAGTCTATAGATTAATATACCT 91282
OY 93298 ATAAAGTATATCCCTTCGATTAACAGAAACAGACACACTTCTCGCCCGCGTGTGCGC 93357
Db 91283 ATAAAGTATATCCCTTCGATTAACAGAAACAGACACACTTCTCGCCCGCGTGTGCGC 91342
OY 93358 TTGCGCACTGGGAATGAGCAGCAATCTTCTTGCGCAGGGTATGCGTCTGCAAT 93417
Db 91343 TTGCGCACTGGGAATGAGCAGCAATCTTCTTGCGCAGGGTATGCGTCTGCAAT 91402
OY 93418 TTTTGGCATTAATATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 93477
Db 91403 TTTTGGCATTAATATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 91462
OY 93478 GCATACACTTTGCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 93537
Db 91463 GCATACACTTTGCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 91522
```

OY	93538	TCGTGATTCGTGAACCTCTTTAACTAGCTCTTCGATGTAAAGTTTACAGACTCTCTGCC	935397
Db	91523	TCGTGATTCGTGAACCTCTTTAACTAGCTCTTCGATGTAAAGTTTACAGACTCTCTGCC	915828
OY	93598	ATTACCCAAAATGTGAAGAGAAACCTGGTAAACCTCCCTAATCGGTGGGACATCAATATGTCC	93657
Db	91583	ATTACCCAAAATGTGAAGAGAAACCTGGTAAACCTCCCTAATCGGTGGGACATCAATATGTCC	916428
OY	93658	ACCTCATCGGAGTCTCTGTCAGGAGAAATTTGACTGGGGAAACCATCTGTTCTGCCATGTTC	937178
Db	91643	ACCTCATCGGAGTCTCTGTCAGGAGAAATTTGACTGGGGAAACCATCTGTTCTGCCATGTTC	917020
OY	93718	TCTCGGGTGAAGCTATAAAAAAGCCAGGGTGGTCCCTGCGCTACAGAAACCGATCTGGGGAC	937777
Db	91703	TCTCGGGTGAAGCTATAAAAAAGCCAGGGTGGTCCCTGCGCTACAGAAACCGATCTGGGGAC	917628
OY	93778	TCCATGCGCGCGGTACTATTGACAGGCCCCAAACATACCTTGGCGCGCTACAGTCGGGCT	938377
Db	91763	TCCATGCGCGCGGTACTATTGACAGGCCCCAAACATACCTTGGCGCGCTACAGTCGGGCT	918222
OY	93838	TTTGTACGCAGTTAGACTCCGCCCTCTGAGAGATGTTGTACCCACGACCTGATCTTA	938977
Db	91823	TTTGTACGCAGTTAGACTCCGCCCTCTGAGAGATGTTGTACCCACGACCTGATCTTA	918827
OY	93898	AGCATCTCAGGGCTTTAAGTTTGTCTGTTTCGAATTTGACAAATTAATACAGATGGTTT	939577
Db	91883	AGCATCTCAGGGCTTTAAGTTTGTCTGTTTCGAATTTGACAAATTAATACAGATGGTTT	919428
OY	93958	TTAAACCTAGCTGTATCCGGTCAGGAGCAAGTCTCGAATATTAACTCGGCCGGTGGCT	940177
Db	91943	TTAAACCTAGCTGTATCCGGTCAGGAGCAAGTCTCGAATATTAACTCGGCCGGTGGCT	920022
OY	94018	GCCTCTCTTTAAAAAATAATTAAGCAGCACTGCTGCTTCAATTTGGAGCCGGCGAC	940777
Db	92003	GCCTCTCTTTAAAAAATAATTAAGCAGCACTGCTGCTTCAATTTGGAGCCGGCGAC	920622
OY	94078	CGGCCGCTCCAACTGCTTAATTGGGCAAGTAATCAAAAGGCCGTCAAAAAATCTGTATTC	941377
Db	92063	CGGCCGCTCCAACTGCTTAATTGGGCAAGTAATCAAAAGGCCGTCAAAAAATCTGTATTC	921222
OY	94138	TGTGCTTCAGGGGTTTCGAAATGAAGACCGACCTCCGTTAAGGGCGACACGTTCCGA	941977
Db	92123	TGTGCTTCAGGGGTTTCGAAATGAAGACCGACCTCCGTTAAGGGCGACACGTTCCGA	921828
OY	94198	GGTCACCAAGGCTTCACTCTCTTAAAAAAGTCAGCTTGGCTTCAAGATCTCTCTTTCG	942577
Db	92183	GGTCACCAAGGCTTCACTCTCTTAAAAAAGTCAGCTTGGCTTCAAGATCTCTCTTTCG	922428
OY	94258	TGTGTACCTTCGATGCGATATTGGCAAGAAGCGATTAATGCTTGGGTATCCCGTAA	943177
Db	92243	TGTGTACCTTCGATGCGATATTGGCAAGAAGCGATTAATGCTTGGGTATCCCGTAA	923022
OY	94318	GCTGAGAGGTTCCGGCGGTTGGGATCAGCGCCAAAAACCTGGCTTGAATAATCCATGTCT	943777
Db	92303	GCTGAGAGGTTCCGGCGGCTTGGGATCAGCGCCAAAAACCTGGCTTGAATAATCCATGTCT	923628
OY	94378	GGGCAATGCTGCGGCCAGGTGCTCCCATCTCTCAAGGAGGGTGGAGCGGCTTAACGC	944377
Db	92363	GGGCAATGCTGCGGCCAGGTGCTCCCATCTCTCAAGGAGGGTGGAGCGGCTTAACGC	924222
OY	94438	CGTCCCAAGTTTGGCAATGGAACAACCCGAGCCAAATGCACTCCGCTCCCAATCCAGAA	944977
Db	92423	CGTCCCAAGTTTGGCAATGGAACAACCCGAGCCAAATGCACTCCGCTCCCAATCCAGAA	924828
OY	94498	ACGAGAGTCCCTCGCCAGATTAACAACATCTCATGAGCTGTTTGCACCGCGTTAAATTACA	945577
Db	92483	ACGAGAGTCCCTCGCCAGATTAACAACATCTCATGAGCTGTTTGCACCGCGTTAAATTACA	925428
OY	94558	TTGCTCTAAAAAATCTCAGCTCCAGCTTGGCGCTCTCGCGCTCAAGTATGCCAAAGCCCA	946177
Db	92543	TTGCTCTAAAAAATCTCAGCTCCAGCTTGGCGCTCTCGCGCTCAAGTATGCCAAAGCCCA	926022

QY	94618	GTTCGGCAAAACAGTCGGGCCAGTCCTTGGACGGCCAAATGCCCAATGATTCGTTCTCTGGC	94677
Db	92603	GTTCGGCAAAACAGTCGGGCCAGTCCTTGGACGGCCAAATGCCCAATGATTCGTTCTCTGGC	92663
QY	94678	CGGCGCTTAAGGCTCTGGTAGGGGCGCTCCGGCCAAAATGCAAGGATTTGACAAATGATA	94737
Db	92663	CGGCGCTTAAGGCTCTGGTAGGGGCGCTCCGGCCAAAATGCAAGGATTTGACAAATGATA	92722
QY	94738	CTGGGCGCTCCAGCGGCATCATCGAGCAGTTCAAAACCAAAATGTTACATCCCTCCACAG	94797
Db	92723	CTGGGCGCTCCAGCGGCATCATCGATGATGTTCAAAACCAAAATGTTACATCCCTCCACAG	92788
QY	94798	GCTCCACACCAAGACTCTCCCTGTGGGGCTTGAGGCATTTGGTAGGCTAATGTTTGCA	94857
Db	92783	GCTCCACACCAAGACTCTCCCTGTGGGGCTTGAGGCATTTGGTAGGCTAATGTTTGCA	92842
QY	94858	AGTTACACAGGAAAGCCTGACCCGCGGTTGCGACAGATTCGCGACAGAGATTTGAAAC	94912
Db	92843	AGTTACACAGGAAAGCCTGACCCCTGGGTTGTGCGACAGATTTCCGACAGAGATTTGAAAC	92902
QY	94918	AGTTTATGGGCTTCCTGGCGTCAACACCAAGTGGTGTGTGTGAGCGGCTCCCTTATGCA	94977
Db	92903	AGTTTATGGGCTTCCTGGCGTCAACACCAAGTGGTGTGTGTGAGCGGCTCCCTTATGCA	92966
QY	94978	GGACGTAGGAGCTCGCGGCTTAAATGACAGTAAATTAAGGCGATACATCATGATTTTA	95037
Db	92963	GGACGTAGGAGCTCGCGGCTTAAATGACAGTAAATTAAGGCGATACATCATGATTTTA	93022
QY	95038	ACGGCAACGAGCTAAGATGTTTGGCAGCGGCACATGCTGTGTATTCAAATCTCAAAAT	95097
Db	93023	ACGGCAACGAGCTAAGATGTTTGGCAGCGGCACATGCTGTGTATTCAAATCTCAAAAT	93082
QY	95098	CGGCAACGCTAGAGTTTATGAGAGATTTTGGCCACACTCTGGCGCAAAACAGGTGCACTGGC	95157
Db	93083	CGGCAACGCTAGAGTTTATGAGAGATTTTGGCCACACTCTGGCGCAAAACAGGTGCACTGGC	93142
QY	95158	CATCTGGGTTTGTTCGTACAGTGGAAAAAAGCTCCGGCACACACAGCCCTGAACA	95217
Db	93143	CATCTGGGTTTGTTCGTACAGTGGAAAAAAGCTCCGGCACACACAGCCCTGAACA	93202
QY	95218	GGTTGTACACCGGCTCCTGATTTCCGCGGACATCTGGGTTCAAAAATATCAAAATCTGAT	95277
Db	93203	GGTTGTACACCGGCTCCTGATTTCCGCGGACATCTGGGTTCAAAAATATCAAAATCTGAT	93266
QY	95278	GATGCAATAGTTCATCTAGGCGCTGGCACCAACAGAGCAGATTTGTTATCTTTGAAAT	95337
Db	93263	GATGCAATAGTTCATCTAGGCACTGGCACCAACAGAGCAGATTTGTTATCTTTGAAAT	93322
QY	95338	ACCCACAGTGCGGCTTTAATTAATTTAAACAGCTGATGTTCTTGTGTCGGCAAAAG	95397
Db	93323	ACCCACAGTGCGGCTTTAATTAATTTAAACAGCTGATGTTCTTGTGTCGGCAAAAG	93382
QY	95398	ACGAGACATCATCCCCACGCGTGCATCTGTACGAGAAAGGGGGACATTTCTCATGAA	95457
Db	93383	ACGAGACATCATCCCCACGCGCTGCATCTGTACGAGAAAGGGGGACATTTCTCATGAA	93442
QY	95458	GTCGTTTAGAGGTTTGTCTTCGCTGCCATTTGACAGCGCTTTAAAAATTAACACGCTAGAA	95517
Db	93443	GTCGTTTAGAGGTTTGTCTTCGCTGCCATTTGACAGCGCTTTAAAAATTAACACGCTAGAA	93502
QY	95518	GCTGACCTCCGCGAAGCCGCGGTGACCTTAATACAGGCGTTTGGCGACACACAAATCTGTG	95577
Db	93503	GCTGACCTCCGCGAAGCCGCGGTGACCTTAATACAGGCGTTTGGCGACACAAATCTGTG	93566
QY	95578	ACGAGATGTAATGGAACGCGTAACCAACAGGTAATCTATCTCACAGTCCGTTTCGCTCT	95637
Db	93563	ACGAGATGTAATGGAACGCGTAACCAACAGGTAATCTATCTCACAGTCCGTTTCGCTCT	93622
QY	95638	CCACACAGGTGCTGAGGGTCTCCCGCAAAACAGGAAATTTATACACTGACAGGCGACAA	95697
Db	93623	CCACACAGGTGCTGAGGGTCTCCCGCAAAACAGGAAATTTATACACTGACAGGCGACAA	93688
QY	95698	AAACAGCCACCTCTATTAACATCTGGGCGACGCTTTCAAAAATGGGTTGAAGAACCTCTGG	95757

|||||
Db 93683 AAACACCAACCCCTCAATAAATCTGGGCCAGCTTTCAAAAAGGGGGAAGAACCTGGG 93742
QY 95758 TTCTCAGCAGTACGTATGCTAAACCTAAGCGCAGACAGGTAGCCGAGTTAACGAAT 95817
Db 93743 TTCTCAGCAGTACGTATGCTAAACCTAAGCGCAGACAGGTAGCCGAGTTAACGAAT 93802
QY 95818 TTGTGTATGCTTGGCTGCTGTTAAAGTCTGTAAAGACCGCTCAGGGCCGCTGCTGT 95877
Db 93803 TTGTGTATGCTTGGCTGCTGTTAAAGTCTGTAAAGACCGCTCAGGGCCGCTGCTGT 93862
QY 95878 TTGACATTAACCGCGACACTGCTGCTTAAGCTTTCCCGAATACCGGAGATACATC 95937
Db 93863 TTGACATTAACCGCGACACTGCTGCTTAAGCTTTCCCGAATACCGGAGATACATC 93922
QY 95938 GCACCGTAAACAGGACACTGCTGCTTAATTTCTGCGCAAGAGACCGGTTAGTACG 95997
Db 93923 GCACCGTAAACAGGACACTGCTGCTTAATTTCTGCGCAAGAGACCGGTTAGTACG 93982
QY 95998 TGGCCCTATATGCTCCATCCAGATGTTCCCTTTAAGAAATTCACGAGTATCGGCCATC 96057
Db 93983 TGGCCCTATATGCTCCATCCAGATGTTCCCTTTAAGAAATTCACGAGTATCGGCCATC 94042
QY 96058 GTTCAGGCTCAAGGCTTGAAGCTACACCCCGAGTTCCCGGCTGAGTACGAGGTTAAG 96117
Db 94043 GTTCAGGCTCAAGGCTTGAAGCTACACCCCGAGTTCCCGGCTGAGTACGAGGTTAAG 94102
QY 96118 GTTTGGCAGATTTTGGCGAGAGAAAGATTGCTGTTCAATGTTTAAAGAAATAGCTT 96177
Db 94103 GTTTGGCAGATTTTGGCGAGAGAAAGATTGCTGTTCAATGTTTAAAGAAATAGCTT 94162
QY 96178 CCAAGACCCCGGATTTGGAAACAACATCCGTAATTTTAAACACCGGTTAAAGACGCTTT 96237
Db 94163 CCAAGACCCCGGATTTGGAAACAACATCCGTAATTTTAAACACCGGTTAAAGACGCTTT 94222
QY 96238 AAAGTAAAGCTTTGAAAGATGTTGTTAAACCGGAGACGCTTCAAGTGTGCAAC 96297
Db 94223 AAAGTAAAGCTTTGAAAGATGTTGTTAAACCGGAGACGCTTCAAGTGTGCAAC 94282
QY 96298 TACGCCGAACGCAAGCCTATTATATACAGGTCTTCTGACAGTGAATGTTTGGTGG 96357
Db 94283 TACGCCGAACGCAAGCCTATTATATACAGGTCTTCTGACAGTGAATGTTTGGTGG 94342
QY 96358 AATACGCGCGTGTAAATATCCCTCAATGGGAGATTTTCACAATATCTTTACCA 96417
Db 94343 AATACGCGCGTGTAAATATCCCTCAATGGGAGATTTTCACAATATCTTTACCA 94402
QY 96418 CTTAATAAACCAGTCTAGCGCGGCTTATTTATTTACCTAATGTAGTTAAGCAAC 96477
Db 94403 CTTAATAAACCAGTCTAGCGCGGCTTATTTATTTATTTGCTTATGTAGTTAAGCAAC 94462
QY 96478 ATTAATAGACAGTGGGCGGCAAAAGCTGTGCGCAGGCTGACGGGCGATAGTCAATC 96537
Db 94463 ATTAATAGACAGTGGGCGGCAAAAGCTGTGCGCAGGCTGACGGGCGATAGTCAATC 94522
QY 96538 TAAATCCAAACATGCTACTAGAAAGCCTAAGGCCAATATGTGTAAACAAGGGCTCT 96597
Db 94523 TAAATCCAAACATGCTACTAGAAAGCCTAAGGCCAATATGTGTAAACAAGGGCTCT 94582
QY 96598 GCGAGTACGTGCTTAAAGCAGACGCTACCTGTTGACAAACGTAAGTGTGACCGT 96657
Db 94583 GCGAGTACGTGCTTAAAGCAGACGCTACCTGTTGACAAACGTAAGTGTGACCGT 94642
QY 96658 TTGAACCAAGCGCCGACCGGCGCAAGAACTGATGAACGAGCCGTTTCCAAATTC 96717
Db 94643 TTGAACCAAGCGCCGACCGGCGCAAGAACTGATGAACGAGCCGTTTCCAAATTC 94702
QY 96718 TTCAAAATTTGGTATATGGCTCAAGTACACGCTCTGCTGCTTACCAACACAGCTAT 96777
Db 94703 TTCAAAATTTGGTATATGGCTCAAGTACACGCTCTGCTGCTTACCAACACAGCTAT 94762
QY 96778 TCTGTTGGTCTGGGGGCGAGATCCGCTCATCTAGACATCGCGGCGAGGAGCTAG 96837
|||||

Db 94763 TCTGTTGCTTGGGGGCGAGATCCCGCTTCATCTAGACATGTCGGCCACGACGCTAG 94822
QY 96838 CGTGAATTAACATGTCAATGGAGGACCCAGTGTGCTGTGTTAAAGAAACAGTATG 96897
Db 94823 CGTGAATTAACATGTCAATGGAGGACCCAGTGTGCTGTGTTAAAGAAACAGTATG 94882
QY 96898 GCCCGAGGTTCTGTGAACTCATGTGTGAGATTAATTCAAAAATTCATACGTTG 96957
Db 94883 GCCCGAGGTTCTGTGAACTCATGTGTGAGATTAATTCAAAAATTCATACGTTG 94942
QY 96958 ACATGTAGGAGACAGATTAATAATCATCTTTGATGGGCTCCACCCGAGTGTGCA 97017
Db 94943 ACATGTAGGAGACAGATTAATAATCATCTTTGATGGGCTCCACCCGAGTGTGCA 95002
QY 97018 CACACATATTTAGAGAGAGATCAGAAACACCTTAGAAAAAGTCGACCGGAGATTA 97077
Db 95003 CACACATATTTAGAGAGAGATCAGAAACACCTTAGAAAAAGTCGACCGGAGATTA 95062
QY 97078 CGAAACCCGGTGAAGGAGCGGCGGCGAGTAGAGCATCAAACTATCTTACGCTTTCAC 97137
Db 95063 CGAAACCCGGTGAAGGAGCGGCGGCGAGTAGAGCATCAAACTATCTTACGCTTTCAC 95122
QY 97138 GTTTGGCTCCGCTGCTTCATGGCGCTGCTCAATTTCTGCGCACGGGCTGATTAACGCTA 97197
Db 95123 GTTTGGCTCCGCTGCTTCATGGCGCTGCTCAATTTCTGCGCACGGGCTGATTAACGCTA 95182
QY 97198 CGAGAACACCGCGGCGCTTTACAAATTAACGCAACCTCTAACGCTGACCGGATGCT 97257
Db 95183 CGAGAACACCGCGGCGCTTTACAAATTAACGCAACCTCTAACGCTGACCGGATGCT 95242
QY 97258 ACACAGCTTAAACTCTGATGAGTGTCCAACTAAACACGATCAACCGGACACCTTT 97317
Db 95243 ACACAGCTTAAACTCTGATGAGTGTCCAACTAAACACGATCAACCGGACACCTTT 95302
QY 97318 AAGCATGCCACCGTGAACCGGCTTTTAAATCTGATTCAAATTAAGACAACCCCTGCT 97377
Db 95303 AAGCATGCCACCGTGAACCGGCTTTTAAATCTGATTCAAATTAAGACAACCCCTGCT 95362
QY 97378 TTCAATTTATCAAAAACACCTGTGTGTTTTTTTAAATGAGAGTCCGAGGCTTCGAGCC 97437
Db 95363 TTCAATTTATCAAAAACACCTGTGTGTTTTTTTAAATGAGAGTCCGAGGCTTCGAGCC 95422
QY 97438 AGTCATTAAGACACCAAGGCGAGAAACGTCACAGCATATCTCCGAGTGTGAA 97497
Db 95423 AGTCATTAAGACACCAAGGCGAGAAACGTCACAGCATATCTCCGAGTGTGAA 95482
QY 97498 TGTCTTAATACAGTATTCGAAACCAACAGCAGTCCCGAGGCGTAAAGACAGATTA 97557
Db 95483 TGTCTTAATACAGTATTCGAAACCAACAGCAGTCCCGAGGCGTAAAGACAGATTA 95542
QY 97558 TCTCGAACACGCTGCCATATGCGCTGCTGCTGAGATACATCATCATCTTACG 97617
Db 95543 TCTCGAACACGCTGCCATATGCGCTGCTGCTGAGATACATCATCTTACG 95602
QY 97618 TACGCCCTCGGGGATCCCGACACACCAATGGGTACAGCATCTACGCTGGTGA 97677
Db 95603 TACGCCCTCGGGGATCCCGACACACCAATGGGTACAGCATCTACGCTGGTGA 95662
QY 97678 GCAAAATTTTACAGAAACCAACCGCAATACTGGAACCTCAACCTCCGAGTCTCAT 97737
Db 95663 ACAAATTTTACAGAAACCAACCGCAATACTGGAACCTCAACCTCCGAGTCTCAT 95722
QY 97738 TATCGACATGCGGAGATGCTGCTGCTGCTGAGAGTGGCTAATCTATGTTGTA 97797
Db 95723 TATCGACATGCGGAGATGCTGCTGCTGCTGAGAGTGGCTAATCTATGTTGTA 95782
QY 97798 AAAACTGCAACTGGACACACCGCCCTATTTCCACCTGTCGACGAACTGGCCGCT 97857
Db 95783 AAAACTGCAACTGGACACACCGCCCTATTTCCACCTGTCGACGAACTGGCCGCT 95842
QY 97858 GGTACCGGCGCACAGAAATGTTTGTCCCTTATCGAGAGTACAGTGAACCTATCATC 97917
Db 95843 GGTACCGGCGCACAGAAATGTTTGTCCCTTATCGAGAGTACAGTGAACCTATCATC 95902
|||||

QY	97918	CATGCCAGTATCAAAACAGCGAGCGTTTGAGATATACAGCGTCTTTGCCAAATCAAAAA	979177
Db	95903	CATGCCAGTATCAAAACAGCGAGCGTTTGAGATATACAGCGTCTTTGCCAAATCAAAAA	959622
QY	97978	CATAGTTGAGCGGACACCAATTTTACCGTTCAACCGACACAGAACTTACACGTTCAACCC	98037
Db	95963	CATAGTTGAGCGGACACCAATTTTACCGTTCAACCGACACAGAACTTACACGTTCAACCC	96022
QY	98038	CGAAGCTTATTCCTGTACGACTTCGTAAATCGAGTCCGTGCAAAAACACGACATACGG	98097
Db	96023	CGAAGCTTATTCCTGTACGACTTCGTAAATCGAGTCCGTGCAAAAACACGACATACGG	96082
QY	98098	GTGTTCGCCGAACGCAATTGAGATTTTATTAAGAAAGGTATCGATTTTATGCGGAGTT	98157
Db	96083	GTGTTCGCCGAACGCAATTGAGATTTTATTAAGAAAGGTATCGATTTTATGCGGAGTT	96142
QY	98158	GGGGGCGTTCATTGAAAAAAGCGTGTGGCTATCGATCAACCGTAAGCGCTCCCAAGTGAG	98217
Db	96143	GGGGGCGTTCATTGAAAAAAGCGTGTGGCTATCGATCAACCGTAAGCGCTCCCAAGTGAG	96202
QY	98218	AGCGGTTAAGCCAGCGCTGCGAGCTGTGGCCTATCCAAAAGAGCGGTGGAAGATTCCG	98277
Db	96203	AGCGGTTAAGCCAGCGCTGCGAGCTGTGGCCTATCCAAAAGAGCGGTGGAAGATTCCG	96262
QY	98278	CGCAATATATCTGATGTACACCGGACGACGACACGCCAAAGTGGGAAAAATTTACGACATT	98337
Db	96263	CGCAATATATCTGATGTACACCGGACGACGACACGCCAAAGTGGGAAAAATTTACGACATT	96322
QY	98338	TTTAAAGATGTAACCAATTTAACTATACGGGTCTATTTTACGAGTGTTAACCA	98397
Db	96323	TTTAAAGATGTAACCAATTTAACTATACGGGTCTATTTTACGAGTGTTAACCA	96382
QY	98398	GTACAGGCCCACTAGCATATCGTGTGGGCAAAATTCAAATATCTTAAACCGAGTGATGC	98457
Db	96383	GTACAGGCCCACTAGCATATCGTGTGGGCAAAATTCAAATATCTTAAACCGAGTGATGC	96442
QY	98458	CGAACAGAGGATCGCGCCCTGTGGCGACATCCATTAAATCGGGTCTTCCGTCCTCCG	98517
Db	96443	CGAACAGAGGATCGCGCCCTGTGGCGACATCCATTAAATCGGGTCTTCCGTCCTCCG	96502
QY	98518	GAAATTTAAACAACGTGCTGGCGCTTTTTTAAGCCTACACCCCGTGGCAACGCTACAAA	98577
Db	96503	GAAATTTAAACAACGTGCTGGCGCTTTTTTAAGCCTACACCCCGTGGCAACGCTACAAA	96562
QY	98578	AATCTACAAAGCAATAACCGTCGTACGTAAATAGAGCTTTGTTCGAATATAGCGGCAACAA	98637
Db	96563	AATCTACAAAGCAATAACCGTCGTACGTAAATAGAGCTTTGTTCGAATATAGCGGCAACAA	96622
QY	98638	ATCGTGGGGTACATCGCGCTCGCAGAGAGCGCCCGGCTAACCGCATACAGACCGCGCA	98697
Db	96623	ATCGTGGGGTACATCGCGCTCGCAGAGAGCGCCCGGCTAACCGCATACAGACCGCGCA	96682
QY	98698	ACCAAGACAGAGGTCGCGTGTGCGGCCCAAGTTATACGAAATATATGACGCGCTCCAAAT	98757
Db	96683	ACCAAGACAGAGGTCGCGTGTGCGGCCCAAGTTATATGCAAAATATATGACGCGCTCCAAAT	96742
QY	98758	AAGCGCAGCAGATTATAGCAGCAGCAATCGTCTCACCGCGGATTTGCGCGGAGTTCTAT	98817
Db	96743	AAGCGCAGCAGATTATAGCAGCAGCAATCGTCTCACCGCGGATTTGCGCGGAGTTCTAT	96802
QY	98818	TAAACCAAAACGTATTCGATCCTTATAGCGAGGTGCTCCGAACACGTCCAAAAAAATCG	98877
Db	96803	TAAACCAAAACGTATTCGATCCTTATAGCGAGGTGCTCCGAACACGTCCAAAAAAATCG	96862
QY	98878	ATCGCTATTCGAAATTTGATAGGCTCAATAGCTTACGCGGACAGAGAACGACGACCTTAC	98937
Db	96863	ATCGCTATTCGAAATTTGATAGGCTCAATAGCTTACGCGGACAGAGAACGACGACCTTAC	96922
QY	98938	CCCTATACAGACGCTCGTGCGCTCGGCGTATTTTCAATATATGACATTTTGAAGAAAA	98997
Db	96923	CCCTATACAGACGCTCGTGCGCTCGGCGTATTTTCAATATATGACATTTTGAAGAAAA	96982

QY	98998	GCATCTCTCCGAGTGTGTTTACAACTGCTGGACATATCTTCAGAGAAACATTTAAGTGCAAT	99057
Db	96983	GCATTCTCCGGGTGTGTTTACAACTGCTGGACATATCTTCAGAGAAACATTTAAGTGCAAT	97042
QY	99058	ACGATAGGTGATACCGGAAAGCCACGCGCCACAGAAATTTGACAAATTAAGTACTGTTACTTT	99117
Db	97043	ACGACAGGTGATACCGGAAAGCCACGCGCCACAGAAATTTGACAAATTAAGTACTGTTACTTT	97102
QY	99118	TCAAACAATTCGAATAGCAGCGAGCTTCATTCAAACATCATGACCTTTGTAGACGACCT	99177
Db	97103	TCAAACAATTCGAATAGCAGCGAGCTTCATTCAAACATCATGACCTTTGTAGACGACCT	97162
QY	99178	CAAAAAGCGCATCCCGGTATACCTGAGACCTGTCTCTTAACTAGTGCCCGCTTTATACAT	99237
Db	97163	CAAAAAGCGCATCCCGGTATACCTGAGACCTGTCTCTTAACTAGTGCCCGCTTTATACAT	97222
QY	99238	GAAATCTAGTTCGATTCGAAGCTTGACACCGCTCGAGATTCGAAGCGAAGAGGGACAC	99297
Db	97223	GAAATCTAGTTCGATTCGAAGCTTGACACCGCTCGAGATTCGAAGCGAAGAGGGACAC	97282
QY	99298	CATCTCGTGAAGCATGTTCTGATTTCAAAATCCAGATTCGCGTCTTGAGAGAGCTCTTACA	99357
Db	97283	CATCTCGTGAAGCATGTTCTGATTTCAAAATCCAGATTCGCGTCTTGAGAGAGCTCTTACA	97342
QY	99358	GGAAACCGTTATCGCGTTAAGTCAAAACGTCGCAACCGATGATGACGACGACATCCGTCT	99417
Db	97343	GGAAACCGTTATCGCGTTAAGTCAAAACGTCGCAACCGATGATGACGACGACATCCGTCT	97402
QY	99418	GATGCAACACCTCAGCTACATCCAAAGATTCGCGGACAGCAAAATATGACGACACACT	99477
Db	97403	GATGCAACACCTCAGCTACATCCAAAGATTCGCGGACAGCAAAATATGACGACACACT	97462
QY	99478	TCCATCCGTTTCAAGAAATACAGAGGAGATATTTGCAAGTGTTTAAGCGTTTAAACG	99537
Db	97463	TCCATCCGTTTCAAGAAATACAGAGGAGATATTTGCAAGTGTTTAAGCGTTTAAACG	97522
QY	99538	TCTCATGTTTACAGCTTACGGGAAGCTGCTGCTAATCTACGTAGCCGATACTTTGGAATTCCT	99597
Db	97523	TCTCATGTTTACAGCTTACGGGAAGCTGCTGCTAATCTACGTAGCCGATACTTTGGAATTCCT	97582
QY	99598	ATATCAACCCCGCTAATACCCGATACATTCGATACAAAAATTTTAACTTAAACGCA	99657
Db	97583	ATATCAACCCCGCTAATACCCGATACATTCGATACAAAAATTTTAACTTAAACGCA	97642
QY	99658	AACGACACACACCGACAGCATCTTAAAGACCTGTACAGCCGCTGACAGCAAGACCTCT	99717
Db	97643	AACGACACACACCGACAGCATCTTAAAGACCTGTACAGCCGCTGACAGCAAGACCTCT	97702
QY	99718	ATCGGCTGA AAAAGTAGAGTGCACCTCAAAAAACAAGTTGAGCTGCTCAAAA	99777
Db	97703	ATCGGCTGA AAAAGTAGAGTGCACCTCAAAAAACAAGTTGAGCTGCTCAAAA	97762
QY	99778	ACTGTACGACGACTTTCGACCGCTCCACAAACAATAACCCACCTGATTTAACTTGA	99837
Db	97763	ACTGTACGACGACTTTCGACCGCTCCACAAACAATAACCCACCTGATTTAACTTGA	97822
QY	99838	ATATTGCGGTATTTTAAAGAAACACAATGTCCGATGATTTGGAGACATATAACCGGT	99897
Db	97823	ATATTGCGGTATTTTAAAGAAACACAATGTCCGATGATTTGGAGACATATAACCGGT	97882
QY	99898	GACATACACCCGACCCGAGATACGTTAAATTTACCCCGTTTAAACGAGGACACTAGA	99957
Db	97883	GACATACACCCGACCCGAGATACGTTAAATTTACCCCGTTTAAACGAGGACACTAGA	97942
QY	99958	TCGCATGTTTGCAGAAATAAGCATGGAATTCGCCCAATTTTTTGCAGAAATTTAAATAGA	100017
Db	97943	TCGCATGTTTGCAGAAATAAGCATGGAATTCGCCCAATTTTTTGCAGAAATTTAAATAGA	98002
QY	100018	GGCGCTGGCAAGCAGCAACCAAGCCGATCGCAGGTTCGGACAATACGCCGCTCGAGT	100077
Db	98003	GGCGCTGGCAAGCAGCAACCAAGCCGATCGCAGGTTCGGACAATACGCCGCTCGAGT	98062
QY	100078	CTTAAGCAACTCGTTATCTACCTCGCACAAAGTTATTTCAATAGAGAGTCCCCGCTGAC	100137

Db 98063 CTTAAGCACTGCGTTATCTACTCGCACAAAGTTATTTCAATAGAGTCCCGCGTGCAC 98122
QY 100138 GGACACTAAAGCACTGAGAGAGCTTTTACGGCAAGGGGAGAGCTTTGACTTTATATCTGAG 100197
Db 98123 GGACACTAAAGCACTGAGAGAGCTTTTACGGCAAGGGGAGAGCTTTGACTTTATATCTGAG 98182
QY 100198 AGGCTCCGGGAGAGCTGCGCTATACCAATATGCCCCAAGTGCACACATACCAAGCTTTAT 100257
Db 98183 AGGCTCCGGGAGAGCTGCGCTATACCAATATGCCCCAAGTGCACACATACCAAGCTTTAT 98242
QY 100258 CAAGACCAAGAGTGAAGCGCGCCATCTTTCAATCTCAGAGTACTTTGAGATATATG 100317
Db 98243 CAAGACCAAGAGTGAAGCGCGCCATCTTTCAATCTCAGAGTACTTTGAGATATATG 98302
QY 100318 ACTTGAAGCGGCGCATCCGGGAACCTTTCAATCGAATCCCTAAATCGATCTTAAGCGGAAA 100377
Db 98303 ACTTGAAGCGGCGCATCCGGGAACCTTTCAATCGAATCCCTAAATCGATCTTAAGCGGAAA 98362
QY 100378 TTACGCGCGGCGCATCTTCAATCTTGTATATGCGGCGACAAAGCGGCGCTAAT 100437
Db 98363 TTACGCGCGGCGCATCTTCAATCTTGTATATGCGGCGACAAAGCGGCGCTAAT 98422
QY 100438 TATCAAAAACAAAAGCTTTTACCTGTTGATCCCATTTGCGTACCCAGCTACCAATAG 100497
Db 98423 TATCAAAAACAAAAGCTTTTACCTGTTGATCCCATTTGCGTACCCAGCTACCAATAG 98482
QY 100498 TCCGGCACAGTATATGTTGCTCAGACCCCAAGCGCATATAGAGTACGTGCACGCGC 100557
Db 98483 TCCGGCACAGTATATGTTGCTCAGACCCCAAGCGCATATAGAGTACGTGCACGCGC 98542
QY 100558 AAGACAGATATACCTGCGAGTTTCTATATACATATAGCCAGCGAATATGTCATACAA 100617
Db 98543 AAGACAGATATACCTGCGAGTTTCTATATACATATAGCCAGCGAATATGTCATACAA 98602
QY 100618 GCACATACATACCAACCACTATAGAACTATAGAGTATAGCGGCGGCGGCGACAT 100677
Db 98603 GCACATACATACCAACCACTATAGAACTATAGAGTATAGCGGCGGCGGCGACAT 98662
QY 100678 AATATATATCCACCGCGCATATAGAGCGCGTGCACATCGAAGACATCCCAAGCGCGCGGATC 100737
Db 98663 AATATATATCCACCGCGCATATAGAGCGCGTGCACATCGAAGACATCCCAAGCGCGCGGATC 98722
QY 100738 GCGGATGAGTGAATCAATCAACCTGCGAGCGCGGCGGAGACCAACCAAGCGACAC 100797
Db 98723 GCGGATGAGTGAATCAATCAACCTGCGAGCGCGTGCAGAGCGGAGACCAACCAAGCGAC 98782
QY 100798 GTCGAGCGGCAACCCCGCACCGGCGAGCTATCCGCTTACGGGCGGCGGAGACCAAGCGAC 100857
Db 98783 GTCGAGCGGCAACCCCGCACCGGCGAGCTATCCGCTTACGGGCGGCGGAGACCAAGCGAC 98842
QY 100858 AAGCTACCGAGACCGGCGCAACCAAGCGAGCGGAGACCAAAAGCTTTAATCCCGCTCCAGC 100917
Db 98843 AAGCTACCGAGACCGGCGCAACCAAGCGAGCGGAGACCAAAAGCTTTAATCCCGCTCCAGC 98902
QY 100918 GGAACCGCGCGTGCAGACCAACCGGAATCCCAACCAACCTGAGAGCGACCTACTTCTTC 100977
Db 98903 GGAACCGCGCGTGCAGACCAACCGGAATCCCAACCAACCTGAGAGCGACCTACTTCTTC 98962
QY 100978 AGAAGTGTGCGATCCAGAGGTCGGAAGAGCAAGCTTTCCAGCTTCCAGCGATATTCGGA 101037
Db 98963 AGAAGTGTGCGATCCAGAGGTCGGAAGAGCAAGCTTTCCAGCTTCCAGCGATATTCGGA 99022
QY 101038 TTCCGACGAAGCGTGTCTGACGAGCAAGGGGCGCCAGCTAGCGGCTACAGAGCATG 101097
Db 99023 TTCCGACGAAGCGTGTCTGACGAGCAAGGGGCGCCAGCTAGCGGCTACAGAGCATG 99082
QY 101098 GATATCCGCGGAGTGTGATGAGAGCATATATCTCTCTATATATTCACCGTGC 101157
Db 99083 GATATCCGCGGAGTGTGATGAGAGCATATATCTCTCTATATATTCACCGTGC 99142
QY 101158 GACTCATGCTTGAAGAGCTGTGAGAGCGCGCCCAATGAGACCGGAGTTTACATAGCA 101217
|||||

Db 99143 GACTCATGCTTTGACAGAGCTGTTGCAGACCCCGCAATGACCCGAGTTTACATAGCA 99202
QY 101218 AGACGGGACAGAGAGCAAGATGCGGCTTTAGAACAGATGCTCGAGCGGAGAAC 101277
Db 99203 AGACGGGACAGAGAGCAAGATGCGGCTTTAGAACAGATGCTCGAGCGGAGAAC 99262
QY 101278 GCGGCTCTGCGGTTGAGAGAGCTTATACGGAGACGAGCTTTCTCCCTGATTAATAA 101337
Db 99263 GCGGCTCTGCGGTTGAGAGAGCTTATACGGAGACGAGCTTTCTCCCTGATTAATAA 99322
QY 101338 AATGAGACGTTATATCAATAGCAAGCGGCTTCGAGACCTGCGCAACATCTCGGACAA 101397
Db 99323 AATGAGACGTTATATCAATAGCAAGCGGCTTCGAGACCTGCGCAACATCTCGGACAA 99382
QY 101398 ACAAAAGCGGCGAGCGGCTCGAGAAAGCGGCGGCTTCAGGCGATGAGACAAATATGAT 101457
Db 99383 ACAAAAGCGGCGAGCGGCTCGAGAAAGCGGCGGCTTCAGGCGATGAGACAAATATGAT 99442
QY 101458 TATATCATCTTTGAACAGAGTCTATTTACAGACGGGAGCGGCGGAGCGGCGGCTG 101517
Db 99443 TATATCATCTTTGAACAGAGTCTATTTACAGACGGGAGCGGCGGAGCGGCGGCTG 99502
QY 101518 CAAAAGCTTTCTCAATTTTTCATCCTGTGGGAGAAAACCTCAACATACCAATAAGCA 101577
Db 99503 CAAAAGCTTTCTCAATTTTTCATCCTGTGGGAGAAAACCTCAACATACCAATAAGCA 99562
QY 101578 CCGCAAGAGGCTCTAGAACTGATCTGCACTGATACCGTTACATACGCTATACGCA 101637
Db 99563 CCGCAAGAGGCTCTAGAACTGATCTGCACTGATACCGTTACATACGCTATACGCA 99622
QY 101638 AGGAAATTCAAAACGAGGCGGCTTCAAAAACCTCAACCTCAAAATCAACCGGCT 101697
Db 99623 AGGAAATTCAAAACGAGGCGGCTTCAAAAACCTCAACCTCAAAATCAACCGGCT 99682
QY 101698 GCGGCTCAATGAGGCGGCGGCGGCTTCAAAAACCTCAACCTCAAAATCAACCGGCT 101757
Db 99683 GCGGCTCAATGAGGCGGCGGCGGCTTCAAAAACCTCAACCTCAAAATCAACCGGCT 99742
QY 101758 CGAAGGCTCAGAGATTTGCTCAGAGAGCAAGAAATATATGCTCGGCGCTCAGAGACA 101817
Db 99743 CGAAGGCTCAGAGATTTGCTCAGAGAGCAAGAAATATATGCTCGGCGCTCAGAGACA 99802
QY 101818 GATCGGCAACCACTGAGTCCAGGCTTTTACGGGCTCTCTCGGCGGAGAGGATTAACA 101877
Db 99803 GATCGGCAACCACTGAGTCCAGGCTTTTACGGGCTCTCTCGGCGGAGAGGATTAACA 99862
QY 101878 TCTACGGGATTAATTTCAAGAGCTTAAACCAAGGATCGAGAGCGGCAACCAAGAAATCA 101937
Db 99863 TCTACGGGATTAATTTCAAGAGCTTAAACCAAGGATCGAGAGCGGCAACCAAGAAATCA 99922
QY 101938 ACAGGAGAGAGCTTTTTGATGCACTGCTCAGAGCGCTGCAACGCTTCAACCCCTTC 101997
Db 99923 ACAGGAGAGAGCTTTTTGATGCACTGCTCAGAGCGCTGCAACGCTTCAACCCCTTC 99982
QY 101998 GAAACGGGATTTCAATGAGATCTTCCGAGCGGTAACCGAAGTATATCTCGACA 102057
Db 99983 GAAACGGGATTTCAATGAGATCTTCCGAGCGGTAACCGAAGTATATCTCGACA 102042
QY 102058 CCTGGGCTCATTAACCAAGGTTAAACGAGAGAGCGCAACGAGCGCTTCAACATTAAT 102117
Db 100043 CCTGGGCTCATTAACCAAGGTTAAACGAGAGAGCGCAACGAGCGCTTCAACATTAAT 100102
QY 102118 GGAGACCCCGCGGACCAAGAGCAAGCACTTACCAACATTTTCATCATGCT 102177
Db 100103 GGAGACCCCGCGGACCAAGAGCAAGCACTTACCAACATTTTCATCATGCT 100162
QY 102178 GGCAAAATATCATATCAGCTTAAATACTTAACGATACGAGAAAGAGATGCAATTA 102237
Db 100163 GGCAAAATATCATATCAGCTTAAATACTTAACGATACGAGAAAGAGATGCAATTA 100222
QY 102238 CATAAGCGGCTGAGAGCTGAGGCTGATGTTGATACCTCGGAGGAGGATTTAGAAC 102297
Db 100223 CATAAGCGGCTGAGAGCTGAGGCTGATGTTGATACCTCGGAGGAGGATTTAGAAC 100282
|||||

QY	102298	CATCTTTAATTTAGAGTGGCCATACGAAACCGTGCACCGGTTTCAAGACTGCCCTCGT	102357
Db	100283	CATCTTTAATTTAGAGTGGCCATACGAAACCGTGCACCGGTTTCAAGACTGCCCTCGT	100342
QY	102358	GGCGGGGGCGAAAGCAAAAATGGAATCGGTAAACAAAATGGAAGAACCAACAGGCTCT	102417
QY	102418	CGACCAATTAATCTGGGAGAGCGCCGAAACGTTACTTTGACACAAATACCGCAACATCCGGAGA	102477
Db	100403	CGACCAATTAATCTGGGAGAGCGCCGAAACGTTACTTTGACACAAATACCGCAACATCCGGAGA	100462
QY	102478	TGAGAACCCCGTTCGGCCGCAATGCTCATACGATCTGTGAGACCTTACATTACAAGCAGG	102537
Db	100463	TGAGAACCCCGTTCGGCCGCAATGCTCATACGATCTGTGAGACCTTACATTACAAGCAGG	100522
QY	102538	CGCCCTGATPAGGCACTTCTCGAAGACAGGGTTCGAAAATGCAAGGGCGGCATCCAGCA	102597
Db	100523	CGCCCTGATPAGGCACTTCTCGAAGACAGGGTTCGAAAATGCAAGGGCGGCATCCAGCA	100582
QY	102598	CCTGGCATCATCGAGATCGTTTCATATAATGCTGCTAAACAACACGGCGCTCGATTAACAT	102657
Db	100583	CCTGGCATCATCGAGATCGTTTCATATAATGCTGCTAAACAACACGGCGCTCGATTAACAT	100642
QY	102658	ATCAGACAAATCTGGCGCCAAAGATGACAGGGCATCTGTGACAAACAACACAGCTTTTCTTCAA	102717
Db	100643	ATCAGACAAATCTGGCGCCAAAGATGACAGGGCATCTGTGACAAACAACACAGCTTTTCTTCAA	100702
QY	102718	CGCCCACTGTTAGCAAAAGCGCTCCAAACGCTGGGAGGACGCTTAATCGGGAATGCGTAGA	102777
Db	100703	CGCCCACTGTTAGCAAAAGCGCTCCAAACGCTGGGAGGACGCTTAATCGGGAATGCGTAGA	100762
QY	102778	AGCGCTAATAATAAAGAGAGCCCTCTTCCCTCAACAACGCGGCTTCTCGCGGTTCAAC	102837
Db	100763	AGCGCTAATAATAAAGAGAGCCCTCTTCCCTCAACAACGCGGCTTCTCGCGGTTCAAC	100822
QY	102838	CATACTGGGGGACAGGCTCCGTTCCAGATACAGAGACGCTGACGGCGAATGCTTTCGGGCGT	102897
Db	100823	CATACTGGGGGACAGGCTCCGTTCCAGATACAGAGACGCTGACGGCGAATGCTTTCGGGCGT	100882
QY	102898	CGCCAGCGCACAAAAGAAATCCGCTGGGCGATATCCAGATAGGTGGACCGCGAATACCGG	102957
Db	100883	CGCCAGCGCACAAAAGAAATCCGCTGGGCGATATCCAGATAGGTGGACCGCGAATACCGG	100942
QY	102958	TCACCTAAACGAGCTGAAGCTGTGAATACCCAAATCGCGTTCGACAAAAGCCACAGCGG	103017
Db	100943	TCACCTAAACGAGCTGAAGCTGTGAATACCCAAATCGCGTTCGACAAAAGCCACAGCGG	101002
QY	103018	CAAACTGTAATGATATAATACCCGAGCACTCAAGAGAGGGGAGGTGCTTCAGAGAAACGCT	103077
Db	101003	CAAACTGTAATGATATAATACCCGAGCACTCAAGAGAGGGGAGGTGCTTCAGAGAAACGCT	101062
QY	103078	CCTGGAACACAGCGTGGCAAGAAAGTGTCTAAAGTTTCAACCGTGCAGCTCCAAAGAAAT	103137
Db	101063	CCTGGAACACAGCGTGGCAAGAAAGTGTCTAAAGTTTCAACCGTGCAGCTCCAAAGAAAT	101122
QY	103138	CGAAGACTTTTACACGTGGGCAACCGTCACGCAAAAGCCGGAATTTGCAAGAAAACACT	103197
Db	101123	CGAAGACTTTTACACGTGGGCAACCGTCACGCAAAAGCCGGAATTTGCAAGAAAACACT	101182
QY	103198	ACGGACGCTGATCACCAATTCOAAGGGCAGAGAGGACCGCGCTCCGAGGCCACCGCGCT	103257
Db	101183	ACGGACGCTGATCACCAATTCOAAGGGCAGAGAGGACCGCGCTCCGAGGCCACCGCGCT	101242
QY	103258	TCGCATGAGTACACGCGGACGCCCATACCCACGCGCACAGGCGGTTTCTAGGCGTCCCG	103317
Db	101243	TCGCATGAGTACACGCGGACGCCCATACCCACGCGCACAGGCGGTTTCTAGGCGTCCCG	101302
QY	103318	GGAAAAGGAAAAGGCCGCGATGGAATPAAAATTCACAGGCGCTTTCAGAGATTTCAACTTCA	103377
Db	101303	GGAAAAGGAAAAGGCCGCGATGGAATPAAAATTCACAGGCGCTTTCAGAGATTTCAACTTCA	101362

QY	103378	CCTCATGACGCTTTCGGATTGGCAAGAGATGGCATCTCGAATACCTCCAGACACGGCTGTC	103437
Db	101363	CCTATCGACGCTTTCGGATTGGCAAGAGATGGCATCGAATACCTCCAGACACGGCTGTC	101422
QY	103438	CCTTCCTGGTACGGTTGGACCAAGAAGCTGTGCTGCTCATGGAGAGCATATCTCAACACCT	103497
Db	101423	CCTTCCTGGTACGGTTGGACCAAGAAGCTGTGCTGCTCATGGAGAGCATATCTCAACACCT	101482
QY	103498	GGAGACATCCTCAACGCGAAGAGCTGGCATCTCTGCTTCCAAACGGGCCGGCTTCAGAAC	103557
Db	101483	GGAGACATCCTCAACGCGAAGAGCTGGCATCTCTGCTTCCAAACGGGCCGGCTTCAGAAC	101542
QY	103558	CCGACGCTTTGACTGATCGCGGCCCTATCAAAACACGCGTTAAACGCTTTCTAAAACCAT	103617
Db	101543	CCGACGCTTTGACTGATCGCGGCCCTATCAAAACACGCGTTAAACGCTTTCTAAAACCAT	101602
QY	103618	AGGCGTGGCCATGGTGGCGCAACCTGGCGGACAGATGCTATCCATACCAATGGCCAAACCTGCAG	103677
Db	101603	AGGCGTGGCCATGGTGGCGCAACCTGGCGGACAGATGCTATCCATACCAATGGCCAAACCTGCAG	101662
QY	103678	TCACGCGGTGCAATCCGCGAGACCTTTCACACAGGCCACGGTGGGAACAGTTTGAAGCAGCC	103737
Db	101663	TCACGCGGTGCAATCCGCGAGACCTTTCACACAGGCCACGGTGGGAACAGTTTGAAGCAGCC	101722
QY	103738	CGCGGCCCAATATCTGTGCATATATCTCTGACATGTGCAAGTGGCGCTTTCACACGACCGAGAT	103797
Db	101723	CGCGGCCCAATATCTGTGCATATATCTCTGACATGTGCAAGTGGCGCTTTCACACGACCGAGAT	101782
QY	103798	CGCGCTTAAGATCGGAGCGCGCGGGCTACACGGACGCATTAACCTCGCGCGGCAACGTCGT	103857
Db	101783	CGCGCTTAAGATCGGAGCGCGGGCTACACGGACGCATTAACCTCGCGCGGCAACGTCGT	101842
QY	103858	GACTGCCCGGAAACCCAACTTAGAAGCCCGCCAGAAAGCTTAATTAACGGCACTGACGGCCT	103917
Db	101843	GACTGCCCGGAAACCCAACTTAGAAGCCCGCCAGAAAGCTTAATTAACGGCACTGACGGCCT	101902
QY	103918	AACGTCGAGACGCTTTCAGATTTCTTAAAAAGCTCAATCTCTTCAACAGAGACGCGACT	103977
Db	101903	AACGTCGAGAGCTTTCAGATTTCTTAAAAAGCTCAATCTCTTCAACAGAGACGCGACT	101962
QY	103978	CATTGCGGTCCAGAGAGCGGAGATTTACAGCACTAGAGGCCAGCATCTGGCGGCCGAGACG	104037
Db	101963	CATTGCGGTCCAGAGAGCGGAGATTTACAGCACTAGAGGCCAGCATCTGGCGGCCGAGACG	102022
QY	104038	GCTCCGCAATCCACCCCTGACGAGATGCGAGGCCAAGATGGCAACCGCTATCAGCGCACT	104097
Db	102023	GCTCCGCAATCCACCCCTGACGAGATGCGAGGCCAAGATGGCAACCGCTATCAGCGCACT	102082
QY	104098	CTTACCCCGCGCCCGCTGTCGCATATATCATCGAGACGTTGAACCTTATCAAAACCTATAGA	104157
Db	102083	CTTACCCCGCGCCCGCTGTCGCATATATCATCGAGACCGTTGAACCTTATCAAAACCTATAGA	102142
QY	104158	CTTTTGGATTCAACGATATGACGCAAAATCCTGSCACAAGAGGCTTACGAGACAGCCAT	104217
Db	102143	CTTTTGGATTCAACGATATGACGCAAAATCCTGSCACAAGAGGCTTACGAGACAGCCAT	102202
QY	104218	AGCGGATATCGCGTGGCTGGAAATCGCGACAAATCCGTAAATGGTCTACAGTCAACAAAA	104277
Db	102203	AGCGGATATCGCGTGGCTGGAAATCGCGACAAATCCGTAAATGGTCTACAGTCAACAAAA	102262
QY	104278	CGAAACGCAACGTTAAAGCTATCTGAGCGAGGTAGAAAAACAGACACCGTCGCGCA	104337
Db	102263	CGAAACGCAACGTTAAAGCTATCTGAGCGAGGTAGAAAAACAGACACCGTCGCGCA	102322
QY	104338	GCGTCTAACGATTTTGGAACTGTGGCGCAAAACACGAGACGATTAAGGTGTGAAGCA	104397
Db	102323	GCGTCTAACGATTTTGGAACTGTGGCGCAAAACACGAGACGATTAAGGTGTGAAGCA	102382
QY	104398	GGCGGTATACGAACTCGCGGCCCTTCAGGGTTAAAGGCGGAAAAACACACCTGAGACGGGTG	104457
Db	102383	GGCGGTATACGAACTCGCGGCCCTTCAGGGTTAAAGGCGGAAAAACACACCTGAGACGGGTG	102442
QY	104458	GAAACAAAAACTGGAAAGCATAGATCCCTGCTTCGCGCCACGAGAGACGGCAGCGAAT	104517

D	102443	GAACAAAACTGGAAAGCATTAATCCGTTCGGCCAGAGGCGCAGCGAAAT	102502
Q	104518	ATCATCGAGACTTGAACGATCGGCACACAGGCGTTGGCACCATCCCGCATTT	104577
D	102503	ATCATCGAGACTTGAACGATCGGCACACAGGCGTTGGCACCATCCCGCATTT	102562
Q	104578	AGAGAGCTCTCCGATCAATGCGGGAGCGGCAATTTCTTCAGAGCGCATCTACC	104637
D	102563	AGAGAGCTCTCCGATCAATGCGGGAGCGGCAATTTCTTCAGAGCGCATCTACC	102622
Q	104638	CGAAGGCTTCTGGACATTAGGCAAAACCTCAGCGAGCTCAGGCGTACATTAGTCAA	104697
D	102623	CGAAGGCTTCTGGACATTAGGCAAAACCTCAGCGAGCTCAGGCGTACATTAGTCAA	102682
Q	104698	AAAACGTTTCTGGAGCATTTTGAACACCCAGCCCTAACGCTTTTCAACGCTTCCGCT	104757
D	102683	AAAACGTTTCTGGAGCATTTTGAACACCCAGCCCTAACGCTTTTCAACGCTTCCGCT	102742
Q	104758	ATCCCAAAACATATACGAAAAAGCTTCGGGCGCGCCGCGCATGACTGCGTGGCCAGCT	104817
D	102743	ATCCCAAAACATATACGAAAAAGCTTCGGGCGCGCCGCGCATGACTGCGTGGCCAGCT	102802
Q	104818	GACCAATACACTTCAGTGGCGGCGAGCGCGCCCACTTACAACTGATAGAAAGCT	104877
D	102803	GACCAATACACTTCAGTGGCGGCGAGCGCGCCCACTTACAACTGATAGAAAGCT	102862
Q	104878	ACCGACCTTCGATCCGAAAAAACCACTACGTCGCGCGCGCAGGAGAGCCCTGTGCA	104937
D	102863	ACCGACCTTCGATCCGAAAAAACCACTACGTCGCGCGCGCAGGAGAGCCCTGTGCA	102922
Q	104938	CGCGCGATACGATCTCAAAAGCTCCTAGAGGCGTGTTCATATATGTTCCACACGCT	104997
D	102923	CGCGCGATACGATCTCAAAAGCTCCTAGAGGCGTGTTCATATATGTTCCACACGCT	102982
Q	104998	AACCCCGGTTCCAGACGGCCCGCGTCTGAAATCGCAACCAAGGAGCAGCGCGGGAGA	105057
D	102983	AACCCCGGTTCCAGACGGCCCGCGTCTGAAATCGCAACCAAGGAGCAGCGCGGGAGA	103042
Q	105058	GGCGCGACGTGATGAGACAGACAGTGGCCGACATGCGTCAGAGCGTCCAGAGCTTCT	105117
D	103043	GGCGCGACGTGATGAGACAGACAGTGGCCGACATGCGTCAGAGCGTCCAGAGCTTCT	103102
Q	105118	CGACAGTACGAGACACACCGCCCAAGCAACCGGAGCGGCGCAATTAACGATTTCTT	105177
D	103103	CGACAGTACGAGACACACCGCCCAAGCAACCGGAGCGGCGCAATTAACGATTTCTT	103162
Q	105178	GGCGATGTGCTTTTACGCAATTCATCAAGGGCGCTAGCAGAGCCGTGACGCTCCGAA	105237
D	103163	GGCGATGTGCTTTTACGCAATTCATCAAGGGCGCTAGCAGAGCCGTGACGCTCCGAA	103222
Q	105238	GTTACCGAGACCGCGCGTGTTCCTCAGAGATGCTTTAACAACCCAGGGAATGAC	105297
D	103223	GTTACCGAGACCGCGCGTGTTCCTCAGAGATGCTTTAACAACCCAGGGAATGAC	103282
Q	105298	AACACTGGTACCGGCGCATGGGCGCAACCGCGGCGCGCAATTTACGATTAATCTTA	105357
D	103283	AACACTGGTACCGGCGCATGGGCGCAACCGCGGCGCGCAATTTACGATTAATCTTA	103342
Q	105358	CTCGGAAGCCCTAGACTAATGATGTTTCCCTCCGCTAATTTCCAGCGCGTGGCGCA	105417
D	103343	CTCGGAAGCCCTAGACTAATGATGTTTCCCTCCGCTAATTTCCAGCGCGTGGCGCA	103402
Q	105418	CCTAACGCTAGAGCGCCAGGCTCAAAAAGCGCCACATTAACACCCCGCTAGTTGAGATG	105477
D	103403	CCTAACGCTAGAGCGCCAGGCTCAAAAAGCGCCACATTAACACCCCGCTAGTTGAGATG	103462
Q	105478	CTTTGGCAAAACAGAGCAATTCCTGATTTCCCGGGGCAATGGCATTCAGCGAAGCTTAA	105537
D	103463	CTTTGGCAAAACAGAGCAATTCCTGATTTCCCGGGGCAATGGCATTCAGCGAAGCTTAA	103522
Q	105538	GGAGAGCTGTGGGAGACAGGCACTTTTGCAAATCTGGAATTAACATCAACGCAAGG	105597
D	103523	GGAGAGCTGTGGGAGACAGGCACTTTTGCAAATCTGGAATTAACATCAACGCAAGG	103582
Q	105598	CAGGTTGGCGGCGCGTCACTTGGCGGCTCAGACGATAGAGCGCGGTGTTTGGACCAACT	105657
D	103583	CAGGTTGGCGGCGCGTCACTTGGCGGCTCAGACGATAGAGCGCGGTGTTTGGACCAACT	103642
Q	105658	GTTGTCACATTTTAAACCCATGACAGCGCGGTGAGAGACAGTACTGACTAGTCA	105717
D	103643	GTTGTCACATTTTAAACCCATGACAGCGCGGTGAGAGACAGTACTGACTAGTCA	103702
Q	105718	GACCTTACACTGACCACTTTGGCGCGCGGTCCCAACCGCAGGCGAAGCAACGACAC	105777
D	103703	GACCTTACACTGACCACTTTGGCGCGCGGTCCCAACCGCAGGCGAAGCAACGACAC	103762
Q	105778	CGAGACCGCGCTACAGTACGAGACAGCCAGGCGCTACTGCTCGGCTCAATGAC	105837
D	103763	CGAGACCGCGCTACAGTACGAGACAGCCAGGCGCTACTGCTCGGCTCAATGAC	103822
Q	105838	GAGCGCGTCCAGGCTTCAAAACACACCGGATCCGCTTTCGAGGCGGTGCTGGAGCAAT	105897
D	103823	GAGCGCGTCCAGGCTTCAAAACACACCGGATCCGCTTTCGAGGCGGTGCTGGAGCAAT	103882
Q	105898	GGTGTTACAGTACGATCAGATATTTTGGCGCGCACGCGCAAGCGCTTGGCCAGGC	105957
D	103883	GGTGTTACAGTACGATCAGATATTTTGGCGCGCACGCGCGCAAGCGCTTGGCCAGGC	103942
Q	105958	GGCGGGCGGATGGGCTCTCTACACCATCTGGAATGCGTCCGAGCTGAGCGCTT	106017
D	103943	GGCGGGCGGATGGGCTCTCTACACCATCTGGAATGCGTCCGAGCTGAGCGCTT	104002
Q	106018	CAAAAGCTGTATTAAGGCAACCGCGCAACCGCGGCAATGG-AAAAGCTAACCGCGATCC	106076
D	104003	CAAAAGCTGTATTAAGGCAACCGCGCAACCGCGGCAATGG-AAAAGCTAACCGCGATCC	104061
Q	106077	TCCACCGCGACGAGCGACAGTCTTTTGAAGACAGCAGTGGTATCTTACCGAT	106136
D	104062	TCCACCGCGACGAGCGACAGTCTTTTGAAGACAGCAGTGGTATCTTACCGAT	104121
Q	106137	TCACACCAACGAAAGCGCGCGTCTGCACTCCCGGCTTGTGTGTCATAGACCTTG	106196
D	104122	TCACACCAACGAAAGCGCGCGTCTGCACTCCCGGCTTGTGTGTCATAGACCTTG	104181
Q	106197	AAAACCTCTGTAAGGCAACGATCTCCAGTGGCGGCGTGCAAATTTTCAGAGACGCGG	106256
D	104182	AAAACCTCTGTAAGGCAACGATCTCCAGTGGCGGCGTGCAAATTTTCAGAGACGCGG	104241
Q	106257	TTTACGTGATGCCCGGACCATACCCCGACACTGGCGCAAAAAGCGTGTGGTAATCAA	106316
D	104242	TTTACGTGATGCCCGGACCATACCCCGACACTGGCGCAAAAAGCGTGTGGTAATCAA	104301
Q	106317	ACACGTCGTTGACGACCTCAGCAGCAGAGAGATATGTAACTTTTACTAGCTATCCG	106376
D	104302	ACACGTCGTTGACGACCTCAGCAGCAGAGAGATATGTAACTTTTACTAGCTATCCG	104361
Q	106377	GAGAACAGGGAACGCGGCAAGGAGGATATCTCCAGCGGCTCCGACAAACGTAAC	106436
D	104362	GAGAACAGGGAACGCGGCAAGGAGGATATCTCCAGCGGCTCCGACAAACGTAAC	104421
Q	106437	CGGAACAAACCGGCAATCTCCGCGATGGGAAAAGGATTAACGATTAATTAACGAAACAG	106496
D	104422	CGGAACAAACCGGCAATCTCCGCGATGGGAAAAGGATTAACGATTAATTAACGAAACAG	104481
Q	106497	AAAACGCAAAAACCTCATATATATTCCTGCTCTTAAAGCGCGGACAGATCCACGG	106556
D	104482	AAAACGCAAAAACCTCATATATATTCCTGCTCTTAAAGCGCGGACAGATCCACGG	104541
Q	106557	TGGAACCAAGCCCGCATTTTCAAGGGCAAGCGCTCGAACAAGCAAGCAAGCAAGTAA	106616
D	104542	TGGAACCAAGCCCGCATTTTCAAGGGCAAGCGCTCGAACAAGCAAGCAAGCAAGTAA	104601
Q	106617	ACCAGCGCGGTCAATTTACTTCAACAGGCTCAAGTAAACAGCGTCAACCGCACTCAG	106676
D	104602	ACCAGCGCGGTCAATTTACTTCAACAGGCTCAAGTAAACAGCGTCAACCGCACTCAG	104661

QY	106677	CCTCATCTTTCACCGAAAAATTCAACACGCACAAACGGTGCCTTGACTAATATCTCAACGT	106736
Db	104662	CCTCATCTTTCACCGAAAAATTCAACACGCACAAACGGTGCCTTGACTAATATCTCAACGT	104721
QY	106737	CGGAAAGGGCCCATTTAAACCGACGACGCTCCGGGCAGGTCAACCGAACCGAAAGGGAACTCT	106796
Db	104722	CGGAAAGGGCCCATTTAAACCGACGACGCTCCGGGCAGGTCAACCGAACCGAAAGGGAACTCT	104781
QY	106797	TTGGAGCCTATTAACCCCGGAGTGTCTACCGAACCAGCCGCAACCCGCAACCGCGCGGCTAG	106856
Db	104782	TTGGAGCCTATTAACCCCGGAGTGTCTACCGAACCAGCCGCAACCCGCAACCGCGCGGCTAG	104811
QY	106857	CCTCTGCCCAACAGAGCAACCCACCGAGGTCCCAAGTTACGATTAATCCACCCACCG	106916
Db	104842	CCTCTGCCCAACAGAGCAACCCACCGAGGTCCCAAGTTACGATTAATCCACCCACCG	104901
QY	106917	CTAGGCGTCTTATAGGGAACGGGCTCCAAACTCTGGCAGCCGTCGAAGAGACCCACGGGG	106976
Db	104902	CTAGGCGTCTTATAGGGAACGGGCTCCAAACTCTGGCAGCCGTCGAAGAGACCCACGGGG	104961
QY	106977	CCACACCCGACGCACATCAGTCGGAAGATAGATCGGGAAAAAATACGCCGAGAGTCCGGCTTC	107036
Db	104962	CCACACCCGACGCACATCAGTCGGAAGATAGATCGGGAAAAAATACGCCGAGAGTCCGGCTTC	105021
QY	107037	GCCGACCCCCACACCTCGAAGAGGGGCCACAGGAGCTTCAGTCAACACTCCACACAGCG	107096
Db	105032	GCCGACCCCCACACCTCGAAGAGGGGCCACAGGAGCTTCAGTCAACACTCCACACAGCG	105081
QY	107097	CACACATTAACGTCCTCCCTCTACCCAAAGGTCAAAAAAGATACACGGGGCGGAAAAATCCGG	107156
Db	105082	CACACATTAACGTCCTCCCTCTACCCAAAGGTCAAAAAAGATACACGGGGCGGAAAAATCCGG	105111
QY	107157	GCCTTTCAAAACAGCAACTCCACAGCGCCGCCCAACCAACCGCATCAAAACCCGCGCATTCAT	107216
Db	105142	GCCTTTCAAAACAGCAACTCCACAGCGCCGCCCAACCAACCGCATCAAAACCCGCGCATTCAT	105201
QY	107217	ACAGCGTCCCAAGAACGAGCGCGCGTGTCTCACAGCAAGTCGAGAGTGGAAATGCACCC	107276
Db	105202	ACAGCGTCCCAAGAACGAGCGCGCGTGTCTCACAGCAAGTCGAGAGTGGAAATGCACCC	105261
QY	107277	CAACCGAGAGGTAAAGATGAGTGGCCAAAAAACAAGATGTGTCTCAAGCGGCCGGAACCGG	107336
Db	105262	CAACCGAGAGGTAAAGATGAGTGGCCAAAAAACAAGATGTGTCTCAAGCGGCCGGAACCGG	105321
QY	107337	ACGACTCCAGGTGAGCCGCCCGCTCGGTCCAACCATAGAGATTCACTGACTGGAAACACC	107396
Db	105322	ACGACTCCAGGTGAGCCGCCCGCTCGGTCCAACCATAGAGATTCACTGACTGGAAACACC	105381
QY	107397	CCCAAAATCTCAAAAATATATACATCATCTACCGTCCGCCACTCCAGAGTCAACCCCATCC	107456
Db	105382	CCCAAAATCTCAAAAATATATACATCATCTACCGTCCGCCACTCCAGAGTCAACCCCATCC	105441
QY	107457	CTCCACTTAACATCTGGAATACCCCTATCCACAGTCAACATCCCAACGCAAGAAATACAC	107516
Db	105442	CTCCACTTAACATCTGGAATACCCCTATCCACAGTCAACATCCCAACGCAAGAAATACAC	105501
QY	107517	GAGCCCAAGATGTGTTAATGCGATTTATCAAAACGTACGAAGAAAACTTCAAGCGTGT	107576
Db	105502	GAGCCCAAGATGTGTTAATGCGATTTATCAAAACGTACGAAGAAAACTTCAAGCGTGT	105561
QY	107577	CTGACAGCTATACGAGGCTATTTGCGAAGAAATGAAGTTTATATCTGTAACCGCCCATTC	107636
Db	105562	CTGACAGCTATACGAGGCTATTTGCGAAGAAATGAAGTTTATATCTGTAACCGCCCATTC	105621
QY	107637	TCACCTGCTTTTATTTATTTGAGAGAGCGTCTTGCTGCACAGATAGTTGCGTCCGTAGG	107696
Db	105622	TCACCTGCTTTTATTTATTTGAGAGAGCGTCTTGCTGCACAGATAGTTGCGTCCGTAGG	105681
QY	107697	TGATTAACGAAGTGAACCTATGCCAGAAAGACGCACACGCTCCGGGGTCCGCCACACGGGG	107756
Db	105682	TGATTAACGAAGTGAACCTATGCCAGAAAGACGCACACGCTCCGGGGTCCGCCACACGGGG	105741

QY	107757	CGCGGGGCCCATCTCGAGCCTATCAATGAATGGGGCCCCGCTGGAGATCTGTAAAGTATT	107816
Db	105742	CGCGGGGCCCATCTCGAGCCTATCAATGAATGGGGCCCCGCTGGAGATCTGTAAAGTATT	105801
QY	107817	TGACCCGAGGGGAGAGGCCACCGGGGGCAACGCTCGGGGGGGCGAGACCGGACCCGGACAA	107876
Db	105802	TGACCCGAGGGGAGAGGCCACCGGGGGCAACGCTCGGGGGGGCGAGACCGGACCCGGACAA	105861
QY	107877	AACGCCCGAGATACTAGAATAGCTGCTCTTTTGGCGGAAAGGCCCGCGGAGGTGTCTTT	107936
Db	105862	AACGCCCGAGATACTAGAATAGCTGCTCTTTTGGCGGAAAGGCCCGCGGAGGTGTCTTT	105921
QY	107937	GGCGAGATTCATTCTCTTTCATATACATGTCTGTATGATGTTTGGCGTTAAAA	107996
Db	105922	GGCGAGATTCATTCTCTTTCATATACATGTCTGTATGATGTTTGGCGTTAAAA	105981
QY	107997	CACCGAGATTAATAGCTTTCGGGATGCGATACAGGGGGGAGACATGTCACCCGGGGAAG	108056
Db	105982	CACCGAGATTAATAGCTTTCGGGATGCGATACAGGGGGGAGACATGTCACCCGGGGAAG	106041
QY	108057	GTTGTTCATCTCGGCACACAGCGGGGTATTGGTAAATGTGCTCAAGGCGTCCCTGAAC	108116
Db	106042	GTTGTTCATCTCGGCACACAGCGGGGTATTGGTAAATGTGCTCAAGGCGTCCCTGAAC	106101
QY	108117	GATTGGCTCTTAACCCCGACAGGACGACATCTCTTTAACTTCTATTACATTTCCACAG	108176
Db	106102	GATTGGCTCTTAACCCCGACAGGACGACATCTCTTTAACTTCTATTACATTTCCACAG	106161
QY	108177	GACAGGGAGATATAGAGAGGTTCAAATTAACAGCTGGGGCACACGCAAAATGCTTAAAT	108236
Db	106162	GACAGGGAGATATAGAGAGGTTCAAATTAACAGCTGGGGCACACGCAAAATGCTTAAAT	106221
QY	108237	AGGCGGCTCGCAGTCCGGCGACCCCAAAACAGGGCAGCAGACGCTAACCAAGGAGTTTC	108296
Db	106222	AGGCGGCTCGCAGTCCGGCGACCCCAAAACAGGGCAGCAGACGCTAACCAAGGAGTTTC	106281
QY	108297	GGCTCTCGATGCGATGTGCGGCTTGTGGGAGACGACACCGTAATATAGGATCTCCA	108356
Db	106282	GGCTCTCGATGCGATGTGCGGCTTGTGGGAGACGACACCGTAATATAGGATCTCCA	106341
QY	108357	ACACAGCGATCTCGAATAGATATTAACCCGCAATGTGGATCCGCCACAATTAAGGCAN	108416
Db	106342	ACACAGCGATCTCGAATAGATATTAACCCGCAATGTGGATCCGCCACAATTAAGGCAN	106401
QY	108417	TATAGCGCCCGGCTGTAGCAGATGCAAAACCTGCTCTCTTTTGGTGGGACGTGAAA	108476
Db	106402	TATAGCGCCCGGCTGTAGCAGATGCAAAACCTGCTCTCTTTTGGTGGGACGTGAAA	106461
QY	108477	AACAGCTGTGGTGGGGAATTTACGGTTTCAAAATTTACCCGCTCGGAATTTCAAAACAG	108536
Db	106462	AACAGCTGTGTGGTGGGGAATTTACGGTTTCAAAATTTACCCGCTCGGAATTTCAAAACAG	106521
QY	108537	TAACCGCACTCGAGGCACACCAACCCCTCGGAGCTGGGACGCTTCTTCCAGTACGCTTC	106591
Db	106522	TAACCGCACTCGAGGCACACCAACCCCTCGGAGCTGGGACGCTTCTTCCAGTACGCTTC	106581
QY	108597	CTGGCGACACCTGTGGGACCAAAACAGATGAGAGATACAGGAAACAGTACGTTATACGCC	108656
Db	106582	CTGGCGACACCTGTGGGACCAAAACAGATGAGAGATACAGGAAACAGTACGTTATACGCC	106641
QY	108657	AATACTTTTTGACCCAGGTGCGGGGATATCTCGCTCGGTGACTCCCTATAGGGCAAC	108716
Db	106642	AATACTTTTTGACCCAGGTGCGGGGATATCTCGCTCGGTGACTCCCTATAGGGCAAC	106701
QY	108717	ACAAACGGGACATGCTCAGCAGAGGGCCCTTAAACGTCAGGCTCTCAGAAAGGCGTTAAAC	108776
Db	106702	ACAAACGGGACATGCTCAGCAGAGGGCCCTTAAACGTCAGGCTCTCAGAAAGGCGTTAAAC	106761
QY	108777	GGGTTTGGCAGCGGAGAGCGTTCGGGCGCAGATTTTCCGAGAGGAGGCCGAAGTCCCGGCTCC	108836
Db	106762	GGGTTTGGCAGCGGAGAGCGTTCGGGCGCAGATTTTCCGAGAGGAGGCCGAAGTCCCGGCTCC	106821
QY	108837	GAAGGGCCCGGACACATCTCATTTACGTTTACGCTCCGACAGCTGTGAAATGTGACGGAAAGC	108896

106822 GAAGGGCCCGGACACTCTTCATTTCAGGTTTACGTCCTCCAGACGTTGGAAATGACGGACG 106881
108897 TTCACGTGATCGAGACACAAACCCCGCTTCCATTCTTCCGCAAAAGGGCAGATCC 108956
108882 TTCACGTGATCGAGACACAAACCCCGCTTCCATTCTTCCGCAAAAGGGCAGATCC 106941
108957 AACGCGTGTGTGGCAAAACAGTAAACAGGGGAAACCCGCTGGGACAGTTAAAGGTTTGG 109016
106942 AACGCGTGTGTGGCAAAACAGTAAACAGGGGAAACCCGCTGGGACAGTTAAAGGTTTGG 107001
109017 CACACGAGACAAACACGCCCTCTGTAAGACACAAACAGATACCTGGACACGCGCTCTG 109076
107002 CACACGAGACAAACACGCCCTCTGTAAGACACAAACAGATACCTGGACACGCGCTCTG 107061
109077 GGAAGCGCGCTTAACTTAAACCTTTCGCTGGGACAGCCACGCGGATGACAGATACAC 109136
107062 GGAAGCGCGCTTAACTTAAACCTTTCGCTGGGACAGCCACGCGGATGACAGATACAC 107121
109137 CTCAGACACCCAGCGCTACGCTCTAACAAACAGACCGCGCATATCTGTGACGCGCATCTC 109196
107122 CTCAGACACCCAGCGCTACGCTCTAACAAACAGACCGCGCATATCTGTGACGCGCATCTC 107181
109197 ACCTCGCGCTTTTATGAGTGGATTATCGGCGCTCCAGCGGATGACATCTGTTCAAGGGG 109256
107182 ACCTCGCGCTTTTATGAGTGGATTATCGGCGCTCCAGCGGATGACATCTGTTCAAGGGG 107241
109257 GTCGTGAAGGATGGGCGAGAAATTAACGTGCAAGCCCATTTTGGGGGCTGCTCCGAC 109316
107242 GTCGTGAAGGATGGGCGAGAAATTAACGTGCAAGCCCATTTTGGGGGCTGCTCCGAC 107301
109317 GCACCGACCGCGCTACGCTACAAACACAGCTACGATTTGGGGGCTGCTCCGAC 109376
107302 GCACCGACCGCGCTACGCTACAAACACAGCTACGATTTGGGGGCTGCTCCGAC 107361
109377 ATGAGGCGCGGAGATCTTAAGCCCGACCGAGACATCCAGCCAGATGGGAGATTA 109436
107362 ATGAGGCGCGGAGATCTTAAGCCCGACCGAGACATCCAGCCAGATGGGAGATTA 107421
109437 GAAAGCGCGCGATGACAGGACGCTTCTTCAGCGAGTTTAAAGCGGCGGCGGAGGCG 109496
107422 GAAAGCGCGCGATGACAGGACGCTTCTTCAGCGAGTTTAAAGCGGCGGCGGAGGCG 107481
109497 ATCCCGCAATGACGATGATGATTTGTTAATTTGGTCATCGCCGCA -CGCTCTCGCGCGC 109555
107482 ATCCCGCAATGATGATGATTTGTTAATTTGGTCATCGCGCACCGCTCTCGCGCGC 107541
109556 CAATATCTTCAACTCCGACCCGAGAGGGGCGCACGAGCGCGTTCGCTCAAGCAC 109615
107542 CAATATCTTCAACTCCGACCCGAGAGGGGCGCACGAGCGCGTTCGCTCAAGCAC 107601
109616 CGAGGCGGTGGAAGTGA -CCCGTCAGGGGCAAAACCGTCTTAAGAAAGGTTTTTAAACGT 109674
107602 CGAGGCGGTGGAAGTGAAGCCCGTCAAGGCAAAACCGTCTTAAGAAAGGTTTTTAAACGT 107661
109675 TTAGCGCTTTTGGATGACAGACCAAAACGTAAACCTGTGCGGTCTCCGTAAGTGA 109734
107662 TTAGCGCTTTTGGATGACAGACCAAAACGTAAACCTGTGCGGTCTCCGTAAGTGA 107721
109735 GTGCGGATATGACATGAGAGCTGTAAAGGTTTAAAGTCTCCGAGAAACAGAGCTGGC 109794
107722 GTGCGGATATGACATGAGAGCTGTAAAGGTTTAAAGTCTCCGAGAAACAGAGCTGGC 107781
109795 TTAAATTTTCAAAATCGTCTGGGCGCAGGAGACAGGAGAGTTCTCTCAAGATACAG 109854
107782 TTAAATTTTCAAAATCGTCTGGGCGCAGGAGACAGGAGAGTTCTCTCAAGATACAG 107841
109855 TCCGATTTATATAGGAGGTTTTTTCAAACGTGGGCTCGGCTACGCTGTTACCAAA 109914
107842 TCCGATTTATATAGGAGGTTTTTTCAAACGTGGGCTCGGCTACGCTGTTACCAAA 107901
109915 AAACATTTTCAGGCTGTGGCGCAACCGTGTGATTAATTAACAAACAGGGGCAAAAGGCG 109974

107902 AAACATTTTCAGGCTGTGGCGCAGACCGCTTCTGATATTAATTAACAAACAGGGGCAAAAGGCG 107961
109975 TAGGCGAGTCTCTAGTTTGTGAGCCAAACTTAACAAATCGAGATGATAGC 110034
107962 TAGGCGAGTCTCTAGTTTGTGAGCCAAACTTAACAAATCGAGATGATAGC 108021
110035 CAGCGGTGTGACAGGGGCAACGGTGCACAGGGGACCGCCCGCTTATAGGTTTACGGGA 110094
108022 CAGCGGTGTGACAGGGGCAACGGTGCACAGGGGACCGCCCGCTTATAGGTTTACGGGA 108081
110095 GCCCGCTCCGACACCTCTCAAGTCCAGGAGATTCAGAGGGTCCAGAGTAAGAGACA 110154
108082 GCCCGCTCCGACACCTCTCAAGTCCAGGAGATTCAGAGGGTCCAGAGTAAGAGACA 108141
110155 ACTAAATCGACAGCTGTCACTAAACGTTTTCCGGAATCAATCGTTATTAAGATCTT 110214
108142 ACTAAATCGACAGCTGTCACTAAACGTTTTCCGGAATCAATCGTTATTAAGATCTT 108201
110215 TAGGTGCTGTGGCTGGCTCCGTTAAACCGGCTCCGTTGATACGATTTTGTAAATGACC 110274
108202 TAGGTGCTGTGGCTGGCTCCGTTAAACCGGCTCCGTTGATACGATTTTGTAAATGACC 108261
110275 TGTTTACGGCGTTTACCTTGGGCTCAGAGACATGAGTCAAGTACAGTACGCGC 110334
108262 TGTTTACGGCGTTTACCTTGGGCTCAGAGACATGAGTCAAGTACAGTACGCGC 108321
110335 GTCGTGACAGATGACAGAGAAATTTTAAATACGACAGTAAATGCGTTGAGC 110394
108322 GTCGTGACAGATGACAGAGAAATTTTAAATACGACAGTAAATGCGTTGAGC 108381
110395 CTGGAATATATGTTGGGAAACATATTTTCAATCTCAGCGGAGCGAGGACCTGCAAGCGC 110454
108382 CTGGAATATATGTTGGGAAACATATTTTATGTCATCGGAGCGAGGACTGCAAGCGC 108441
110455 AATTAATCGTCAACCGAAATCACTACGTGAGAGAGTAAAGATGCTCACCGCGGTACCG 110514
108442 AATTAATCGTCAACCGAAATCACTACGTGAGAGAGTAAAGATGCTCACCGCGGTACCG 108501
110515 CGTAACAGCGAGCACGACCCCTTAATATTTTACCTTAAAGCGGCGCCCTTAA 110574
108502 CGTAACAGCGAGCACGACCCCTTAATATTTTACCTTAAAGCGGCGCCCTTAA 108561
110575 GTGCTCACTACGCTTAAACCTCTACCATTAATGTTGCTGCGCGTCACTGAGAGC 110634
108562 GTGCTCACTACGCTTAAACCTCTACCATTAATGTTGCTGCGCGTCACTGAGAGC 108621
110635 CCTCATGAGACACTGGCCCTCTCTGCGGGAGCTGTAGAACAATCCTTCCGCCGCTAC 110694
108622 CCTCATGAGACACTGGCCCTCTCTGCGGGAGCTGTAGAACAATCCTTCCGCCGCTAC 108681
110695 CCCGAGCGAGCTTTTAAACGCGCGGTATTAATCACTACAGACTCTCTACACCGCG 110754
108682 CCCGAGCGAGCTTTTAAACGCGCGGTATTAATCACTACAGACTCTCTACACCGCG 108741
110755 CTCACTGTCAGGCTGTATAGCTCTGTCACCTGTGCTGCGGACATTCGCAACCCCGCA 110814
108742 CTCACTGTCAGGCTGTATAGCTCTGTCACCTGTGCTGCGGACATTCGCAACCCCGCA 108801
110815 CTCTTCTTCAAGAGTACGGCTGTGTTGCGCTCACTGCTCTATACGCGCCCGATCATG 110874
108802 CTCTTCTTCAAGAGTACGGCTGTGTTGCGCTCACTGCTCTATACGCGCCCGATCATG 108861
110875 GACGCTACCTTCATGCTGTGCTGCGACCTTTTGAAGTAAACGACGCTTACTCCGCA 110934
108862 GACGCTACCTTCATGCTGTGCTGCGACCTTTTGAAGTAAACGACGCTTACTCCGCA 108921
110935 ATGCGTAAAGATGGGCGAGTATACACCGCCCAACACATCTCGGAATGAGCTACGCT 110994
108922 ATGCGTAAAGATGGGCGAGTATACACCGCCCAACACATCTCGGAATGAGCTACGCT 108981
110995 GCACCTTCTTCAAGACCGCTGCTTCCGACCAATCGACAGAGAAATTAATCTCACACATC 111054
108982 GCACCTTCTTCAAGACCGCTGCTTCCGACCAATCGACAGAGAAATTAATCTCACACATC 109041

OY	111055	TCATTTAATTTTTTTTACAAACCGAGTTTATTAAGGGCATGTTAGAAGCCACGATTC	CGGG	111114
OY	111055	TCATTTAATTTTTTTTACAAACCGAGTTTATTAAGGGCATGTTAGAAGCCACGATTC	CGGG	111114
Db	109042	TCATTTAATTTTTTTTACAAACCGAGTTTATTAAGGGCATGTTAGAAGCCACGATTC	CGGG	109101
OY	111115	ATCGTTCGTTTTAAACGTCCTGGCCGGCGCACAAAAAGSAGCCACACACTTC	CCGT	111174
Db	109102	ATCGTTCGTTTTAAACGTCCTGGCCGGCGCACAAAAAGSAGCCACACACTTC	CCGT	109161
OY	111175	TGCGTGTTGTTCCGTTGGCCGGCGGAAAGTCACACCAACCGGGATTAACCGCTCAC	CGGAGA	111234
Db	109162	TGCGTGTTGTTCCGTTGGCCGGCGGAAAGTCACACCAACCGGGATTAACCGCTCAC	CGGAGA	109221
OY	111235	CCTGGAAAGAGCGCTTCAACTCCAGACAGCCGAGGAAAAAGCCAGCTCTCTGGG	CTTT	111294
Db	109222	CCTGGAAAGAGCGCTTCAACTCCAGACAGCCGAGGAAAAAGCCAGCTCTCTGGG	CTTT	109281
OY	111295	TTTGGCAACGTGGGGAGAAATCCACACTTCTTGCTCCGACACACAACAGGCAAGAT	ACCA	111354
Db	109282	TTTGGCAACGTGGGGAGAAATCCACACTTCTTGCTCCGACACACAACAGGCAAGAT	ACCA	109341
OY	111355	TTTACAAACCTCCGCTTCCCAACCCAGAAAGATCTGCACAAATCACAAGGGCCCT	GTGCT	111414
Db	109342	TTTACAAACCTCCGCTTCCCAACCCAGAAAGATCTGCACAAATCACAAGGGCCCT	GTGCT	109401
OY	111415	GATGCACCCAAACGCTCAACCTTAATAAACAACCAACACCGCATCATATGGGTCTA	AG	111474
Db	109402	GATGCACCCAAACGCTCAACCTTAATAAACAACCAACACCGCATCATATGGGTCTA	AG	109461
OY	111475	CGAGTGTTGGCCCGCACACCCGAGCCGGCTCCGGTTCTGAAAGATCTGTCGGCACA	T	111534
Db	109462	CGAGTGTTGGCCCGCACACCCGAGCCGGCTCCGGTTCTGAAAGATCTGTCGGCACA	T	109521
OY	111535	TCGTGAAAACATGAAAAACAACGTTAAGCTCGTCAATGCGATATGCTATCCTTAACA	GA	111594
Db	109522	TCGTGAAAACATGAAAAACAACGTTAAGCTCGTCAATGCGATATGCTATCCTTAACA	GA	109581
OY	111595	TCCGAGCTACACTGTACACAGTGGCGGAGCAACATCTGCCGGCCCTTAATTAAGCG	GTCT	111654
Db	109582	TCCGAGCTACACTGTACACAGTGGCGGAGCAACATCTGCCGGCCCTTAATTAAGCG	GTCT	109641
OY	111655	GGCACAAGAAATCCACAAGCATTTTTTTTGGCAGACCCGGGTGTCGTCCTGACACG	TACTC	111714
Db	109642	GGCACAAGAAATCCACAAGCATTTTTTTTGGCAGACCCGGGTGTCGTCCTGACACG	TACTC	109701
OY	111715	GCAGTGTCCCGGGTTTTATTTAAATGCCCACCTCCGAAAGATTAAGAGCTCAAGC		111774
Db	109702	GCAGTGTCCCGGGTTTTATTTAAATGCCCACCTCCGAAAGATTAAGAGCTCAAGC		109761
OY	111775	TGCTGTGGCAACCGGAGAGTTCCTGACGTGCAACAGAAATATTGACTGGAGACCTTA	CA	111834
Db	109762	TGCTGTGGCAACCGGAGAGTTCCTGACGTGCAACAGAAATATTGACTGGAGACCTTA	CA	109821
OY	111835	GACCTGTGCGCTCTTTAAGGGGCTCTCACTGGCCAAATATCGGCAAAACACGTCGT		111894
Db	109822	GACCTGTGCGCGTCTCTTTAAGGGGCTCTCACTGGCCAAATATCGGCAAAACACGTCGT		109881
OY	111895	CGAGATTAATCCGTGAAGTTCGATTTCAACTGCTGACACAACATTTCAATCACCCACC		111954
Db	109882	CGAGATTAATCCGTGAAGTTCGATTTCAACTGCTGACACAACATTTCAATCACCCACC		109941
OY	111955	GTTTCAACCTCCACACTATACATTTAATCTTCAGAAAGGCAACAGACATGCGCAAAACA		112014
Db	109942	GTTTCAACCTCCACACTATATATTTAATCTTCAGAAAGGCAACAGACATGCGCAAAACA		110001
OY	112015	GCCCAAGAAGTGGATTGGCGTCTCGAGCGCGCTACGCACTACGCTAGAGCGACGAGCG		112074
Db	110002	GCCCAAGAAGTGGATTGGCGTCTCGAGCGCGCTACGCACTACGCTAGAGCGACGAGCG		110061
OY	112075	GCCCCAGTTCACAGCGACCGGCAATCAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGG		112134
Db	110062	GCCCCAGTTCACAGCGGCAATCAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGG		110121

QY	112135	GAAAAAGTTAGTTTACGACAGCAGT	TTTTTCTGCGCCTAACGCGCGCCACGAGCTGGG	112194
Db	110122	GAAAAAGTTAGTTTCAGACAGCGAC	TTTTTTTCTGCGCCTAACGCGCGCCACGAGCTGGG	110181
QY	112195	GGTGACCTTTTAAAGAAATGGGGAG	CCCGATATGACCTCCAAAGTCCGTTATGTTGGC	112254
Db	110182	GGTGACCTTTTAAAGAAATGGGGAG	CCCGATATGACCTCCAAAGTCCGTTATGTTGGC	110241
QY	112255	GTTAAACCTAAAAACATCGCCCCG	GGGTGCGTCTCTCTCATCTTTCGAGCACTC	112314
Db	110242	GTTAAACCTAAAAACATCGCCCCG	GGGTGCGTCTCTCTCATCTTTCGAGCACTC	110301
QY	112315	GTCAAACATGCGGTTCAACTGTTCG	TGTCACGCGCACTGACGCGTGTCTCT	112374
Db	110302	GTCAAACATGCGGTTCAACTGTTCG	TGTCACGCGCACTGACGCGTGTCTCT	110361
QY	112375	GGAGCGCAACGGCGTCCGGGGAAG	ATTCGGCCGAGGAAAAACGAGCGAGCTGTTCAGTGGC	112434
Db	110362	GGAGCGCAACGGCGTCCGGGGAAG	ATTCGGCCGAGGAAAAACGAGCGAGCTGTTCAGTGGC	110421
QY	112435	GTTAAACCTTTTACACACACAGCG	CGGAAAGGTCTGTGACGACAAAGGGCTTTTACCTGTCTCT	112494
Db	110422	GTTAAACCTTTTACACACACAGCG	CGGAAAGGTCTGTGACGACAAAGGGCTTTTACCTGTCTCT	110481
QY	112495	GCTCAGCCACATCTCATGGAAGTC	GTTAGGAAAAAGCTTCACGCAACCCGGGTGTCTACGC	112554
Db	110482	GCTCAGCCACATCTCATGGAAGTC	GTTAGGAAAAAGCTTCACGCAACCCGGGTGTCTACGC	110541
QY	112555	CCACCTACTGCGTAAAAACCTTTG	GGCGACGATCTTACCTATTTTACAGTGAGTCCGA	112614
Db	110542	CCACCTACTGCGTAAAAACCTTTG	GGCGACGATCTTACCTATTTTACAGTGAGTCCGA	110601
QY	112615	TGAGAGACTCGCATCTGTGGGGG	GTTCACACTAGAGACCTACACCTGGGGAAACAG	112674
Db	110602	TGAGAGACTCGCATCTGTGGGGG	GTTCACACTAGAGACCTACACCTGGGGAAACAG	110661
QY	112675	TCTGCGACTCATATGACAACTTCC	CAAAATATGACATACGGTGGACTGCATYAGCA	112734
Db	110662	TCTGCGACTCATATGACAACTTCC	CAAAATATGACATACGGTGGACTGCATYAGCA	110721
QY	112735	AACGTACATATGAAGTTTACACCC	TGGGACCGGCAACGCAACCGGTACGGTTCCTGT	112794
Db	110722	AACGTACATATGAAGTTTACACCC	TGGGACCGGCAACGCAACCGGTACGGTTCCTGT	110781
QY	112795	CAACGACATTTTGGCGAGGCGGTG	GGCCACCCCTAGACTGCACCGGAGATTTTCGAGAAAGAAAT	112854
Db	110782	CAACGACATTTTGGCGAGGCGGTG	GGCCACCCCTAGACTGCACCGGAGATTTTCGAGAAAGAAAT	110841
QY	112855	TCAAAGGGGACGCGCCATCATTAAC	TCCAGGGGCTATTTGTAACCTTTCCTTAGACGAA	112914
Db	110842	TCAAAGGGGACGCGCCATCATTAAC	TCCAGGGGCTATTTGTAACCTTTCCTTAGACGAA	110901
QY	112915	ACAGATGTAATTCACCTACTTCAAT	TGCAAAATGTTTGTTCGAACATACACCAATTAANA	112974
Db	110902	ACAGATGTAATTCACCTACTTCAAT	TGCAAAATGTTTGTTCGAACATACACCAATTAANA	110961
QY	112975	ACAACTTATGTTTACACAAATTTGA	GAGCGCTTTCATTTTACCATTAACATAGCAAAAC	113034
Db	110962	ACAACTTATGTTTACACAAATTTGA	GAGCGCTTTCATTTTACCATTAACATAGCAAAAC	110211
QY	113035	CACGGTAACATAACTCAATAGCATA	TTCGATGGGATCCCTAGAGACCAATCGACGTG	113094
Db	111022	CACGGTAACATAACTCAATAGCATA	TTCGATGGGATCCCTAGAGACCAATCGACGTG	111081
QY	113095	CGCGCGTATTAATTACGCGGAACG	ACGCTTAACGTCTCCACGAATTCGCAAACTCCGGC	113154
Db	111082	CGCGCGTATTAATTACGCGGAACG	ACGCTTAACGTCTCCACGAATTCGCAAACTCCGGC	111411
QY	113155	TTTTTACGACCATTTGACGCGCGT	TATATATTTGGCAGTAACGTGCGAAAGGGCTACATCG	113214
Db	111142	TTTTTACGACCATTTGACGCGCGT	TATATATTTGGCAGTAACGTGCGAAAGGGCTACATCG	111201
QY	113215	CAGTATGATTTTACGATGTGCACAC	CTTTCCGCGGTTCCGCCCAACAAACAAAGCGGG	113274

Db	111202	CAGTAGTATTTTACGATGTGACACACTTTCGCGGTTACCGCCCAACAAACGCGG	111261
OY	113275	TCACGAGCAGCTAAATGCGCCGCGCTTTTATGCCAAAGTACAAAAGGAGCGCGTTC	113344
Db	111262	TCACGAGCAGCTAAATGCGCCGCGCTTTTATGCCAAAGTACAAAAGGAGCGCGTTC	111321
OY	113355	TACGTTACGAAACAACACTGTTGATTCGCAAAATACAAATAGTGTGTGGTGACCGCAACT	113394
Db	111322	TACGTTACGAAACAACACTGTTGATTCGCAAAATACAAATAGTGTGTGGTGACCGCAAACT	111381
OY	113395	GCCAAATCCTAAATATGATGAGACATAGTCCCTCAAAATCTAGAAAGAACTCCAAAACAT	113454
Db	111382	GCCAAATCCTAAATATGATGAGACATAGTCCCTCAAAATCTAGAAAGAACTCCAAAACAT	111411
OY	113455	GGCGCAATTAACAAACCCCTTGCAAGTTAAATGCATCTGAACGAGACGGAATCCAAAGAC	113514
Db	111442	GGCGCAATTAACAAACCCCTTGCAAGTTAAATGCATCTGAACGAGACGGAATCCAAAGAC	111501
OY	113515	ACGCCGAGTCTTAAGACCAAGGAGCAGTCTTTGGGTTCCGGGGCGTTAGCATGGAAG	113574
Db	111502	ACGCCGAGTCTTAAGACCAAGGAGCAGTCTTTGGGTTCCGGGGCGTTAGCATGGAAG	111561
OY	113575	TTGATCAGCAATATCCCATCAACCGTATACAAAAGCGTAAAGATTAATGGTTTACAATA	113634
Db	111562	TTGATCAGCAATATCCCATCAACCGTATACAAAAGCGTAAAGATTAATGGTTTACAATA	111621
OY	113635	AACAAATAAAAAATAGTGCAGCAAGTATCAATCCGATACAAAGCGGAGCCCAAAAAACAC	113694
Db	111622	AACAAATAAAAAATAGTGCAGCAAGTATCAATCCGATACAAAGCGGAGCCCAAAAAACAC	111681
OY	113695	CCCAACGCAAAAACAACCTGAGACCTGTCTTTGGGTCCTTCCACGCTCCCAATGAAATTT	111741
Db	111682	CCCAACGCAAAAACAACCTGAGACCTGTCTTTGGGTCCTTCCACGCTCCCAATGAAATTT	111741
OY	113755	CTGGGACCGGTGCTGCTTACCGGCTTACAGTGTGTTATPAGGTAGCTAAACACAC	113814
Db	111742	CTGGGACCGGTGCTGCTTACCGGCTTACAGTGTGTTATPAGGTAGCTAAACACAC	111801
OY	113815	AATCTAGAATGCTTAACAGGTGCACCGCGCTTAGGGCGCTTGTGCAACTAAGTGTGTCA	113874
Db	111802	AATCTAGAATGCTTAACAGGTGCACCGCGCTTAGGGCGCTTGTGCAACTAAGTGTGTCA	111861
OY	113875	GGTACTACTCTTATTTTAAACAATAGCATACCAACTGCATTAATTTGCACATAAACCA	113934
Db	111862	GGTACTACTCTTATTTTAAACAATAGCATACCAACTGCATTAATTTGCACATAAACCA	111921
OY	113935	GTTTAGTCTTTTACTGAGTGGCGCAATAGTCTCATGGAAGAACCATATCATCTCGG	113994
Db	111922	GTTTAGTCTTTTACTGAGTGGCGCAATAGTCTCATGGAAGAACCATATCATCTCGG	111981
OY	113995	TCAACGGCGGTGCTTACCGTGTATTTGCGGGCAAAAACAGGCTGGGGGAAAAAAGAG	114054
Db	111982	TCAACGGCGGTGCTTACCGTGTATTTGCGGGCAAAAACAGGCTGGGGGAAAAAAGAG	112041
OY	114055	CAACATATGCTGATTTTAAAAACACTCAAGTCTTAAATCTCAACCCACTGTGAACAAA	114114
Db	112042	CAACATATGCTGATTTTAAAAACACTCAAGTCTTAAATCTCAACCCACTGTGAACAAA	112101
OY	114115	AACATCGAGTTAAGGTATGCTATCCGAACATTAACAACAGAGTTTAAAAACAGCT	114174
Db	112102	AACATCGAGTTAAGGTATGCTATCCGAACATTAACAACAGAGTTTAAAAACAGCT	112161
OY	114175	GGGTAATTAACCCCATTTGCGACCGGTGCGCTGAAGTGTTTTAAAAATTACATGG	114234
Db	112162	GGGTAATTAACCCCATTTGCGACCGGTGCGCTGAAGTGTTTTAAAAATTACATGG	112221
OY	114235	TGCGTTTACACACCGACAGTAAATCTCAGAGGGCGGTTAAACGAGCGATATACATATTC	114294
Db	112222	TGCGTTTACACACCGACAGTAAATCTCAGAGGGCGGTTAAACGAGCGATATACATATTC	112811
OY	114295	CCTAAACACGGGAACGGCGCTGACCGCCTTCCCAATACACAACGGGACTACAAAGC	114354

Accession	Source	Organism	Reference Authors	Title
Db	112282	CCCTAAACACGAGGAGCGGCGGTGACGCGCCCTCCCAAAATGACAACACGAGGACTACAAAGC		112333
QY	114355	CTAGTGTATATATATATCAAAATTAATAAAACACAGAAACCTTTAGTGTGCGCAACACTA		114411
Db	112342	CTAGTGTATATATATATCAAAATTAATAAAACACAGAAACCTTTAGTGTGCGCAACACTA		112400
QY	114415	GGAAGGTGCTACAGACTTTCCCTTACTTC-AAAAACAGGGGTGGTATTTGACCA		114477
Db	112402	GCAAAAGTACCTAGACTTTCCCTTACTTC-AAAAACAGGGGTGGTATTTGACCA		112466
QY	114474	CACGTTAAGTAAACACCCGTAAGAAATTAATTCGCTTATCAAAATGGAATAAATTAAGCT		114533
Db	112462	CACGTTAAGTAAACACCCGTAAGAAATTAATTCGCTTATCAAAATGGAATAAATTAAGCT		112522
QY	114534	TTGCGTTAAATCTGCTAAACGCAAGGAGCACTTAATTTTCAGATTGACCTCGAAGCTT		114599
Db	112522	TTGCGTTAAATCTGCTAAACGCAAGGAGCACTTAATTTTCAGATTGACCTCGAAGCTT		112581
QY	114599	TACCGCTAACGTTAAATTTAATATGCAAAAGGACATTAATTTTGTGTATACCTCA		114655
Db	112582	TACCGCTAACGTTAAATTTAATATGCAAAAGGACATTAATTTTGTGTATACCTCA		112644
QY	114654	AAACTCTACAGCTAAAGTTAATTAACGCGGCACTTTGGGACAGATCAGTCTGTGCGAA		114711
Db	112642	AAACTCTACAGCTAAAGTTAATTAACGCGGCACTTTGGGACAGATCAGTCTGTGCGAA		112700
QY	114714	ACCGTGTAAATTTAATAACACACAGGAGCGGACGACTAAACAGGACTAACGTGTCATCGG		114777
Db	112702	ACCGTGTAAATTTAATAACACACAGGAGCGGACGACTAAACAGGACTAACGTGTCATCGG		112763
QY	114774	GCCGCTTTGAAGAAGTTGGTGTGCAATGATTAAGGAATCTAATAAGAAATCTGCTC		114833
Db	112762	GCCGCTTTGAAGAAGTTGGTGTGCAATGATTAAGGAATCTAATAAGAAATCTGCTC		112820
QY	114834	GCTAACACGGAATTTCTTTAGTTCCTACACAGATCACAACAATGTAATACCATAAACG		114893
Db	112821	GCTAACACGGAATTTCTTTAGTTCCTACACAGATCACAACAATGTAATACCATAAACG		112886
QY	114894	TACGCGCGGTGGGTGGTGTGTAATGCTTTGGTGCACGTTTACATGAGGCGGATTTG		114955
Db	112881	TACGCGCGGTGGGTGGTGTGTAATGCTTTGGTGCACGTTTACATGAGGCGGATTTG		112944
QY	114954	TAAATGTGTGCTTGTGTGCAACGCTGTGGGTGCA		114989
Db	112941	TAAATGTGTGCTTGTGTGCAACGCTGTGGGTGCA		112976
RESULT 3				
AF210726/c		130733 bp	DNA	linear
LOCUS				VRL 27-MAR-2000
DEFINITION				Macaca mulatta rhadinovirus 26-95 unique region L-DNA, complete sequence.
ACCESSION				AF210726
VERSION				AF210726.1
KEYWORDS				GI:7329990
SOURCE				
ORGANISM				
REFERENCE				
AUTHORS				
TITLE				
JOURNAL				
MEDLINE				
PUBMED				
REFERENCE				
AUTHORS				
TITLE				
JOURNAL				
MEDLINE				
PUBMED				
REFERENCE				
AUTHORS				
TITLE				
JOURNAL				
MEDLINE				
PUBMED				
REFERENCE				
AUTHORS				
TITLE				
JOURNAL				
MEDLINE				
PUBMED				
REFERENCE				
AUTHORS				
TITLE				
JOURNAL				
MEDLINE				
PUBMED				
REFERENCE				
AUTHORS				
TITLE				
JOURNAL				
MEDLINE				
PUBMED				
REFERENCE				
AUTHORS				
TITLE				
JOURNAL				
MEDLINE				
PUBMED				
REFERENCE				
AUTHORS				
TITLE				
JOURNAL				
MEDLINE				
PUBMED				
REFERENCE				
AUTHORS				
TITLE				
JOURNAL				
MEDLINE		</		

Research Center, One Pinehill Dr, Southborough, MA 01772, USA

FEATURES

Location/Qualifiers
1..130733

/organism="Macaca mulatta rhadinovirus 26-95"

/mol_type="genomic DNA"

/isolate="Macaca mulatta rhadinovirus isolate 26-95"

/db_xref="taxon:119193"

gene

/gene="R1"

CDS

/gene="R1"

/codon_start=1

/product="ORF1"

/protein_id="AAFS9980.1"

/db_xref="GI:7329991"

gene

/gene="ORF2"

CDS

/gene="ORF2"

/codon_start=1

/product="ORF1"

/protein_id="AAFS9981.1"

/db_xref="GI:7329992"

gene

/gene="ORF4"

CDS

/gene="ORF4"

/codon_start=1

/product="complement binding protein"

/protein_id="AAFS9982.1"

/db_xref="GI:7329993"

gene

/gene="ORF06"

CDS

/gene="ORF06"

/codon_start=1

/product="sDBP"

/protein_id="AAFS9983.1"

/db_xref="GI:7329994"

gene

/gene="ORF07"

CDS

/gene="ORF07"

/codon_start=1

/product="transport protein"

/protein_id="AAFS9984.1"

/db_xref="GI:7329995"

gene

/gene="ORF08"

CDS

/gene="ORF08"

/codon_start=1

/product="ORF08"

/protein_id="AAFS9985.1"

/db_xref="GI:7329996"

gene

/gene="ORF08"

CDS

/gene="ORF08"

/codon_start=1

/product="ORF08"

/protein_id="AAFS9986.1"

/db_xref="GI:7329997"

DVDEDLAEALVSVYKNSLAFEETNVLDVDPDSLSYARKLNGALTRACGQIQFVAT
TLHLCTPVLQTTDAEEYPHVLGSAALATPAVLAETIGRALTALVQTPARQPVATGRL
RPVITVPMVNNKYATGVNNGNNGVFCGLGFAGRGDRALMPESSPEPKSGAMALGK
RHVMPTITDRLIKRAAGORTISFPEAEVSRYSOALIEDKDNMLKSYLETILRHIG
KGCODLSSDEVQYITLGDYCMITDEVLFTLDNIQSGSPRTIEDAGALIEDROADDLQ
FVSDSDATATASCPEEQPLTPSAGALLACKRRKINALSDLDL"

7636..9696

/gene="ORF07"

7636..9696

/gene="ORF07"

/codon_start=1

/product="transport protein"

/protein_id="AAFS9984.1"

/db_xref="GI:7329995"

gene

/gene="ORF08"

CDS

/gene="ORF08"

/codon_start=1

/product="ORF08"

/protein_id="AAFS9985.1"

/db_xref="GI:7329996"

gene

/gene="ORF08"

CDS

/gene="ORF08"

/codon_start=1

/product="ORF08"

/protein_id="AAFS9986.1"

/db_xref="GI:7329997"

gene

/gene="ORF09"

CDS

/gene="ORF09"

/codon_start=1

/product="polymerase"

/protein_id="AAFS9986.1"

/db_xref="GI:7329997"

/translation="MDFNFYLDGRGRPHSHKGTAPAPAGAGANVPDPDVCALTA
CLRTPGAGMIPVITIPPTPYFENGAGDVLNENRSMWAPARCKPAPADPODSTF
HAYDVPTTYAARCAVAPSRFQTDIIPSGVTIKLRLTDRDGSVCANVROOVYFA
KPVAGIINWTHILLOALKNVAGRAAGSTRVNKRILKTYDVNHPTEITLSGSMIL
STLSDRVACGCEVSENVADVAREVLFDEHFTFGWAGSCARAPRLAARARALAE
CSMEDLSVQADRSADMPYRTIADIDCTGAGPCARDDVAYOISCVYTRREGAP
NPRIILFVSTGCPDIPDTDLVLEPSEDTLVSPFAMTRDEVDVFLINJSDNPLPL
ITRAQVYINRLNEVYTIKTKGSIFEVHEPRGGGGFKRSVSKITIAIVTIDYQVCR
EKLSDISYKIDTAAAOCLGKRGKDVSKDIPPLRSQPGGAGVAGSVLVDML
LKRMHILSEITLAKLAKIDARVLTGDCQOLRPFSCLEAAARENFLLPRTPEGQCG
YOGATVINPILPGYDEVLVADVASLPSITIOAHNLCTSTMIGRDLHLHPNLTPDY
EFTVLGSGPVHPVKKHRSILGRLITVWLEKERRAIPRTIAACDDPSLTKYITLQKOLA
IKYTCANAYFTGVSAGSLIPCINIAEYVTLRGRTMLEMSYVEALTTDELRLRIGCE
VTARHGARFVVYGDNDLSLFIADGVSAAEVSAPCDLARIATADLEPPRIKLEAET
FKCLLLLTRKRYIGVLLNDKMWKGVDLIRKTAACKFQVQERCAILDLVLVLDPEVKA

[illegible]

AUTHORS Searles, R.P., Berguam, E.P., Athelme, M.K. and Wong, S.W.
 TITLE Direct Submission
 JOURNAL Submitted (26-JUN-2000) Division of Pathobiology and Immunology,
 Oregon Health Sciences University/ Oregon Regional Primate Research
 Center, 505 NW 185th Avenue, Beaverton, OR 97006, USA
 REMARK Sequence update by submitter
 COMMENT On Jun 26, 2000 this sequence version replaced gi:5508840.
 FEATURES
 source
 1. 133719
 /organism="Macaca mulatta rhadinovirus 17577"
 /mol_type="genomic DNA"
 /db_xref="taxon:83534"
 1. 840
 /note="partial terminal repeat"
 1353..2624
 /codon_start=1
 /product="R1"
 /protein_id="A021330.1"
 /db_xref="GI:4494908"
 /translation="MEVLVLFMLQPVSELLPAKLTQVPTWCPRPHGDTYLLTQCT
 STARDSTQWEPNNLTLMRNSFGRLVSVTPATISDRACOTKTTTSSNIDFRS
 SSLTLOERSSXYGYANTRTVLRGYSGGNVLIRNFIHNTAVANGTTHIFV
 LEKTKGTGYFCSAFIGNERKYSQTIWVFESFPEKPPNDIIPNSHKNKQIQOTFASV
 QHEENVVSPSPFSGVLTGTLAISTLMCLPTIRCNENSSNSYASOTYSIOSH
 NQSNSTNCSRATITRNAHDESETEELPNOITSTPDSCCQVLELVKNVARDQENETI
 NEMWEDQDVVKNITPOTSEEDVNEHMDSDTINPNPNYSGILLEVDVEYNELEN
 QYHGLILENDLHNEYHNLNMLNMEIQYDME"
 complement (2692..3258)
 /note="ORF 2: similar to Kaposi's sarcoma-associated
 herpesvirus ORF 2"
 /codon_start=1
 /product="dihydrofolate reductase"
 /protein_id="A021331.1"
 /db_xref="GI:4494909"
 /translation="MDITVNCIAVDVDQLGKNGTMPMYLENEMXYPQKMTSTPSV
 VGKRNINWIKGRTWFSIPEKKPLNVRNITLSRELRPEHGAFIARTIDDAFNFYR
 QYKLSKOLNTWVWVIGKSYSESVLANKCPKLTITRMSEFDQDVEFSPINTEYML
 SELGKDNTEENEGIKYKQYVEKNNK"
 3676..5613
 /note="ORF 4: similar to Kaposi's sarcoma-associated
 herpesvirus ORF 4"
 /codon_start=1
 /product="complement binding protein"
 /protein_id="A021332.1"
 /db_xref="GI:4494910"
 /translation="MFKLPPLFLHINMWHDCDECKRPHFTEYVKSSTEDLXSY
 GETAELICRPGVYTKRIITTECLQNGWSTPFCPCRKCPYADLLNGAHIHGSD
 NAKPFSNITSDENGEYDLGNSWRCILIDQENWKSNEPCELOKICRPAVHG
 DYLPNDVNYGDAITFFKSLISTYLGSTLTIVTSKMSNSPTCLIMCESPDIDN
 GYDILSRRYHNGOISITKASDGVNIGVEGTEICNTNTWVPLPKCVLITNRPSP
 PEMPEPTEPPDPOKINLSAKATNPMAFVTVVSPEDQDVCAVPHFERFANRSM
 DKRTYSVGSVELICRPGFTKQSTYSVECLSGVTATAPAKCRHKRCPTROLLNGE
 YVITSEDAFKGTGNTITVYCNESGTYQLGSSNVRILKLDLITVDMKAPITQIECK
 PPQITGVYHPKDYQYLDVTFSCNDRPFSVIGDMETGICNTNTPKAPRPEQTECK
 SVAHINAGRLTGSSSVYKXGQSVLTIGCEGFLIGSEISTCQSSMDPPLPCVAV
 SMSDIPKPEKTKPNTPEAPKGPQNPVNGTHPFPQPQNPDIAPMSKWKRRVLYV
 LFSVSLVSLFVLAATCYCFEK"
 6045..9443
 /note="ORF 6: similar to Kaposi's sarcoma-associated
 herpesvirus ORF 6"
 /codon_start=1
 /product="sDNA binding protein"
 /protein_id="A021333.1"
 /db_xref="GI:4494911"
 /translation="MASKSNAGPLIEDNGSRAPICAGGVYVAKODPEEASTIG
 NRPSSGVFSPLPLTGLIVHEHPPLTVKAKYKVDITTLAAKYTCRREYIVHNASL
 FRVEFGTGINELCEEARALFGYTOPLEGPPSINPLEPQLPKRDEKFLGAVTE
 GFERLIRMGCLPVAVQTOOVQIAGQARFPLYLDLPAHGRMPRHRKHSAYL
 YSFLFSIAQALRKLQVTAIVIAHTEQFMODHKIAKIYQAKQFSTLLEKTTDSSSH
 IYDSVVALEIALSYGCMELPCPODACELIWDSPIDFGDSDPARVNALERMGAEOAV
 HVAQGLFANSVYITLKVQKQARQGRQGVNYYNSFLDHGIGELINAKITKENGSAF
 KQVPSALDGSSFTPTHLIAVASFSLHAKLQCTYQFQJHRSKSTNQAQNNVHYVGT
 AANSEACITGHGNTPATCINTLTLEYRLTKDFFPAVTPQDIPVYVSTQACTFNDLEILG

NPASFEDEEDGNPADEHPKYYTWOLOQVTEKLSAIGITTEHDHNVNLTITNQSFL
VFKGIDSIADGEVCKEYVNSMKNKNNFNEBHVSVHHILQFCCNVYQACAVFLNLY
KSLMTIIOQICLYCMYIEQDNPAMGILPESMLKMHFOITLMTNFKAACDQCVLTGCE
LKIHVDMFCDEFDPDAGNSGLAPFKMOVRIARAAVVPKSIKIKRIIIFSTTASE
AVOSGFVKPPTGPDYVVAQPYKFLNSLRALFPPTKTRALYLMHKISOTNTPYK
DVPDDLAELVSVKTNLSAFETNVLDVVPDSLMYARKIKLNGALILRCGQIOFYAT
TLHCLTPVLOTIDAEYPHYLSAAIATPVAYLAETRGRLALTVOPTAQRPVAMRL
RPVITPVMVKNKTYGVNNGNNVHCNGLGFAGRGVDRNLMPESPCKRTGVSAARK
RHVMMPIDRLIKRAAGOTISTFEAEVSKRSQALLEDNDNLKSLYTEILRHG
KGGODLSSEVOYIGDYCMITDEFLTNDINAOISGVPTMTEDNAGALIEDROADLO
FYDSDIATASCPPEEQLPFSAGALLAGKRRKRIALLSDLL

CDS

/note="ORF 7: similar to Kaposi's sarcoma-associated
herpesvirus ORF 7"
/codon_start=1
/product="transport protein"
/protein_id="A021334.1"
/db_xref="GI:4494912"
/translation="MARLEALYALYALAVLSLIVFADPRSIDGARILKTKQIEN
LNEDLPLREQNSVETSSLSLEVEHLANIEDKLESLRQYSSREHETLHR
PECHYSTVTFQYGGGLIDVNMCLINDVELCKRLGSVYEGIGANBALSGLRVLT
LSTLRGISPIPHDILVYTSVPCVQCLRETELAVNOCSSILAVADRCHCKVAAE
PIHGLFETELSQLKVTYKRSATQHGVSASADQLSESLAIQDNNIRKVSATME
LSNLTWNAGQGTLOGTENESQMARLTHEADMEHRLALITPKLSATHFYDCEFRD
PIESLCGGLFNSIDIDTINALSDCSVTFEQOANYNMKONELTRLSILRQSA
GSGKPAATPEPRTTVAATAASVDIKDAQYRKQYAKADGKDEKLEOTQOSAVL
ANALCKRWGVAVYGEASELVNHEFLRRRVAPLPMWRCRSDLEKENSYYIKNSYS
ORLSRHEVELITLOFYGLITGRTGSDLPFGANALAOFCFAAMKPHMKLYSEM
IMPQIDPKMIDTNNRYQOLPBGDILNANQSWKCTRELVSALYNRTWEKTLTLE
SLAREKLSINLDVKLTSGLYLTEDAPVLTISONTGWIFKDYALLYHLILSDG
HSDN"
11515..14004
/note="ORF 8: similar to Kaposi's sarcoma-associated
herpesvirus ORF 8"
/codon_start=1
/product="glycoprotein B"
/protein_id="A021335.1"
/db_xref="GI:4494913"
/translation="MMITNTRRLRAMVYIIAIGTAVGENTTPPKGATTAATKTPGP
STPTPENPRPAFAKFRVCSASATGELFENLEKPECGEDTHOEGILMVKKNV
PIHFKYRRKRVATSVYRGWTEYAVTKQEVIRVPOVEINHMPTTQOCSEMYN
VNGIVNTYDRODTNFTVLOPYEGSLDNIORYESQVLTTPGMPGTYRVITVNC
EIVDMARSAEPTSYFVTAAGDVEVSPCHNDSTSVAKETNGCGARVLTITVD
FATQPTTEREYFADGEYVSWKADPKSACALMLKMTFTGPAIQTTHASVYEV
DVAFTSTPLSQVNTFTGYPCLDNIOLKNTIKLSLSTHATNSSEOVYEEGGF
LMQPLTSLADEMRENGTTPAPPTTSTARVRSRSTNOADDLAAPOLOGAY
DKRASINKYLELSRAMCREQVRYOTMYMELSKINPTSMYTIYGRPSAKYVGAI
SYTDCVAVDQASVYIHSKLTSTPGICYSRPVTEFLNSTLTKQGLRKNELIILD
NOVEACKETCEHYFIASNVYIYKDVFKKIMTBSITLGTFLANLSIENIDERY
IELYSRAEKKLSGVFDIETMREYNYTORLGLPREDLNTIDLNDRLARLSEIV
ADLGDYGRIVNVASSVITLFGISVGFINEIKSPGGMILVITAVVILVALRR
TNAIAQPIRMVYPOIDKMQPSGKQDODIKKIIILAGMLQOEEERRRDEQORSAPS
LRRASDGLKRRRGYKPLENEAOYEMSK"
14122..17166
/note="ORF 9: similar to Kaposi's sarcoma-associated
herpesvirus ORF 9"
/codon_start=1
/product="DNA polymerase"
/protein_id="A021336.1"
/db_xref="GI:4494914"
/translation="MDFENYVLPGRGPRPHSHRGTDAPAPAGAVOPPPDQRLIPA
CLRTPGAGMIPVTPPTPYENGARGDVLANERSMTARDRKVPADPOQOSITF
HAIVVETTYAADRCACAEPSRFOTDIIPSGTVYKILKRTEDGTSVAVNEBOVYEA
KVPAGINVTIIOQALKNTAGRAAGFSTRVNRKRIKITYDAVEHPTVETLSSGSL
STLSRDLVACGCVESNVDAVRPVLIDGFTTFGWYSCARATYAAARALALEFD
CSMEDLSVADRSMDPPYRIVAFDICTGBAGPCATRGDAVITQISCVFTTBEAP
NPNLILSVGTCPIPTDVLLEPSEYDMVGSFAMIRDFEVDPLGYNISNDELVL
ITRASGVNMLNNEYTKIKTGSIFEVHEBPBGSGGFMRSYSKIKIAGIYIDIMDYCR
EKLSIDYKIDYAROCIGKEDVYKDIPLFRSGPGRAKVSYCVWSDSLVMD
LKMFMHVEISEIAKLAKIOARVYLDGKDIPLRFSCILLEAARENFILVPEEGGG
YOGATYINPIRGYDEPVLYVDPASLYPSITQAHNICYTHMGRDLHLPNITPDY
ETFEVLSGPFVFKKRRRESLGRLLTWLEKRAIRLTLAACDDSLTTLIDKQOLA
IVTCAVYVGTGVAAGLLPCINIAETVTLRGRTMLEMSKSYEALTTEDLRTLRIGRE

CDS

CDS

VTARHARRRVYGYDTSLEFIACDGSAAVSAFCODLAAITATADLPPPIKLEAKT
FKCLLLTFRKRYIGVLLINDRMKMGVDLIRTKACKFQVQRCRAIIDLVLHDEPVKAA
RLCKRKYVAYEGGLPAGPIKIVELVNSYDLDRSVVPIEQLTFSTELSRVCDYK
TNMLPLAYOKLASRCELPQVHDIPVYFVDAVPSGLSDLAHEHDDYRQHIIPAV
DLTFDLVIGANIILOCLGNNADTIVALLNPLNYLFS"
17261..18511
/note="ORF 10: similar to Kaposi's sarcoma-associated
herpesvirus ORF 10"
/codon_start=1
/product="unknown"
/protein_id="A021337.1"
/db_xref="GI:4494915"
/translation="MLVNELSVVLGDMETVFNHGRSPVNLTRLOTFKGGHYARVL
PESLDLQHQHFAFLVTRKLELPESDCVALLAPLDSGDADAAVAGFVYDSSRP
LTVWVASGRHTIRFCLFLFKPLIDLRAYTVYVGGGARSSECTPCTATESLPGSR
LYSGASOTSPPSFVAYPTANISVACISILRQVRFPSDAAHRRARISPKYFESN
SGGNVCKASVHTISPSRCKTAQKEIITVYADPRAEVLVGSQGVLTTHHGRVLYA
DAKTTIQPGSSAEVRVOLIFQOGAAARGDLAVTVGAPLFFVTPALLISCTTHL
RLRPNGTPTTIKRDVLVAAAPCPVVRUSSLADARDLVASDGTALSNAPTVIG
FPGVYAECHVSLRDGVHERMNH"
18520..19749
/note="ORF 11: similar to Kaposi's sarcoma-associated
herpesvirus ORF 11"

CDS

CDS

Query Match 0.1%; Score 33; DB 1; Length 133719;
Best local Similarity 100.0%; Pred. No. 4.5e-07;
Matches 33; Conservativity 0; Mismatches 0; Indels 0; Gaps 0;

QY 117543 ATGTATATAGGAGACTGTGTAACAAACCAAC 117575
Db 23911 ATATATATAGGAGACTGTGTAACAAACCAAC 23879

RESULT 5
AF083424
LOCUS AF083424 108409 bp DNA linear VRL 07-JAN-2000
DEFINITION Ateine herpesvirus 3 complete genome.
ACCESSION AF083424
VERSION AF083424.1 GI:4019231
KEYWORDS
SOURCE Ateine herpesvirus 3
ORGANISM Ateine herpesvirus 3
Virus; dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Rhadinovirus.

REFERENCE 1 (bases 1 to 108409)

Aubrecht, J.C.

Primary structure of the Herpesvirus ateles genome
JOURNAL 7 Virology 74 (2), 1033-1037 (2000)

MEDLINE 20091363

PUBMED 10623770

2 (bases 1 to 108409)

Albrecht, J.-C. and Fleckenstein, B.

Direct Submission

Submitted (11-AUG-1998) Institut fuer klinische und molekulare

Virologie, Universitaet Erlangen-Nuernberg, Schlossgarten 4,

Erlangen, Bayern 91054, Germany

location/Qualifiers

1. 108409

/organism="Ateine herpesvirus 3"

/mol_type="genomic DNA"

/strain="73"

/db_xref="taxon:85618"

complement(join(90..730,1339..1507))

/note="C10: similar to Tip and Srp-C of herpesvirus

salmali-C-488"

/codon_start=1

/evidence="experimental"

/product="tlo"

/protein_id="A021338.1"

/db_xref="GI:4019240"

/translation="MANEORHEHGGPFPPLDSCSEEGPPNIPDPTTCTPPGPIINS
KEDNPPLEPNPNSSEGPDSGSSSPVYMLVNNQDRKQDVSESGGNNSANS
VSKHSTSSSSSAGNGNETKCPDEONTQOECITTIYIPWEDAKPLMLVLDSSDEE

RSPFNKPKNKTKLRYDGMENPPICIPPOPLPPRANICGOKOSATSKNGPOLILREAT
 EVESQOATDGOINHERVEKTKVLCILGILVLLILFLMLGFLILMK"
 snRNA
 complement(2144..2264)
 /product="HAUR 1"
 snRNA
 complement(2752..2865)
 /product="HAUR 2"
 CDS
 3224..6961
 /note="orf10; similar to FGARAnts"
 /codon_start=1
 /protein_id="AAC95537.1"
 /db_xref="GI:4019239"

CDS

CDS

CDS

translation="MLVLPHTSYREALLPEELIATSAILOPPIQVNTSHNPAVSQV
 VYVRHNASFEPIVIGKFFRSYSPKPTPTSPAEOTLSFSGPOLSLDTTTSRELVDI
 LKLSMFTPOGKKNADILIERICTYITITICDINPMTMHORHLKLCVPTGIGTKF
 ILPOKSLNLOAEPARALSTPIIDPLWMCNGFTLPYSDKYSIFRRGOLPKYFVE
 KNSRLGIYDIDYTPWSTNTLYEGLYVNGEYVYTGFTQPTNLMGYNMALHMR
 APLFACOTGHITSLAOSMDHPVQAPOMKMHALNLLKCSMPTIOGFPFVSDI
 ATILPOTKYNGEVSATLRTPVCAATASIREKYLQIOLNFPYRNHRYLIMTODSG
 EIGSTILASFPNOCVKTRESGITVGMSTSLIPESKAKLAACVCHSARILLSLPM
 OYTKLAFSNSSTKHKVEYLKOHFNITLSDLIITAIKININAEALKTADMAKCK
 FKIGLVLHRKGTIVVDGRDKPYKIQDFRKPPEPLKSPINITTOGINMSELD
 LADITFKLLEHPSVCKEPIVSHIDKLVSGRARAIVGPMQLPVSDYSIIVYLOGN
 NRDGMENPMDYETDIDRCVFEELAKPGICSSIGESTLIAQADLKIGTMRATTEALN
 LAMASMNIGSIIIOVALITPLTQAATSLQVMDTAKTCEALSVCTPFAASADGG
 ASIYASATVFNENAKCKMTPMLKHNDSFLILIPTEKRYNHGGSVQOICGKPTGDLR
 OATSPTELKILQVICTIREDOISVSGHVDGGLALYEMALISGGGVRYYPQGE
 DTLQFLESEPGIYIEVSTLYIVQVGLNRVDFOLVGCISLEPLEAVSONSIDIM
 SEPDLISLOIWRKESDACEADVOHPQVEMHITPIKPCPAGVCFHSVYVYLPHNS
 VPHGLISAIAEGEQPKLISIDHPQVNSIYDPYAMGEFIVGASNMEEINIGIALK
 AQLKSHVALQDFERIMLAKPEYFCVAGIAMACELFEYKTIYGNPSTQYCVNNS
 EKFSERNMIIYIPENTKAIAROSLKNLSILPCMTQGTHLRHPKMLEKMAEHGVNS
 MEYGNLSAGPAOHPILPNGSNATAGICSDAGRILALHNPISLCNNICQMPYEPPTD
 PPKVSPKRIWFLDHLKMGITVQGASPPSRDPLSLVSP
 7470..8552
 /note="orf 04a"
 /codon_start=1
 /product="complement control protein homolog ceph"
 /protein_id="AAC95530.1"
 /db_xref="GI:4019232"
 /db_xref="GI:4019232"
 /translation="MHTLAFIILPCVIEFWSSSCPKRRNRYSLRYVNTSSGSY
 PNGTTLQVTCRKGYIGROIQVTCVNGMIVPNECQKRCSTPADILNGWYTVNGLY
 YGSYVTCNTGYLQIGSPSSCLLPGDGRVNMPPRIPICETKCKRPPPTVANGHTN
 IKEYTYIYDAVYSCNDETKLITNGSSKOCSEGRWVDEBTEKCEFKVCIPOANG
 HVEWRKSNMVOYOVNIKCDKGRFLOSETPNMCKNGWFPALPTCEKPRAPRGDMPI
 IDSGEDISTPSGRNOCNCTTSVSTNITITITGHTSHIYPTGKNYKLPQGVLTIL
 TTSIIILAILITGVCLHRCRLMFPV"
 9205..12591
 /note="orf 06"
 /codon_start=1
 /product="major sedna binding protein"
 /protein_id="AAC95531.1"
 /db_xref="GI:4019233"
 /translation="MATKATQPIADNLGSRAPVAGCYIYVPEKGFPOBASLLGNR
 NMGADAMSLPLSGILVEANFSFNKAVHKIKIDMTLSVRVSAVHREAIIVPPNNFET
 PIFRPGIDSLCSABRNLEGYTSPTRPKADIKIDIKIYLAPYTKRYSNMTAEVTS
 FKRLRYRNLVPLISQCKQVQINGREANKITLYDEDLFESKSHLPRYITPSVKYTLH
 DSLFTSIAQALRIRDESIVRAIEKQSHIDQYKLAKVYNSKFEALQACODNAAEFV
 IDCIAELAELIYGSLEFETPOPCALIDYTEMJEDTETEGEGRKAIADOMNAAEFV
 VYTHLFSTNSVLYLTKIKNOTKNSDONIYNSFMQGLSYAAEOTKENGDAFSG
 AVFNGSGYTLFHLALASSPFLIARNCYMOGCOHKSTTNSYSAOVYVYAVS
 ELCELCQCKPAACITHTLFYRLKDRFVYSSQRDRPVYVYGVSGOYVDDMLGNFAT
 FREKEDDVQVOTBECKITVQIOLNVEKLAITIGTSTLGSDLITDQSLFKYFREL
 DNVDVNEIKYINCLVKNINIFRETIKGVHVLHAGCNVQWQAPCAMLNLVPSVLA
 IIDQICLIPVAMIEEDQNSMGMPSEMKMHQIIMTFKSSCIDKYGTAEBKRVH
 GDMFCDFINVSALNGOIVPYKMOVRLAKALITVPTIKINRIYVSSMSTEAIOAG
 FIRSTKDSYIVGYPMKPLNSLHAYFPDAKISALYIMHTFESOKROIPIPLIGSKE
 NITELANTIEAGSKMHDMDVLDITPTTLAYAKRYRLNMTLRTKCGOTQFATTLQCL
 LPTLQVVSATIEPVHLHQOSTVVDVYLSIKKQALIVQTLTKLEDIATIGKHRIYV
 VPLVYKNTGTINGNTQIFQCGNLGYFMQGRVDRNLIPDSGFRROONVYAKRKHIFM
 TPVIANLKRTSNLNLNLEVEETIRKNVQITFDKDNINIPDNVILEVKGISGSEN
 MTEDDLOIYGLDYIMSEIDMSRLOLTDGSTPVSVESTYIIGLSRKQEDCNLEBVG
 EEOISCAPOIDEVPOATLSTIAGRKRIAHILSDIL"
 12598..14640

CDS

CDS

CDS

/note="orf 07"
 /codon_start=1
 /product="transport protein"
 /protein_id="AAC95539.1"
 /db_xref="GI:4019241"
 /translation="MAOHLAAVYQIYGFRTLDVSLVFPVPSHINRKIFETNMOKINK
 IYLOIMPLDOONNVESTLSVELOHLLTNKTMADITLKLHNTYETFDNHSSTP
 CSKHKILVIOEYFNCSVSVMCIINDIEIFLKLSSVYCIIRADHATYGLNKLVIDFLG
 HLRGISPIPLDPIYLSNIPCIYCLMEHMLNNOESLOMKTSVNCHVQNLDEPV
 OGMEFENELORHIIYVDQPKPEPTQOCSINKRIDETLSKSHHTIENETSPAYLELS
 NLIYWSGTHTRKCTNIEWNTSEIVKLSHETKMOVRYKICKSTHEFPKRYPSIETI
 FCGIFENSVDTVSRSKSDCSLAPMKRANVOOLIKOMELFVPLNMLIKGSDTSTP
 PPVPISEKAAVNEQVYINDHARKDAILQVATKDLGSLYACLDTOGAVYLSNLSMR
 VWGAVVDEIYKLNHNFLEFROFISLMDIIEEBSVSGFENSKYIKNLISQKLSSEH
 ISSLQGLYOLITGDSQNVSEYFPLPYNIALHCLADAGALPHHKLITEMIWPTIEP
 KDMVSOAKNRYETITSGDLNNIQEWFIEELIYSLVYRALEAKNLQIYSVNFKEK
 NCVRKSPNKGSGIYLFEDRSPIELFIYRNOGWFKDLTYLWYHHLQSLVKNHDS"
 14627..17050
 /note="orf 08"
 /codon_start=1
 /product="glycoprotein B"
 /protein_id="AAC95532.1"
 /db_xref="GI:4019234"
 /translation="MTLNRGVLLIYLFSTACQSTTPASDNGKTPAIKEKYKRYV
 CSASTGELFEPNIDRACSPSTEDVYHREGILLYKKNIVPPIFYRRYKKAJATSVRIE
 NGMSREGVATINKNELSAVPKYEINLMKRYIQCHNCQIIEYKGLNSYCRDGNKTI
 VDLKRVDELTAITRYVSQPIEDADGLWQYVTRTYVNCIEIVEMERSADPVTYFV
 TALGDVDEYSPCEAENSCPNASDVLSSQVDFNHTVNDVYGNRARSQOGRKIPATLD
 YSAGVEALINKTSQCSVMFQFORAIDTDEDSYHFYANBITAGFSTKSTLASFS
 EYSCMLSDINSTLNDKIGRVNNTNTPYTAQYFTEGMIYVMOPLTIELEEMIAE
 TTSPPTPLSTAHITLDRKIGRVNNTNTPYTAQYFTEGMIYVMOPLTIELEEMIAE
 TWCRQVQVQYHWEIYKINPTSVYATIKGYPVAKALGDIYSTECINVOYTSYSH
 KSLRTNNDVQYSRPVYEFKFNSSQGLQGLARNEILLSESLVENQHQAHEHFTA
 KNEYHFNKYNLHVEITPLNTISLDTFLALWPLENIDFAKVELVSSGERKLANVPD
 LEFMREXYNYAOSISGLKEDPDNSQNRRIIIODESEIILADISIGKVIYVNIASSA
 FSLRGVITGILNFKPLGMLFLLGAILIYVILVYRRTNMNSQAPIMYIYDIE
 KRSRSVPTPEPEVYKQILLGMHNNQDEBYKKREBKKSQPEFLKATDAPFLKRAYKY
 QISTEDKMI"
 17123..20152
 /note="orf 09"
 /codon_start=1
 /product="DNA polymerase"
 /protein_id="AAC95533.1"
 /db_xref="GI:4019235"
 /db_xref="GI:4019235"
 /translation="MEFTNPLYTKLAGSKMKLQSCCTTKOPICILVPCERNPSRGIV
 SVSFAPTPYRNGSENNVYLGNNQSMHMLRPOKTEPEVQSTFHAHYDIVEYTSSE
 DRCDNDPEKRFQTDIIPNGTVLKLGRITDGSVCANVFGQKIYFVYVKEGNGITNYLC
 KOALNEKRGPCSYOTELVYKIKILSRYPDBEHEVEKVISSHSYKASDYLVANGC
 IEFNTNVAIRREITIDNNSRTGWYCKSACRRTNRDSYDIEFDGQNDLEFHAERT
 EMPYNTIARPIECIGKEGFPKACNEBDLIIOISCVNQVSTPPTKRMILSTGCA
 VEDESVIEFPESEADMLGEFTILRDFNEIITGYNISFEDLPIYLDRTQYLNKILSD
 YSRVSGSIFQVHMKDNGFMGSVSKIKISGIIAIDMYIVCKDKSLSNYKIDTVA
 DHCIGAKKEEDVSYDILPLFMSCGEGRAKIRYCVIISVILVILKLMFKTVEISEIA
 KLAKIPRRVITDGOQIIRFESCLAAARAENYIIPVSNVKSQDVEFMLSGSPLHPYK
 NNAIVYDRAISLYSITIOAHNLQYLSITLPHSLILNYPYKTSQDVEFMLSGSPLHPYK
 KHIQTSLSKLITLYWLSKRAIKROKLACEODPRTKILDKOQALIKYCANVYPTGY
 ASGLPCTISAEYTVLQGRIMLESKAFIEEMTPVQROIEVPHLHEHKEHKEPVITG
 DTSGLFVECVASYDVTVYRFGDLTSESEIFNAPKILBESEKFOCLILAKRYIG
 IISNDKIKLGVLDVDAKTFACVFOYTSKILNLLIKPEYVAAOOLSKRPDVAFRE
 GLDPGLFKVIDILINESVNTERTGVMSDILFESLSEIPYSYTEMNPLHYVKKII
 KROEPRQIHRIYVYVGRKATQISTMADEPYYAONINIIADLYFDKILHGVANI
 IQCLFKDSNKTQSVLYNVSIFPLFSTELKDSHSET"
 20192..21412
 /note="orf 10; similar to Raji Lf1"
 /codon_start=1
 /protein_id="AAC95534.1"
 /db_xref="GI:4019236"
 /translation="MNBSTNITWGRWTVYSSGLFSJSSNNEIAPATPVARYHLDP
 SIESIILIKRSHNGIYVPTLLOQOYTNSPAYFSDTSPQCKPYVLPMTISDFINLAV
 FVKGPIILKRSNGLKFIYFISLPRDIDISFIPDPNDKDTLALAGFRINENVA
 IGRPRTKNTNGSYMLFRCEKIPLEVININVADEKILPEYVAAOOLSKRPDVAFRE
 MCGSPKQDIOEVQVHLVNTNPTLYVKKHALLPHELASGSGIILPIYLEADKILKPGSS
 VEISFSEYFNGLVDNOSALFVASSNHTKYVVKPOIWIPTITPLSTIYVNPGRNITF

CDS	IKRGCVAAVAPCFEYLKAPGDCEDKVTLDSDTSIHMSDVLIRKPGEGPIVHAHNL VLKEINFTEEMPE" 21415..22632 /note="orf 11; similar to Raj1 LP2" /codon_start=1 /protein_id="AAC95535.1" /db_xref="GI:4019237" /translation="MATPKHIRGVMRGSAKROSEKRNFLFMSSSVHEHFTITNNO ETIOLPDVILARCPISREIVGKOLPNKFGSRGPGGTTTSFYVVGHCNVIKIP MTISDQDELIFKTFPALECIITPGSKKIFLPTPLTKLDDLILCLEDESSITMTS CMQGITLTSETPQVFLKSPVLTKEPLPLMKQKTFPKKMARVHTVONECEVN SIYKGDHILRLAKSEDEVNEFEVPIGLTMKALIAFQHNYYFCPMWQNSIP IIYVPSIRIPADRAVAVKNNMYSSTANTAMTNCCTPDHISCEKMPSPVY INVTNIAITTISSGTRKLGAEVFLAPFKICKIKISKHVQTLPSAVTLPGNVTINS NKLPLADITTYK" Complement(23207..24028)
Query Match	0.1%; Score 26; DB 1; Length 108409;
Best Local Similarity	100.0%; Pred. No. 0.0043;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
cy 111659	CACAGAAATCCACAGCATTTTGTG 111684 95614 CACAGAAATCCACAGCATTTTGTG 95639
RESULT 6	
LOCUS	U93872 133661 bp DNA linear VRL 09-JUL-2001
DEFINITION	Kaposi's sarcoma-associated herpesvirus glycoprotein M, DNA replication protein, glycoprotein, DNA replication protein, FLICE inhibitory protein and v-cyclin genes, complete cds, and tegument protein gene, partial cds.
ACCESSION	U93872 GI:14627174
VERSION	U93872.2
KEYWORDS	
SOURCE	Human herpesvirus 8 (Kaposi's sarcoma-associated herpesvirus - Human herpesvirus 8) Human herpesvirus 8 Viruses; dsDNA viruses, no RNA stage; Herpesviridae; Gammaherpesvirinae; Rhadinovirus.
ORGANISM	Human herpesvirus 8
REFERENCE	1 (bases 29032 to 30108; 117733 to 118431) Zhong, W., Wang, H., Herndler, B., and Ganem, D. Restricted expression of Kaposi sarcoma-associated herpesvirus (human herpesvirus 8) genes in Kaposi sarcoma (human Natl. Acad. Sci. U.S.A. 93 (13), 6641-6646 (1996)
JOURNAL	96270595
MEDLINE	8692871
PUBMED	2 (bases 17242 to 17856) Neipel, F., Albrecht, J. C., Ensser, A., Huang, Y. Q., Li, J. J., Friedman-Kien, A. E., and Fleckenstein, B. Human herpesvirus 8 encodes a homolog of Interleukin-6 J. Virol. 71 (1), 839-842 (1997)
REFERENCE	3 (bases 123309 to 124082) Li, M., Lee, H., Yoon, D. W., Albrecht, J. C., Fleckenstein, B., Neipel, F., and Jung, J. U. Kaposi's sarcoma-associated herpesvirus encodes a functional cyclin J. Virol. 71 (3), 1984-1991 (1997)
JOURNAL	97184528
MEDLINE	9032330
PUBMED	4 (bases 122660 to 123226) Thome, M., Schneider, P., Hofmann, K., Fickenscher, H., Mehl, E., Neipel, F., Matlmann, C., Burns, K., Bodmer, J. L., Schrotter, M., Scheidt, C., Kramer, P. H., Peter, M. E., and Tschopp, J. Viral FLICE-inhibitory proteins (FLIPIs) prevent apoptosis induced by death receptors Nature 386 (6624), 517-521 (1997)
REFERENCE	5 (bases 1 to 133661) Neipel, F., Albrecht, J. C., and Fleckenstein, B.
JOURNAL	97242415
MEDLINE	9087414
PUBMED	
AUTHORS	
TITLE	
JOURNAL	
MEDLINE	
PUBMED	
AUTHORS	
TITLE	Cell-homologous genes in the Kaposi's sarcoma-associated rhadinovirus human herpesvirus 8: determinants of its pathogenicity?
JOURNAL	J. Virol. 71 (6), 4187-4192 (1997)
MEDLINE	97296220
PUBMED	9151804
REFERENCE	6 (bases 1 to 133661) Neipel, F., Albrecht, J. C., Ensser, A., Huang, Y. Q., Li, J. J., Friedman-Kien, A. E., and Fleckenstein, B. The genome of human herpesvirus 8 cloned from Kaposi's sarcoma Unpublished
JOURNAL	7 (bases 1 to 133661) Neipel, F., Albrecht, J. C., Ensser, A., Huang, Y. Q., Li, J. J., Friedman-Kien, A. E., and Fleckenstein, B. Direct Submission.
REFERENCE	Submitted (17-MAR-1997) Virology, University of Erlangen, Schlossgarten 4, Institut für Klinische und Molekulare, Erlangen 91054, Germany
JOURNAL	8 (bases 1 to 133661) Neipel, F., Albrecht, J. C., Ensser, A., Huang, Y. Q., Li, J. J., Friedman-Kien, A. E., and Fleckenstein, B. Direct Submission
REFERENCE	Submitted (09-JUL-2001) Virology, University of Erlangen, Schlossgarten 4, Institut für Klinische und Molekulare, Erlangen 91054, Germany
JOURNAL	Sequence update by submitter On Jul 9, 2001 this sequence version replaced g1:2246466. Location/Qualifiers
FEATURES	1..133661 /organism="Human herpesvirus 8" /mol_type="genomic DNA" /db_xref="taxon:37296" /note="sequence derived from overlapping lambda phage clones isolated from two libraries of Sau3a partially digested DNA from Kaposi's sarcoma biopsies" 105..959 /note="ORF K1" /codon_start=1 /protein_id="AAB62619.1" /db_xref="GI:2246494" /translation="MFLYVCSLAVCFGLSLSIQSSPNCPCGYISPTPLTCSNT SLPTSWCNDRLRLTQOTFTVDTLQCNFSCVQSGSRHSLMTWYQPVQLTQCG PSNVTGCOHVTLCSTSGNVTWHLPGNGENYVSCRYNFTLMDVYMEASCSNG LSRSINRLCSARCANLTPETHVSVSTGFRFSTNRGRTLLDVLVMEASCSNL HIOYHFLVFMVLVALIGTMGILGIIIFAHQOKQDSKVTYQQLQDYYSLDCTED YTOQPDWY" 1127..2779 /note="ORF 04, complement control protein homolog" /codon_start=1 /protein_id="AAB62602.1" /db_xref="GI:2246477" /translation="MFLRQTLMLTMTPTWYIGDNEKCSQKTLIGYRLKSRQDDIA VGEVVELRCNGCYTTTARNTATATCLQSGTSEPTPKCKKSPNGLQNGVITFGG QDALRYGANISYVCSNEGFLVGREVRYCMIGASQGMSSSPFCEKCHRPETEN GDFPKDXYEYNDVAHFECNDEGYTLVGRHSIACAVNNTWTSNMPTCLACKRPST HGYPLOGSLTYKHKQSVTFACNDGCVFGRSGPTTICANTENDPPLPKVLIEDIDPN SNQRLHTPEKRPKRGVNFORSNTEPTKEDDTATCNCEQPKILPTSGFN ETTSNRTTQLEDEKTSQPNHTTSLTSMKAKGNTKNTNSDTLHASTPSOD DATSIPSVOPTPNNTNAPRTTLTSLHIEEGPSNSTSEKATSLSNSKNDTGCI YTLTKTQTLQSTNKPNSQAKSSSTRPVEVHNKTSIPALSLTDSADVPQPREPTL PIPRFPASKNRYLEKOLVIGLITLVAVALTCLTLFHLVFR" 3194..6592 /note="ORF 06, major ssDNA binding protein homolog" /codon_start=1 /protein_id="AAB62603.1" /db_xref="GI:2246478" /translation="MALGQPTLEENIGSAAPTGPCGYLVAVLTHNPDIGEASLGG YPAKVESLPPLHLGLVSDPLPWKAHKKIDATYAAVCLYSREAVIHNHLLFO PIFOGKELCRRESRELFGSTVEOQHKGMLMEACPOLPCANETFMVAVIYEGF KERLYGKLVVPSQTPPVHIGENHAKTPIYDEPLFGSRAOELCRFYNNDISYLIH DSITFGIAQALRVKDVSTVYIASERQPHDOYKIKPLVQAKDFQCCASRGDGSILWY IDSILVAELGMSYGLSFTGPDSCVLLVYDWMPLENEETDPARALEVHAEDALH IGAOIFAANSVLYLTRVAKLPQKNQKRGDANNYSFYLOHGLGYLSEATVKNENASAFK

CDS

```
GPVSAIDGSSYTLQHLAVASFSFPHLLARMCYVIOELPHHKNTNOSQYVWVYVGTNA
APSMDCIDGCGPANCINTLFYRMKDRPPTVSNKRDPRVYITGTAGTINDIELIGN
PATFREREENGVEDAPKTYIMOLCONITEKLASMSISEGDAIRLVIDISEVAV
FKGIDSTVEALELFLNQMKNVNFENIKSVHHLQFCANVWQAPCPVFLTYLK
SLTIVDIDICLSCMYEDBNPAVIGYSEMLKMHQTMNTNFKGACFDGALITGLYL
KIVHOSFECIDFTDAIGGAPARQVRIARMAVPTIKIKNIIFISNFGAS
IOAGFMKPAROSDYIYIGPYMKFLNHLKTLFPTSTSLYIMKHIGOTTPIIDPG
VSEHLETELONVYKASQAFEEINLDIYPTDITLSTAKITLNSIILRACQOTPYAT
LSCLSPTOLVPAREPYPHVLGVLGSPDEYRAKAVAGRSVITVOSTLQKQVSTNGRR
PITVPLVANKYTGSGNGNTNWFHCANLGYPSGKGVBNLRESEVPEKKNVSMRLRR
HVIMTPLVDRIVKRVIGINSGEAEVAKRSVONVDRPNPLPKVIVIELVHLGSS
SCASILEEDVYIIGPYAVLGEDEVLSLTSGVAGVPTDEGVASVQDIIIDCELOF
VGPDEPCLIQGQSVLELPPSPGVSLTVEKKRIASLSLDL"
```

6609..8696

/note="ORF 7, processing and transport protein homolog
(ICP18.5)"

/codon_start=1
/protein_id="AAB62620.1"

/db_xref="GI:2246495"

```
/translation="MAKELAAVYADVSAIAMDCLISYADPAIIDLKSLATLTGKRS
LHGTLLPLLRQNAHSCGLSLDELHLEVNADALATLVGTCRKSLSEHESLHLHD
TTCNKHRSVRENFYGMWALKLKSLINDVEIFKRLSVSYCGSGSLAGEVLEHD
VGLKISIPVGPDLVYVNLPCLEIOEVLTPNQGLQAMLPDACHICTPACE
PVRLGEENELKQLOTRESIPTPCOSRVRODETIROSSIAMVGDHIGEVTSVL
EISNLIYSSGSHDATCGDRCDSLALSLFTHADMKRRVDIAGCGEGRPKHNEP
CERPDLSFTLFCGGLFSVSDTIESLOKCSSAFYQOVANTLQOKNERVYRLSKIL
AAQOLNIGKSTSCSPSEARKQLVGGKPEEVLDAHRELTLQKVARGEFKLSIC
IRHOGHILSQTLRLMGSVIYNEASLQNLHFRKQFISLPVQDILVDCPTREMSK
YIKNSQILQGLREHVEILTFEYKLTGLSRHRLFPISLPVQDILVDCPTREMSK
OKMAMSEIMWPSIEPKDIEPNQFSPFNQDINHLOKAMEYIRELVKDYLLANT
WERELKILTPGSPGPEPKPAGLTGLITFETSPALVLVAKKGMIFKDLALLY
HHTOLSNHNSQY"
```

CDS

/note="ORF 08, glycoprotein B (gB) homolog"

/codon_start=1
/protein_id="AAB62592.1"

/db_xref="GI:2246467"

```
/translation="MPRSRLATLTVIILVCCAGAAHRCGTPOTSSPTPPGSSS
KAPYKGEBAKSPKSYDPTQRYCASAITELEFRNIEQCPPTKDXHROEGLLYK
KNIVPHIFKVRIRKILATSVTVRGLTESAITNKLREPRVPLEISHMSTQCFSS
MKVNVGVENTFTDRDQVNTVTELQVEGLIDNQLORFSQPVYAEAGMPGTYRAT
TVNCEIIVDIARAEPPYNEFVSLGDTVEVSPSCSTPKNKGNGVYVNVNH
TVVYISDRGTSPTPNRIEFTGATVLSMASEKTAVCGLAMTKPEPSTIOYTHDS
FHFVANEIITAFAPLTPVANTDYSCITSDINTLNSKATLASHVNGVQVQFH
TNGGLIWNQPMANILTRQGDSCNPTSPSPASAPMTTSASRRKRSASTAAGG
GSTDNLSYQLOFAYDKLRGINQVLEESRAVCRQVRNMLWELSKINPVSMTA
IYGRPVSAFVGAISVTECINDVOSVNIHKSILRNSKQVCAAPLVFEPKINSNL
FTGQLGARNEIILTNNOVETCKDCEHYETTRMETLVYKQVAILRTINTDITLNF
IALNLSFIONIDKALEIYSSAKRLASVFELEMERRENYTHRLGARELDNMTI
DMNKEFVRDLASIEVADIGIGIKTYVNASVYVLTGSLVYTGFINFKHPLGMLMI
IYVAILIIFMLSRNTNTIAQAPYKMIYEDVVRARPPSGAPRREIKNILLGMOLO
QSEKQADLDKSTPSVFOETANGLRQRLRGXPLTQSDIDISPTGE"
```

CDS

/note="ORF 09, DNA polymerase homolog"

/codon_start=1
/protein_id="AAB62593.1"

/db_xref="GI:2246468"

```
/translation="MDFENFIDPTRGPPRNVRQPTPSQSPVSETRVCRILPACF
QTPRGVVAADVTPPTPYFOGKRGVAGEGSEIMTKRCGARAAPMSHLTFHYD
IYETVYTADEVEDPSPQDILIPSTGLVILKGTLDGASVGNORRCQVFTLADP
GVLTLVLOALQAGFRAAGSCGSTEPRVKILRAVDQOQVAKQITLSSPMMRSL
DRLTCCGCEVPSBNDAIRFVLDHGFSTFGWEGCNAPRVARASVTELEKDSME
DKFTPERTEMPPTTLISFDIECMGKGFNPATQDDMTIISCVLTHVGNDPYRM
LVGLGCDPLPGEVEFPEYDMLAALISMLDYVEETITGNINPDLPIYIARAT
QVDFKLODFTKIKTGSEVFEVHQPRGSGNMRQSKISGIVPIDMYQVCREKL
SLSDYKLTIVAKOCLGRKODISYKDIPPLFGSGPGRKGVGIVPVDGANDLLR
FOHVEISIAKAKIPTRVRLTDGOIIVFSCLLAEATTEGTVIPVPGDANSVCG
ATVISPSPGTDPPVYVDPASILPSITIAHNICSTLIPGSLHHPHUSPDITET
VLSSGCVHFKKHKRESLAKLTIVLAKRKEIKRLACSTPALMTIIDQOOLAKY
TCLNAVYGTGVAAGSILPCINIAETVILQGRKMERQAOVEALSPRLGLRRPIDV
SPDARKVYIGDTSLEIFCMGFMNDVSDFAEELIASITNTLFRPILKEAKIFKC
LLTLTKRRVYGVLSDDKVLAMKGVDLIRKTACRQVOKSSQVLDLITRPSVAAAKLI
SGOATDMVYREGLPBGFKVITIOVLNASHLELERSVPVYKLTFTTSLRPLADYKTN
```

AUTHORS Russo, J. J., Bohenzky, R. A., Chien, M.-C., Chen, J., Yan, M.,
Maddalena, D., Parry, J. P., Peruzzi, D., Edelman, I. S., Chang, Y. and
Moore, P. S.

TITLE Nucleotide sequence of the Kaposi sarcoma-associated herpesvirus
(HHV8)

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 93 (25), 14862-14867 (1996)

MEDLINE 97121480

PUBMED 8962146

REFERENCE 7 (bases 1 to 137508)

AUTHORS Russo, J. J., Bohenzky, R. A., Chien, M.-C., Chen, J., Yan, M.,
Maddalena, D., Parry, J. P., Peruzzi, D., Edelman, I. S., Chang, Y. and
Moore, P. S.

TITLE Direct Submission

JOURNAL Submitted (17-OCT-1996) Dept of Pathology/Genome Center/Division of
Epidemiology, Columbia University, 650 West 168th Street, New York,
NY 10032, USA

REFERENCE 8 (bases 1 to 137508)

AUTHORS Russo, J. J., Bohenzky, R. A., Chien, M.-C., Chen, J., Yan, M.,
Maddalena, D., Parry, J. P., Peruzzi, D., Edelman, I. S., Chang, Y. and
Moore, P. S.

TITLE Direct Submission

JOURNAL Submitted (02-MAY-1997) Dept of Pathology/Genome Center/Division of
Epidemiology, Columbia University, 650 West 168th Street, New York,
NY 10032, USA

REMARK
COMMENT Sequence update by submitter
FEATURES
Source
On May 3, 1997 this sequence version replaced gi:1718251.
Location/Qualifiers
1..137508
/organism="Human herpesvirus 8"
/mol_type="genomic DNA"
/db_xref="taxon:37296"
/cell_line="BC-1; virally infected primary effusion
lymphoma derived cell line"
/note="sequence derived from overlapping lambda phage and
cosmid clones isolated from libraries; A prototype
sequence for the terminal repeat (tr) unit is deposited
under GenBank Accession Number U75699. The left junction
variant tr sequence unit immediately preceding base pair 1
of the LUR is deposited under GenBank Accession Number
U75700. The remaining LUR sequence extending from this
sequence to the right tr unit is not available due to
difficulties in cloning and sequencing of this region"
1..137508
/note="long unique region LUR"
105..974
/note="ORF K1"
/codon_start=1
/protein_id="AAC57081.1"
/db_xref="gi:1718252"
/translation="MFLYVCSLAVCFRGLSLSLSSPILCPGVISTPYTLTCLSA
SLPISMCNTRRLRLTERVILDTIACFTCEVSGHROSIMTWRAPVLOTCAQ
PSNTVTCOHTVLYCSTGNNTVWHLPGRNETHVSORTYVETLMSOEGCYTSGN
LSSRLSNRCFWRACANITPETHVVSSTGSEFRLSTNSLVKTIHATRDVVVKEA
KSTHIEVHEVPTLVALLTMCGLIGTIIFAHCQRDSNKTVPQOLQDIYSLHD
LCTEDTQPDVMT"
1142..2794
/note="ORF 4: The HVS ORF 4 homolog has alternatively
spliced messages encoding membrane bound and secreted
proteins; complement binding protein VCBP homolog"
/codon_start=1
/protein_id="AAC57082.1"
/db_xref="gi:1718253"
/translation="MAFLQRLIMLTFTVYIGDNKCSOKTLIGYRLKMSRSDGIA
VGEIVELRSGSYTYARNTATCLOGGWSSEPTCNKKSQPNGETIONGKVIHGG
ODALKYANISYVNEGYELRGREVRCMIGASOMASSPPCEKREKRPITKN
GDFKPKDYIERNDVHFECHNGITLVGPHSACVANNITWTSNMPTCELAGKPSVT
HGYPLOGFSLYLKHQSVTFACNDGFVFGSGPTTCANTWDPLPKCVLEIDIDPN
SNPGLRHPTEPKPMGNVFORSNTEPTPKBEDTAACTDNCOPKILPTSGEN
ETTSNTITKOLEDEKTIISOPHTITSAITSKAKGNFTKNTNNSTDLHISTPSOD
DATPISVOTPNVNTAPRTLTSLHIEGNSNSTSEKATSTSLSHNSKNDGKI
YTLNKTOLDSJTNKPTNSQAKSSKRPVEYHNKTSNPAISLIDSAVDPORPEPTL
PIRFPASKNRTEKQVLIGLIVALTGCLITLFFHLFFR"
3210..6611

CDS

/note="ORF 6; ss DNA binding protein ssDB homolog; EBV
BALF2 homolog"
/codon_start=1
/protein_id="AAC57083.1"
/db_xref="gi:1718254"
/translation="MALKGPQLEENIGSAAFTGCGYLAVYATHNPFIGENSLGNG
YPAKVFSLPLHGLTVESDPLNKAIVAKIKDATTAASKLTSYREIAVFNTHLFO
PIFOGKLEKLCRESRELFGFSTFVEODKHTLMSPEACPOLCPALNEMATVIEFG
KERLFGKLVPPSOTTPVTHOHAFTKPIYDEDLFSPSRQELCERYNDISRYLH
DSIFVIGKALNVKDVSTVYQASERQPHDQKIKRLVQAKFCPCASGDFGSLYLM
IDSLVAELGMSYGLSIFEGPODSCVLNWDWPIFENCEETPARALKALEVMAEOLH
IGAOLFANNSYLYLTVAKLPQKNORGANMNSFYLOHGLTYSEAVYKAGSAAFK
GVPSALDOSSYTLQHLAVASSEPSHLLARMOYLOFPLHKNNTSGYNNVDYGA
APSOACDLOGGCCPAVCINTLTFEKKDRPDLTSMVKDKDYPITGTAGTIVDELIGN
FATREPEREGCPVPDARKYTWQICONTETELASMSGEGDALRTIIVDPSPVYK
FKGIDSYBAELKFTINCKIKNTNIRENISVHIILOFACVNTQAPCPVFLTYLK
SLUTVYIDICITSCMAYKEDNPVAVGVSEWLMKMFQTMNFKACGDKAITGGL
KIVHOSMCDLEDTDAAIGMFAFARMQVRIKRAMLYPKTIKINRIIFSNSTGAE
IOAGFMKPASQDSYIVGGPYMKFLNALHKTLPSTKTSALIMHKIGOTNPIPG
VSGHELTETCNVAKASQAFEEINVLDPDLTYSAKIKLSSITLRACGOTQFAT
LSCSLPQIVAPVAAEYPHYIGPVGLSSDPEYAKAKAGRSYTVOSTIQOAVSTNRLR
PIITYPLVYNNKTSNGNTNVRHCNLCYFSRCYDRNLRPSYFPKKNVSMILRPR
HYIMPLVDRLVKRLVGINSGFEAEAKRSYQNVLEDRDNELKRYLVELKPRRW
SSCASLTEDEDYIVLYGPAVALGDEVLSLSTVGQAGVPTAGVASVYIDIIDCELO
FVGPPEPCLIQGOVSVELFSPGVSLTVGKKRIASLSDLDL"
6628..8715
/note="ORF 7; transport protein homolog; EBV BALF3
homolog"
/codon_start=1
/protein_id="AAC57084.1"
/db_xref="gi:1718255"
/translation="MAKELAAVYADVASLANDLCLISYADPATLDTKSLATLTKFOS
LHGTLPLLRQNAHEGSLGLELHPFKMTKMLPMRWCALEACNLSKISFPSCIMT
QATNSNRSYRFRFGYNNALIELSLINDEVEFRKLSVFTYIGSGALSEGELFR
VEKLIGISVPEGLVSNLPCLEQCLTPNGTSLQALPOTPACHSITPTGCE
EVRGLPELNEKOLGIQTPESIPPTQGSVRODDRIROSSLAVDGHHIFGVETSVL
EISNLIVWSSGSHDATCDGRDCHSLAFTFEDAMHRRVLDALBERGPKPFF
CPRDSELTFCGGLFSSVEDTIESLOKCSAFQOQVNTALLOKONFEYVRLSLC
AAGNLNCKSTESGSEARQVLGGVGRVLEIRAKRHOELYALQVADRGKRTKSDC
IRHOCHITISORTGLRIMGSYIENASALQNHHLNAPISLPMODLTYDCPRFENSK
YKNSLTCORLAREIVEITTEFTKLTIGPLSKRHLTPSPPNVLAOCFEAGMLPH
QKMAVSEMIWPSIEPRKDWLEPNFOFYFENDODIHLQKRAVEYIRELVASLVNRT
WERELKILLTPQSGSPGFEPKPAGLTGTGLYTFETSAPLVLDKRYGMIFKOLVALLY
HILQLSNHDQV"
8699..11236
/note="ORF 8; glycoprotein B gb homolog; EBV BALF4
homolog"
/codon_start=1
/protein_id="AAC57085.1"
/db_xref="gi:1718256"
/translation="MTPRSRLATLTGTVILVLCFCGAHNRGDTFOTSSPPRESS
KAPTRGGEASQSVDPYOPPYRVCASITGCLFERNLEQDGTDPDKYHQBGLLYVK
KNIVPHIKRRIKRIATSVYVRLBETLSATLNKLELRPVLYEIRSHMDSYOCFSS
MKVANVGEVNETDRDDVNTVFQVRLGVLNDIQRYTSQVTVIAPEWPFQIVRT
TYNCIEIVMIAKSABEYNYEYVSLDGTVEVSFCNESSCSTPSNKNGLSVQVVLN
TVYVTSRGTSTPQNRIFEVETGATTLWASBSKTTAVCPALMTKTPFRSIOETHEDS
FHEVANEITATPTAPLTPVANETDYSCTSIDINTLNTASKAKLASTHVPNGTVOYFI
TTGGILYLMOPMSAINLTHAGDSGNPSSPPRSAPMTTASRRKRSASASAAAGG
GSTDLNSTQLOPARDKLRDGINOYLELSRACKEQYRDNLMTLELSKINPTSVTA
ITGRPVNASFVGDAISVTECINVDQSSVINHSLSLSTNKSADCYAPLVTFELNSNL
FTGQIGARNEIILTNNQVECKDCEHETFRNELVYKDAVLAFTINTTDLSTLNT
IALNLSFIONIDEFKALIELYSSAEKRLASVADLEMGFEYENYTHRLGAGMDLNTI
DMNKEFVRQDISEIYADLGGIGKTVANVASSVLTGGLNGVETIHTHPLGEGMMIT
IYVAILIILYMSRRTNINIAAPKYMITYPDVDRAPRPSGAPRTREIKNILLGHQLO
QBERKADLDLKSIPSVYQRTANGRLQRLKRPLOSLSISPETGE"
11363..14401
/note="ORF 9; DNA polymerase homolog; EBV BALF5 homolog"
/codon_start=1
/protein_id="AAC57086.1"
/db_xref="gi:1718257"
/translation="WDFENPPIIDTPRGGRNTVNRQPPSQSPVPSSETRVCLIPAC
QTPGPPVAVADTTFPPPYFGQPKRGVEFAGETGSIWTRGQARNAHMSHLIFHYVD
IVETTYTADRCEDVDFSPQDILIPSGYVLKILGRLDGAASVCVNVNRQRCYFTYLAPO

CDS

Query Match	0.1%	Score 23	DB 1	Length 137508
Best Local Similarity	100.0%	Pred. No. 0.22		
Matches 23	Conservative	0	Mismatches 0	Indels 0
			Gaps 0	
QY	110359	GTTTTAATCTACTGACACTACTT	110381	
Db	114702	GTTTTAATCTACTGACACTAGTT	114724	
RESUT 8				
HEPA18F				
LOCUS	HEPA18F	7423 bp ss-RNA	linear	VRL 02-AUG-1993
DEFINITION	Hepatitis A virus polyprotein RNA, complete cds.			
ACCESSION	M59808			
VERSION	M59808.1	GI:329585		
KEYWORDS	hepatitis A; polypeptide.			
SOURCE	Hepatitis A virus			
ORGANISM	Hepatitis A virus			
REFERENCE	1 (bases 1 to 7423)			
AUTHORS	Plomaviridae; Hepatovirus.			
	1 (bases 1 to 7423)			
	Lemon, S.M., Murphy, P.C., Shields, P.A., Ping, L.H., Feinstone, S.M.,			
	Cromeans, T., and Jansen, R.W.			
	Antigenic and genetic variation in cytopathic hepatitis A virus			
	variants arising during persistent infection: evidence for genetic			
	recombination			
	1 (bases 1 to 7423)			
	Plomaviridae; Hepatovirus.			
	1 (bases 1 to 7423)			
	Lemon, S.M., Murphy, P.C., Shields, P.A., Ping, L.H., Feinstone, S.M.,			
	Cromeans, T., and Jansen, R.W.			
	Antigenic and genetic variation in cytopathic hepatitis A virus			
	variants arising during persistent infection: evidence for genetic			
	recombination			
	1 (bases 1 to 7423)			
	Plomaviridae; Hepatovirus.			
	1 (bases 1 to 7423)			
	Lemon, S.M., Murphy, P.C., Shields, P.A., Ping, L.H., Feinstone, S.M.,			
	Cromeans, T., and Jansen, R.W.			
	Antigenic and genetic variation in cytopathic hepatitis A virus			
	variants arising during persistent infection: evidence for genetic			
	recombination			
	1 (bases 1 to 7423)			
	Plomaviridae; Hepatovirus.			
	1 (bases 1 to 7423)			
	Lemon, S.M., Murphy, P.C., Shields, P.A., Ping, L.H., Feinstone, S.M.,			
	Cromeans, T., and Jansen, R.W.			
	Antigenic and genetic variation in cytopathic hepatitis A virus			
	variants arising during persistent infection: evidence for genetic			
	recombination			
	1 (bases 1 to 7423)			
	Plomaviridae; Hepatovirus.			
	1 (bases 1 to 7423)			
	Lemon, S.M., Murphy, P.C., Shields, P.A., Ping, L.H., Feinstone, S.M.,			
	Cromeans, T., and Jansen, R.W.			
	Antigenic and genetic variation in cytopathic hepatitis A virus			
	variants arising during persistent infection: evidence for genetic			
	recombination			
	1 (bases 1 to 7423)			
	Plomaviridae; Hepatovirus.			
	1 (bases 1 to 7423)			
	Lemon, S.M., Murphy, P.C., Shields, P.A., Ping, L.H., Feinstone, S.M.,			
	Cromeans, T., and Jansen, R.W.			
	Antigenic and genetic variation in cytopathic hepatitis A virus			
	variants arising during persistent infection: evidence for genetic			
	recombination			
	1 (bases 1 to 7423)			
	Plomaviridae; Hepatovirus.			
	1 (bases 1 to 7423)			
	Lemon, S.M., Murphy, P.C., Shields, P.A., Ping, L.H., Feinstone, S.M.,			
	Cromeans, T., and Jansen, R.W.			
	Antigenic and genetic variation in cytopathic hepatitis A virus			
	variants arising during persistent infection: evidence for genetic			
	recombination			
	1 (bases 1 to 7423)			
	Plomaviridae; Hepatovirus.			
	1 (bases 1 to 7423)			
	Lemon, S.M., Murphy, P.C., Shields, P.A., Ping, L.H., Feinstone, S.M.,			
	Cromeans, T., and Jansen, R.W.			
	Antigenic and genetic variation in cytopathic hepatitis A virus			
	variants arising during persistent infection: evidence for genetic			
	recombination			
	1 (bases 1 to 7423)			
	Plomaviridae; Hepatovirus.			
	1 (bases 1 to 7423)			
	Lemon, S.M., Murphy, P.C., Shields, P.A., Ping, L.H., Feinstone, S.M.,			
	Cromeans, T., and Jansen, R.W.			
	Antigenic and genetic variation in cytopathic hepatitis A virus			
	variants arising during persistent infection: evidence for genetic			
	recombination			
	1 (bases 1 to 7423)			
	Plomaviridae; Hepatovirus.			
	1 (bases 1 to 7423)			
	Lemon, S.M., Murphy, P.C., Shields, P.A., Ping, L.H., Feinstone, S.M.,			
	Cromeans, T., and Jansen, R.W.			
	Antigenic and genetic variation in cytopathic hepatitis A virus			
	variants arising during persistent infection: evidence for genetic			
	recombination			
	1 (bases 1 to 7423)			
	Plomaviridae; Hepatovirus.			
	1 (bases 1 to 7423)			
	Lemon, S.M., Murphy, P.C., Shields, P.A., Ping, L.H., Feinstone, S.M.,			
	Cromeans, T., and Jansen, R.W.			
	Antigenic and genetic variation in cytopathic hepatitis A virus			
	variants arising during persistent infection: evidence for genetic			
	recombination			

LOCUS	HPA24A	7436 bp ss-RNA	linear	VRL 02-AUG-1993
DEFINITION	Hepatitis A virus polyprotein RNA, complete cds.			
ACCESSION	M59810			
VERSION	M59810.1	GI:329587		

KEYWORDS hepatitis A; polypeptide.
SOURCE Hepatitis A virus
ORGANISM Hepatitis A virus
REFERENCE 1 (bases 1 to 7436)
AUTHORS Lemmon, S.M., Murphy, P.C., Shields, P.A., Pling, L.H., Felstone, S.M., Cromeans, T., and Jansen, R.W.
TITLE Antigenic and genetic variation in cytopathic hepatitis A virus variants arising during persistent infection: evidence for genetic recombination
JOURNAL J. Virol. 65 (4), 2056-2065 (1991)
MEDLINE 91162758
PubMed 1705995
COMMENT Original source text: Hepatitis A virus (strain HM175, isolate 24a), cDNA to genomic RNA.
FEATURES
source location/Qualifiers
1..7436
/organism="Hepatitis A virus"
/mol_type="genomic RNA"
/db_xref="taxon:12092"
719..7399
/note="putative"
/codon_start=1
/product="viral protein"
/protein_id="AA45468.1"
/db_xref="GI:329588"
/translation="MMSRGGIFQTVSGSLDHLISLADIEEOMQISVDRTAVTASY
FTSVDSVHTAEVSGHVEPLRTSYDKSGSKTQGEKFLHSADMULTTHAFHVA
KIDVAKLYNEQFAVOGLRHTYARFGIEIOVNPPEQGLICAMPGDQSTGS
IASLYVPHGLNCINNNVRIKVPETRGARHFDPOVPELIRVWSELINISGT
TSAYSLNVLARNTDLEHLPLSTOMMRNEFVSTENNVLNVEEDARAKMSAL
DOEDKSDSQGGIKITHFTTWSIPTLAOPFNASAVGOQIVIPDPYFQMT
NPNDDKCTALASICOMCFMGWDLVDFQVPTPHASRSLFCVCPGDELDSGI
TIKQATACAVMDITQVSTLFRPMTSDPRNRTKSHQGEYTAIGKLYV
CINRLTSPNSVASHRVNLYLAINLECAPLHADVTTQVDSGSGSTVSTQDN
VDPQVGIITMDLKGARKMDVSGVAPVAGITTTIEDVLAKEVPEFLPKGE
SRTSDHMSIYKFMGRSHFLCTFTSPNNKEVFPITLSTSNPGLSTLWPFNL
FOLYRGLDITITVGTADVGMAFTPGVADTVMVERESALSIDYKALGAVEN
TTRTGSIORLPMYSYLVAVSGALDGLGDTSGFGLVSIQIANNHSDYLSFCYL
SVTEQSEFFRPRPLNMLSTESVSRISAGDLSVDDPSDEEDKRESHIECK
PYKELLEVQKQKLYAQEELNVEVLPKRMKGLSQANISLTYEEHMMKFSMG
VTAADTRALRRFGSLAAGSVWTEMDAGVLTGLRLINDEKTEKKDQIVSLIEK
TSNKKYSKVFNFPGMLDLBEIANSKEFPMSBTDLCTFLHMLNPKKINLADMLGS
GVOEIKQGVLAECRTFLHSIAGTLKSMFGFHSVVEIINTVLCFVSGILYV
IOOLNDESHIIGLIRVMNVYDGGSVISCGVFSKMETEVNMQMDSMMELTOS
FSNMLDICSGITIFKFKDGLTLYTKLQDFEVNKGKKDILNLKQOKIEKAI
EADKFCILQIDVERSEQIQGVLDLQKLVYSMAQVDPNMLHUSPLRDCIARYH
OKLNLGFIQNAVTRCEPVYCYLHGRGGKSLTIALATICKHGVPEPKNIATYK
PVASDWYDVSQGLVCIIDDIGQNTDESDSCQVSCPMRLNMAISLEKGRHFS
PFIIATSNMSPKTVYVKEAIDRLHFEVYKPAFSEFNPNDMLNVLAKTDAI
KOMSCVDLMDGNVSLMDLSLVTVDIRKQNMPEMELMOSGTSDDNSAVAEF
OSRPSSEPSNLSKSGFOSYTNKRWAGAVALILVYVGNVYVYKHSKEEPIPA
EGYHGVTPKHYIKLADVESOSTLEIAGLVKRLVQGVGEKNGCVAVNALLGV
KDWMLVPSHAYKFEKDYEMMEYFNRRGYYSISGNNVYISLQDFODVVMKVP
IPKFRDITEHFIRKGDVPRALNRLATLVNTGPMISGPKMEKAKVYAKKNG
TIVDLVDOAMRGEGELPMCGALVSSONAILGIHAGVANSILAKLVTEM
FOINDKIESORIMKVEPTQCSNMVVSKITLFRSPYHHIDKMINPAMPASKAI
DPMAYVLSKSLPIVEPEBEKASIFYQKLYGKQVDDPDLDMATGACGIDAI
NMDSGPEFVDEKLTAKRLIWDENGLLVGHPRLAQRLYFLTMVNMESDIDVET
TCKDELRLPELVKLEKTRAIACPLDYLITLCMVGPALSHLNGEFTGVAIGD
PKOMDELFTMTIRFGVDGLDFASFDASISPFMIREAGRISLSEGTSPHGTAL
NTIYSKHLIYNCYHVGSGMPSGPTALNLSIINNVLNYYVYSKIFGSPFQOA
LKLICVGDVILVFSRDVQINDLIGOKVDEKFKGMATGADNVPLKVSSELT
ELKRSFNLVEDRIRPAISEKTTSLIANKRSNAEPQONLENAMQFAMHGYEYQAFY
YFVQSCLEKEMLEYRLUKSYDMMWRPYDDCFIDLS"

mat_peptide /label=vp2
1454..2191
/product="viral protein"
/note="putative"
/label=vp3
2192..3091
/product="viral protein"
/note="putative"
/label=vp1
3092..3658
/product="viral protein"
/note="putative"
/label=2A
3659..3979
/product="viral protein"
/note="putative"
/label=2B
3980..4984
/product="viral protein"
/note="putative"
/label=2C
4985..5203
/product="viral protein"
/note="putative"
/label=3A
5204..5272
/product="viral protein"
/note="putative"
/label=3B
5273..5929
/product="viral protein"
/note="putative"
/label=3C
5930..7396
/product="viral protein"
/note="putative"
/label=3D
7397..7436
/product="viral protein"
/note="putative"
BASE COUNT 2167 a 1202 c 1632 g 2435 t
ORIGIN
Query Match 0.1%: Score 21; DB 1; Length 7436;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 98116 TGAGCATTTATTAAAGG 98136
|||||
Db 5572 TGAGCATTTATTAAAGG 5592
RESULT 10
AY149710
LOCUS AY149710 207 bp RNA linear VRL 27-NOV-2002
DEFINITION Hepatitis C virus isolate BB88263 NS5 gene, partial cds.
ACCESSION AY149710
VERSION AY149710.1 GI:25807869
KEYWORDS
SOURCE Hepatitis C virus
ORGANISM Hepatitis C virus
REFERENCE 1 (bases 1 to 207)
AUTHORS Chinchai, T., Bedl, K., Jantaradsamee, P., Theamboonlers, A. and Poovorawan, Y.
TITLE Direct Submission
JOURNAL Submitted (11-SEP-2002) Pediatrics, Chulalongkorn University, Ramat, Bangkok 10330, Thailand
FEATURES
source location/Qualifiers
1..207
/organism="Hepatitis C virus"
/viation
/mol_type="genomic RNA"
/isolate="BB88263"
/db_xref="taxon:11103"

CDS

<1..>207
/codon_start=2
/product="NS5"
/protein_id="AAN74604.1"
/db_xref="GI:25807870"
/translation="LEPARKYISLTERLYCGPMFNSKGAQCCYRCRACGVLPTS
FGNTTCYIKATAAKAAGLRNPD"

BASE COUNT 42 a 65 c 60 g 40 t

ORIGIN

Query Match 0.0%; Score 20; DB 1; Length 207;
Best Local Similarity 100.0%; Pred. No. 7.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 86659 AGCGGCTGCGAAGCGCCGAG 86678
|||||
169 AGCGGCTGCGAAGCGCCGAG 188

RESULT 11
HPCNS5AD 222 bp DNA linear VRL 03-JAN-1994
LOCUS Hepatitis C virus type 3a (14) nonstructural protein 5 (NS5) gene,
partial cds.
ACCESSION L23464.1 GI:385086
VERSION nonstructural protein 5.
KEYWORDS Hepatitis C virus type 3a
SOURCE Hepatitis C virus type 3a
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.
REFERENCE 1 (bases 1 to 222)
AUTHORS Simmonds,P., Holmes,E.C., Cha,T.A., Chan,S.W., McOmish,F.,
Irvine,B., Beall,E., Yap,P.L., Kolberg,J. and Urdea,M.S.
TITLE Classification of hepatitis C virus into six major genotypes and a
series of subtypes by phylogenetic analysis of the NS-5 region
J. Gen. Virol. 74 (pt 11), 2391-2399 (1993)
JOURNAL 94065665
MEDLINE 8245854
PUBMED
COMMENT Original source text: Hepatitis C virus type 3a (individual isolate
Italy 14) DNA.
FEATURES
source Location/Qualifiers
1..222
/organism="Hepatitis C virus type 3a"
/mol_type="genomic DNA"
/isolate="Italy 14"
/db_xref="taxon:31652"
1..222
/gene="NS5"
<1..>222
/gene="NS5"
/codon_start=1
/product="nonstructural protein 5"
/protein_id="AAN45634.1"
/db_xref="GI:385087"
/translation="IYCCNLEPARKYISLTERLYCGPMFNSKGAQCCYRCRAS
GVLPTSFGNTTCYIKATAAKAAGLRNPD"

BASE COUNT 47 a 67 c 63 g 45 t

ORIGIN

Query Match 0.0%; Score 20; DB 1; Length 222;
Best Local Similarity 100.0%; Pred. No. 7.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 86659 AGCGGCTGCGAAGCGCCGAG 86678
|||||
186 AGCGGCTGCGAAGCGCCGAG 205

RESULT 12
HPCNS5AE 222 bp DNA linear VRL 03-JAN-1994
LOCUS Hepatitis C virus type 3a (S21) nonstructural protein 5 (NS5) gene,
partial cds.

ACCESSION L23465
VERSION L23465.1 GI:385088
KEYWORDS nonstructural protein 5.
SOURCE Hepatitis C virus type 3a
ORGANISM Hepatitis C virus type 3a
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.
REFERENCE 1 (bases 1 to 222)
AUTHORS Simmonds,P., Holmes,E.C., Cha,T.A., Chan,S.W., McOmish,F.,
Irvine,B., Beall,E., Yap,P.L., Kolberg,J. and Urdea,M.S.
TITLE Classification of hepatitis C virus into six major genotypes and a
series of subtypes by phylogenetic analysis of the NS-5 region
J. Gen. Virol. 74 (pt 11), 2391-2399 (1993)
JOURNAL 94065665
MEDLINE 8245854
PUBMED
COMMENT Original source text: Hepatitis C virus type 3a (individual isolate
Sweden S21) DNA.
FEATURES
source Location/Qualifiers
1..222
/organism="Hepatitis C virus type 3a"
/mol_type="genomic DNA"
/isolate="Sweden S21"
/db_xref="taxon:31652"
1..222
/gene="NS5"
<1..>222
/gene="NS5"
/codon_start=1
/product="nonstructural protein 5"
/protein_id="AAN45635.1"
/db_xref="GI:385089"
/translation="IYCCNLEPARKYISLTERLYCGPMFNSKGAQCCYRCRAS
GVLPTSFGNTTCYIKATAAKAAGLRNPD"

BASE COUNT 48 a 65 c 63 g 46 t

ORIGIN

Query Match 0.0%; Score 20; DB 1; Length 222;
Best Local Similarity 100.0%; Pred. No. 7.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 86659 AGCGGCTGCGAAGCGCCGAG 86678
|||||
186 AGCGGCTGCGAAGCGCCGAG 205

RESULT 13
AY149712 223 bp RNA linear VRL 27-NOV-2002
LOCUS Hepatitis C virus isolate BH1025 NS5 gene, partial cds.
ACCESSION AY149712
VERSION AY149712.1 GI:25807873
KEYWORDS
SOURCE Hepatitis C virus
ORGANISM Hepatitis C virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.
REFERENCE 1 (bases 1 to 223)
AUTHORS Chinchai,T., Bedi,K., Jantaradsamee,P., Theamboonlers,A. and
Poovorawan,Y.
TITLE Direct Submission
JOURNAL Submitted (11-SEP-2002) Pediatrics, Chulalongkorn University,
Rama4, Bangkok 10330, Thailand
FEATURES
source Location/Qualifiers
1..223
/organism="Hepatitis C virus"
/viral
/mol_type="genomic RNA"
/isolate="BH1025"
/db_xref="taxon:11103"
<1..>223
/codon_start=2
/product="NS5"

/protein_id="AA074606.1"
/db_xref="GI:25807874"
/translation="LEPEARKYISLTERLYCGGPMFNSKGAQCGYRRCRASGVLPTS
FGNTTCYIKATRAAKAAGLRNPDPLVCGD"
BASE COUNT 44 a 68 c 66 g 45 t
ORIGIN

Query Match 0.0%; Score 20; DB 1; Length 224;
Best Local Similarity 100.0%; Pred. No. 7.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 86659 AGCGGCTGCGAAGCCGCAG 86678
|||||
169 AGCGGCTGCGAAGCCGCAG 188

RESULT 14
AY149695 224 bp RNA linear VRL 27-NOV-2002
LOCUS Hepatitis C virus isolate BB70646 NS5 gene, partial cds.
DEFINITION
ACCESSION AY149695
VERSION AY149695.1 GI:25807839
KEYWORDS
SOURCE Hepatitis C virus
ORGANISM Hepatitis C virus
REFERENCE 1 (bases 1 to 224)
AUTHORS Chinnchal,T., Bedl,K., Jantaradsamee,P., Theamboonlers,A. and
Poovorawan,Y.
TITLE Direct Submission
JOURNAL Submitted (11-SEP-2002) Pediatrics, Chulalongkorn University,
Ramath, Bangkok 10330, Thailand
FEATURES
source Location/Qualifiers
1..224
/organism="Hepatitis C virus"
/viralon
/mol_type="genomic RNA"
/isolate="BB70646"
/db_xref="taxon:11103"
<1..>224
/codon_start=2
/product="NS5"
/protein_id="AA074589.1"
/db_xref="GI:25807840"
/translation="LEPEARKYISLTERLYCGGPMFNSKGAQCGYRRCRASGVLPTS
FGNTTCYIKATRAAKAAGLRNPDPLVCGD"
BASE COUNT 43 a 69 c 66 g 46 t
ORIGIN

Query Match 0.0%; Score 20; DB 1; Length 224;
Best Local Similarity 100.0%; Pred. No. 7.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 86659 AGCGGCTGCGAAGCCGCAG 86678
|||||
169 AGCGGCTGCGAAGCCGCAG 188

RESULT 15
AY149697 224 bp RNA linear VRL 27-NOV-2002
LOCUS Hepatitis C virus isolate BB1885 NS5 gene, partial cds.
DEFINITION
ACCESSION AY149697
VERSION AY149697.1 GI:25807843
KEYWORDS
SOURCE Hepatitis C virus
ORGANISM Hepatitis C virus
REFERENCE 1 (bases 1 to 224)
AUTHORS Chinnchal,T., Bedl,K., Jantaradsamee,P., Theamboonlers,A. and
Poovorawan,Y.

TITLE Direct Submission
JOURNAL Submitted (11-SEP-2002) Pediatrics, Chulalongkorn University,
Ramath, Bangkok 10330, Thailand
FEATURES
source Location/Qualifiers
1..224
/organism="Hepatitis C virus"
/viralon
/mol_type="genomic RNA"
/isolate="BB11885"
/db_xref="taxon:11103"
<1..>224
/codon_start=2
/product="NS5"
/protein_id="AA074591.1"
/db_xref="GI:25807844"
/translation="LEPEARKYISLTERLYCGGPMFNSKGAQCGYRRCRASGVLPTS
FGNTTCYIKATRAAKAAGLRNPDPLVCGD"
BASE COUNT 43 a 68 c 67 g 46 t
ORIGIN

Query Match 0.0%; Score 20; DB 1; Length 224;
Best Local Similarity 100.0%; Pred. No. 7.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 86659 AGCGGCTGCGAAGCCGCAG 86678
|||||
169 AGCGGCTGCGAAGCCGCAG 188

RESULT 16
AY149699 224 bp RNA linear VRL 27-NOV-2002
LOCUS Hepatitis C virus isolate BB10442 NS5 gene, partial cds.
DEFINITION
ACCESSION AY149699
VERSION AY149699.1 GI:25807847
KEYWORDS
SOURCE Hepatitis C virus
ORGANISM Hepatitis C virus
REFERENCE 1 (bases 1 to 224)
AUTHORS Chinnchal,T., Bedl,K., Jantaradsamee,P., Theamboonlers,A. and
Poovorawan,Y.
TITLE Direct Submission
JOURNAL Submitted (11-SEP-2002) Pediatrics, Chulalongkorn University,
Ramath, Bangkok 10330, Thailand
FEATURES
source Location/Qualifiers
1..224
/organism="Hepatitis C virus"
/viralon
/mol_type="genomic RNA"
/isolate="BB10442"
/db_xref="taxon:11103"
<1..>224
/codon_start=2
/product="NS5"
/protein_id="AA074593.1"
/db_xref="GI:25807848"
/translation="LEPEARKYISLTERLYCGGPMFNSKGAQCGYRRCRASGVLPTS
FGNTTCYIKATRAAKAAGLRNPDPLVCGD"
BASE COUNT 43 a 70 c 66 g 45 t
ORIGIN

Query Match 0.0%; Score 20; DB 1; Length 224;
Best Local Similarity 100.0%; Pred. No. 7.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 86659 AGCGGCTGCGAAGCCGCAG 86678
|||||
169 AGCGGCTGCGAAGCCGCAG 188

RESULT 17

AY149703 224 bp RNA linear VRL 27-NOV-2002
LOCUS
DEFINITION Hepatitis C virus isolate bb07893 NS5 gene, partial cds.
ACCESSION AY149703
VERSION AY149703.1 GI:25807855
KEYWORDS
SOURCE
ORGANISM Hepatitis C virus
Hepatitis C virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.
REFERENCE 1 (bases 1 to 224)
AUTHORS Chinchai,T., Bedl,K., Jantaradsamee,P., Theamboonlers,A. and
POOVORAWAN,Y.
TITLE Direct Submission
JOURNAL Submitted (11-SEP-2002) Pediatrics, Chulalongkorn University,
Rama4, Bangkok 10330, Thailand
FEATURES
source
1..224
/organism="Hepatitis C virus"
/vlon
/mol_type="genomic RNA"
/isolate="BB07893"
/db_xref="taxon:11103"
<1..>224
/codon_start=2
/product="NS5"
/protein_id="AA074597.1"
/db_xref="GI:25807856"
/translation="LEPARKYVSSLTRELYCGGPMFNSKGAQCGYRRCRASGVLPST
FGNTTCYIKATATAKAGLNRPDLVCGD"
BASE COUNT 44 a 68 c 66 g 46 t
ORIGIN
Query Match 0.0%; Score 20; DB 1; Length 224;
Best Local Similarity 100.0%; Pred. No. 7.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 86659 AGCGGCTGCGAAGGCCGCGAG 86678
Db 169 AGCGGCTGCGAAGGCCGCGAG 188
RESULT 18
AY149713 224 bp RNA linear VRL 27-NOV-2002
LOCUS
DEFINITION Hepatitis C virus isolate BB1671 NS5 gene, partial cds.
ACCESSION AY149713
VERSION AY149713.1 GI:25807875
KEYWORDS
SOURCE
ORGANISM Hepatitis C virus
Hepatitis C virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.
REFERENCE 1 (bases 1 to 224)
AUTHORS Chinchai,T., Bedl,K., Jantaradsamee,P., Theamboonlers,A. and
POOVORAWAN,Y.
TITLE Direct Submission
JOURNAL Submitted (11-SEP-2002) Pediatrics, Chulalongkorn University,
Rama4, Bangkok 10330, Thailand
FEATURES
source
1..224
/organism="Hepatitis C virus"
/vlon
/mol_type="genomic RNA"
/isolate="BB1671"
/db_xref="taxon:11103"
<1..>224
/codon_start=2
/product="NS5"
/protein_id="AA074607.1"
/db_xref="GI:25807876"
/translation="LEPARKYVSSLTRELYCGGPMFNSKGAQCGYRRCRASGVLPST
FGNTTCYIKATATAKAGLNRPDLVCGD"

BASE COUNT 44 a 68 c 66 g 46 t
ORIGIN
Query Match 0.0%; Score 20; DB 1; Length 224;
Best Local Similarity 100.0%; Pred. No. 7.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 86659 AGCGGCTGCGAAGGCCGCGAG 86678
Db 169 AGCGGCTGCGAAGGCCGCGAG 188
RESULT 19
AY149715 224 bp RNA linear VRL 27-NOV-2002
LOCUS
DEFINITION Hepatitis C virus isolate BB08720 3a NS5 gene, partial cds.
ACCESSION AY149715
VERSION AY149715.1 GI:25807879
KEYWORDS
SOURCE
ORGANISM Hepatitis C virus
Hepatitis C virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.
REFERENCE 1 (bases 1 to 224)
AUTHORS Chinchai,T., Bedl,K., Jantaradsamee,P., Theamboonlers,A. and
POOVORAWAN,Y.
TITLE Direct Submission
JOURNAL Submitted (11-SEP-2002) Pediatrics, Chulalongkorn University,
Rama4, Bangkok 10330, Thailand
FEATURES
source
1..224
/organism="Hepatitis C virus"
/vlon
/mol_type="genomic RNA"
/isolate="BB08720 3a"
/db_xref="taxon:11103"
<1..>224
/codon_start=2
/product="NS5"
/protein_id="AA074609.1"
/db_xref="GI:25807880"
/translation="LEPARKYVSSLTRELYCGGPMFNSKGAQCGYRRCRASGVLPST
FGNTTCYIKATATAKAGLNRPDLVCGD"
BASE COUNT 42 a 67 c 68 g 47 t
ORIGIN
Query Match 0.0%; Score 20; DB 1; Length 224;
Best Local Similarity 100.0%; Pred. No. 7.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 86659 AGCGGCTGCGAAGGCCGCGAG 86678
Db 169 AGCGGCTGCGAAGGCCGCGAG 188
RESULT 20
AY149717 224 bp RNA linear VRL 27-NOV-2002
LOCUS
DEFINITION Hepatitis C virus isolate BB92597 3a NS5 gene, partial cds.
ACCESSION AY149717
VERSION AY149717.1 GI:25807883
KEYWORDS
SOURCE
ORGANISM Hepatitis C virus
Hepatitis C virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.
REFERENCE 1 (bases 1 to 224)
AUTHORS Chinchai,T., Bedl,K., Jantaradsamee,P., Theamboonlers,A. and
POOVORAWAN,Y.
TITLE Direct Submission
JOURNAL Submitted (11-SEP-2002) Pediatrics, Chulalongkorn University,
Rama4, Bangkok 10330, Thailand
FEATURES
Location/Qualifiers

source
1. .224
/organism="Hepatitis C virus"
/vifion
/mol_type="genomic RNA"
/isolate="BB92597.3a"
/db_xref="taxon:11103"
<1. .>224
/codon_start=2
/product="NS5"
/protein_id="AA074611.1"
/db_xref="GI:25807884"
/translation="LEPEARKVISLTERLYCGGPMFNSKGAQCGYRCRASGVLPFS
FGNTITCYIKATAAKAAGLRNPDLVCGD"
BASE COUNT 42 a 67 c 68 g 47 t
ORIGIN

Query Match 0.0%; Score 20; DB 1; Length 224;
Best Local Similarity 100.0%; Pred. No. 7.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 86659 AGCGCTGCGAAGCGCGCAG 86678
|||||
Db 169 AGCGCTGCGAAGCGCGCAG 188

RESULT 21
AY149724 226 bp RNA linear VRL 27-NOV-2002
LOCUS Hepatitis C virus isolate BB09152 NS5 gene, partial cds.
DEFINITION AY149724
ACCESSION AY149724.1 GI:25807897
VERSION
KEYWORDS
SOURCE Hepatitis C virus
ORGANISM Hepatitis C virus
REFERENCE 1 (bases 1 to 226)
AUTHORS Chinchai,T., Bedi,K., Jantaradamee,P., Theamboonlers,A. and Poonvorawan,Y.
TITLE Direct Submission
JOURNAL Submitted (11-SEP-2002) Pediatrics, Chulalongkorn University, Ramat, Bangkok 10330, Thailand
FEATURES
Location/Qualifiers
1. .226
/organism="Hepatitis C virus"
/vifion
/mol_type="genomic RNA"
/isolate="BB09152"
/db_xref="taxon:11103"
<1. .>226
/codon_start=2
/product="NS5"
/protein_id="AA074618.1"
/db_xref="GI:25807898"
/translation="LEPEARKVISLTERLYCGGPMFNSKGAQCGYRCRASGVLPFS
FGNTITCYIKATAAKAAGLRNPDLVCGEM"
BASE COUNT 44 a 67 c 68 g 47 t
ORIGIN

Query Match 0.0%; Score 20; DB 1; Length 226;
Best Local Similarity 100.0%; Pred. No. 7.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 86659 AGCGCTGCGAAGCGCGCAG 86678
|||||
Db 169 AGCGCTGCGAAGCGCGCAG 188

RESULT 22
AF388468 253 bp RNA linear VRL 08-JAN-2002
LOCUS Hepatitis C virus isolate 680 NS5B (NS5B) gene, partial cds.
DEFINITION AF388468
ACCESSION AF388468

VERSION AF388468.1 GI:18087222
KEYWORDS Hepatitis C virus
SOURCE Hepatitis C virus
ORGANISM Hepatitis C virus
REFERENCE 1 (bases 1 to 253)
AUTHORS Kalina,O., Norder,H., Vetrov,T., Zhdanov,K., Barzunova,M., Plotnikova,V., Mukomolov,S. and Magnus,L.O.
TITLE Shift in predominating subtype of HCV from 1b to 3a in St. Petersburg mediated by increase in injecting drug use
JOURNAL J. Med. Virol. 65 (3), 517-524 (2001)
MEDLINE 21479638
PUBMED 11596087
REFERENCE 2 (bases 1 to 253)
AUTHORS Kalina,O., Norder,H., Vetrov,T., Zhdanov,K., Barzunova,M., Plotnikova,V., Mukomolov,S. and Magnus,L.O.
TITLE Direct Submission
JOURNAL Submitted (06-JUN-2001) Department of Virology, Swedish Institute for Infectious Disease Control, 171 82 Solna, Sweden
FEATURES
Location/Qualifiers
1. .253
/organism="Hepatitis C virus"
/vifion
/mol_type="genomic RNA"
/isolate="680"
/db_xref="taxon:11103"
/note="subtype: 3a"
<1. .>253
/gene="NS5B"
<1. .>253
/gene="NS5B"
/codon_start=1
/product="NS5B"
/protein_id="AA158782.1"
/db_xref="GI:18087223"
/translation="TYOCNLEPEARKVISLTERLYCGGPMFNSKGAQCGYRCRAS
GVLPFSFGNTITCYIKATAAKAAGLRNPDLVCGDLYV"
BASE COUNT 50 a 71 c 75 g 57 t
ORIGIN

Query Match 0.0%; Score 20; DB 1; Length 253;
Best Local Similarity 100.0%; Pred. No. 8;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 86659 AGCGCTGCGAAGCGCGCAG 86678
|||||
Db 186 AGCGCTGCGAAGCGCGCAG 205

RESULT 23
AF388469 253 bp RNA linear VRL 08-JAN-2002
LOCUS Hepatitis C virus isolate 590 NS5B (NS5B) gene, partial cds.
DEFINITION AF388469
ACCESSION AF388469.1 GI:18087224
VERSION
KEYWORDS
SOURCE Hepatitis C virus
ORGANISM Hepatitis C virus
REFERENCE 1 (bases 1 to 253)
AUTHORS Kalina,O., Norder,H., Vetrov,T., Zhdanov,K., Barzunova,M., Plotnikova,V., Mukomolov,S. and Magnus,L.O.
TITLE Shift in predominating subtype of HCV from 1b to 3a in St. Petersburg mediated by increase in injecting drug use
JOURNAL J. Med. Virol. 65 (3), 517-524 (2001)
MEDLINE 21479638
PUBMED 11596087
REFERENCE 2 (bases 1 to 253)
AUTHORS Kalina,O., Norder,H., Vetrov,T., Zhdanov,K., Barzunova,M., Plotnikova,V., Mukomolov,S. and Magnus,L.O.
TITLE Direct Submission

JOURNAL Submitted (06-JUN-2001) Department of Virology, Swedish Institute for Infectious Disease Control, 171 82 Solna, Sweden

FEATURES
source
1.253
/organism="Hepatitis C virus"
/vifion
/mol_type="genomic RNA"
/isolate="580"
/db_xref="taxon:11103"
/note="subtype: 3a"
<1..>253
/gene="NS5B"
<1..>253
/gene="NS5B"
/codon_start=1
/product="NS5B"
/protein_id="AAL58783.1"
/db_xref="GI:18087225"
/translation="TYCCCNLEPEARKVYSSITERLYCGGPMFNSKGACGYRRCRAS
GVLPISFGNTTTCYIKATPAKAAAGLRNDFLVCGDDLVV"

BASE COUNT
51 a 71 c 74 g 57 t

ORIGIN
Query Match 0.0%; Score 20; DB 1; Length 253;
Best Local Similarity 100.0%; Pred. No. 8;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 86659 ACCGGCTGGAGAGCCGCAG 86678
|||||
Db 186 ACGGCTGGAGAGCCGCAG 205

RESULT 24
AF388473 253 bp RNA linear VRL 08-JAN-2002
LOCUS Hepatitis C virus isolate 665 NS5B (NS5B) gene, partial cds.
DEFINITION AF388473
ACCESSION AF388473.1 GI:18087232
VERSION
KEYWORDS
SOURCE Hepatitis C virus
ORGANISM Hepatitis C virus
VIRUSES: ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.
REFERENCE 1 (bases 1 to 253)
AUTHORS Kalinina,O., Norder,H., Vetrov,T., Zhdanov,K., Barzunova,M.,
Plotnikova,V., Mukomolov,S. and Magnus,L.O.
TITLE Shift in predominating subtype of HCV from 1b to 3a in St.
Petersburg mediated by increase in injecting drug use
JOURNAL J. Med. Virol. 65 (3), 517-524 (2001)
MEDLINE 21479638
PUBMED 11596087
REFERENCE 2 (bases 1 to 253)
AUTHORS Kalinina,O., Norder,H., Vetrov,T., Zhdanov,K., Barzunova,M.,
Plotnikova,V., Mukomolov,S. and Magnus,L.O.
TITLE Direct Submission
JOURNAL Submitted (06-JUN-2001) Department of Virology, Swedish Institute
for Infectious Disease Control, 171 82 Solna, Sweden
FEATURES
source
1.253
/organism="Hepatitis C virus"
/vifion
/mol_type="genomic RNA"
/isolate="665"
/db_xref="taxon:11103"
/note="subtype: 3a"
<1..>253
/gene="NS5B"
<1..>253
/gene="NS5B"
/codon_start=1
/product="NS5B"
/protein_id="AAL58787.1"
/db_xref="GI:18087233"

/translation="TYCCCNLEPEARKVYSSITERLYCGGPMFNSKGACGYRRCRAS
GVLPISFGNTTTCYIKATPAKAAAGLRNDFLVCGDDLVV"

BASE COUNT
51 a 69 c 74 g 59 t

ORIGIN
Query Match 0.0%; Score 20; DB 1; Length 253;
Best Local Similarity 100.0%; Pred. No. 8;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 86659 ACCGGCTGGAGAGCCGCAG 86678
|||||
Db 186 ACGGCTGGAGAGCCGCAG 205

RESULT 25
AF388475 253 bp RNA linear VRL 08-JAN-2002
LOCUS Hepatitis C virus isolate 759 NS5B (NS5B) gene, partial cds.
DEFINITION AF388475
ACCESSION AF388475.1 GI:18087236
VERSION
KEYWORDS
SOURCE Hepatitis C virus
ORGANISM Hepatitis C virus
VIRUSES: ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.
REFERENCE 1 (bases 1 to 253)
AUTHORS Kalinina,O., Norder,H., Vetrov,T., Zhdanov,K., Barzunova,M.,
Plotnikova,V., Mukomolov,S. and Magnus,L.O.
TITLE Shift in predominating subtype of HCV from 1b to 3a in St.
Petersburg mediated by increase in injecting drug use
JOURNAL J. Med. Virol. 65 (3), 517-524 (2001)
MEDLINE 21479638
PUBMED 11596087
REFERENCE 2 (bases 1 to 253)
AUTHORS Kalinina,O., Norder,H., Vetrov,T., Zhdanov,K., Barzunova,M.,
Plotnikova,V., Mukomolov,S. and Magnus,L.O.
TITLE Direct Submission
JOURNAL Submitted (06-JUN-2001) Department of Virology, Swedish Institute
for Infectious Disease Control, 171 82 Solna, Sweden
FEATURES
source
1.253
/organism="Hepatitis C virus"
/vifion
/mol_type="genomic RNA"
/isolate="759"
/db_xref="taxon:11103"
/note="subtype: 3a"
<1..>253
/gene="NS5B"
<1..>253
/gene="NS5B"
/codon_start=1
/product="NS5B"
/protein_id="AAL58789.1"
/db_xref="GI:18087237"
/translation="TYCCCNLEPEARKVYSSITERLYCGGPMFNSKGACGYRRCRAS
GVLPISFGNTTTCYIKATPAKAAAGLRNDFLVCGDDLVV"

BASE COUNT
53 a 72 c 72 g 56 t

ORIGIN
Query Match 0.0%; Score 20; DB 1; Length 253;
Best Local Similarity 100.0%; Pred. No. 8;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 86659 ACCGGCTGGAGAGCCGCAG 86678
|||||
Db 186 ACGGCTGGAGAGCCGCAG 205

RESULT 26
AF388516 253 bp RNA linear VRL 08-JAN-2002
LOCUS Hepatitis C virus isolate 631 NS5B (NS5B) gene, partial cds.
DEFINITION

ACCESSION	AF388516
VERSION	AF388516.1 GI:18087318
KEYWORDS	
SOURCE	Hepatitis C virus
ORGANISM	Hepatitis C virus Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepadnavirus.
REFERENCE	1 (bases 1 to 253) Kalinina,O., Norder,H., Vetrov,T., Zhdanov,K., Barzunova,M., Plotnikova,V., Mukomolov,S. and Magnius,L.O. Shift in predominating subtype of HCV from 1b to 3a in St. Petersburg mediated by increase in infecting drug use J. Med. Virol. 65 (3), 517-524 (2001)
AUTHORS	J. Med. Virol. 65 (3), 517-524 (2001)
MEDLINE	21479638
PUBMED	11596087
REFERENCE	2 (bases 1 to 253) Kalinina,O., Norder,H., Vetrov,T., Zhdanov,K., Barzunova,M., Plotnikova,V., Mukomolov,S. and Magnius,L.O. Direct Submission Submitted (06-JUN-2001) Department of Virology, Swedish Institute for Infectious Disease Control, 171 82 Solna, Sweden
TITLE	location/Qualifiers
JOURNAL	1..253
FEATURES	/organism="Hepatitis C virus" /vifion /mol_type="genomic RNA" /isolate="631" /db_xref="taxon:11103" /note="subtype: 3a" <1..>253 /gene="NS5B" <1..>253 /gene="NS5B" /codon_start=1 /product="NS5B" /protein_id="AA158830.1" /db_xref="GI:18087319" /translation="TTCGCCHEPPARVISLTERLYCGGFMENSKAGQCYRRCRAS GVLPSTSGNITTCIKATPAAKAGLNRPDLVGGDDLIV"
BASE COUNT	51 a 69 c 74 g 59 t
ORIGIN	
Query Match	0.0%; Score 20; DB 1; Length 253;
Best Local Similarity	100.0%; Pred. No. 8;
Matches	20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY	86659 AGCGCTGCGAAGCCGCGAG 86678
DB	186 AGCGCTGCGAAGCCGCGAG 205
RESULT 27	
LOCUS	AF506554 318 bp RNA linear VRL_04-JUN-2002
DEFINITION	Hepatitis C virus isolate RIG398 polypeptide precursor gene, NS5B region, partial cds.
ACCESSION	AF506554
VERSION	AF506554.1 GI:21321465
KEYWORDS	
SOURCE	Hepatitis C virus
ORGANISM	Hepatitis C virus Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepadnavirus.
REFERENCE	1 (bases 1 to 318) Shustov,A.V., Gavrilova,I.V. and Netesov,S.V. Genetic variability of hepatitis C virus in Western Siberia Unpublished 2 (bases 1 to 318) Shustov,A.V., Gavrilova,I.V. and Netesov,S.V. Direct Submission Submitted (26-APR-2002) Inst. Molecular Biology, State Research Center "Vector", Src VB "vector", Koltsovo, Novosibirskaya obl. 630559, Russia
AUTHORS	
JOURNAL	
TITLE	

FEATURES	location/Qualifiers
SOURCE	1. .318 /organism="Hepatitis C virus" /mol_type="genomic RNA" /isolate="RIG398" /db_xref="taxon:11103" /country="Russia" 1. .>318 /codon_start=1 /product="polyprotein precursor" /protein_id="AA047211.1" /db_xref="GI:21321466" /translation="OCCTLPPEAKKVVSLTERLYCGGPMFNKSGAOCGYRRRASGV LPFSFGNTITCYIKATATAAKAAGLRDPFLVCGDDLVYVAESDGVDEDRKALAFRTDA MTKY"
CDS	
mat_peptide	<1. .>318 /product="NS5B"
BASE COUNT	65 a 87 c 98 g 68 t
ORIGIN	
Query Match	0.0%; Score 20; DB 1; Length 318; Best Local Similarity 100.0%; Pred. No. 8.1; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	86659 AGCGGTCGCAAGCGCCAG 86678
Db	180 AGCGGTCGCAAGCGCCAG 199
RESULT 28	
AF506566	323 bp RNA linear VRL 04-JUN-2002
LOCUS	Hepatitis C virus isolate RIG403 polyprotein precursor gene, NS5B
DEFINITION	region, partial cds.
ACCESSION	AF506566
VERSION	AF506566.1 GI:21321487
KEYWORDS	Hepatitis C virus Hepatitis C virus viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepacivirus.
ORGANISM	1 (bases 1 to 323) Shustov,A.V., Gavrilova,I.V. and Netesov,S.V. Genetic variability of hepatitis C virus in Western Siberia Unpublished 2 (bases 1 to 323) Shustov,A.V., Gavrilova,I.V. and Netesov,S.V. Direct submission Submitted (26-APR-2002) Inst. Molecular Biology, State Research Center 'Vector', SRC VB 'Vector', Koltsovo, Novosibirskaya obl. 630559, Russia
FEATURES	Location/Qualifiers
source	1. .323 /organism="Hepatitis C virus" /mol_type="genomic RNA" /isolate="RIG403" /db_xref="taxon:11103" /country="Russia" 1. .>323 /codon_start=1 /product="polyprotein precursor" /protein_id="AA047221.1" /db_xref="GI:21321488" /translation="VTNAVTLTKPARKVISLTERLYCGGPMFNKSGAOCYLLARCA SGVTFSGNTITCYIKATATAAKAAGLRNDPLVCGDDLVYVAESDGVDEDRVALRAAF TEAMT"
CDS	<1. .>323 /product="NS5B"
BASE COUNT	68 a 86 c 99 g 70 t
ORIGIN	
Query Match	0.0%; Score 20; DB 1; Length 323; Best Local Similarity 100.0%; Pred. No. 8.1;

Matches 20: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 86659 ACCGGCTGCGAAGCCGCAG 86678
|||||
Db 189 ACCGGCTGCGAAGCCGCAG 208

RESULT 29
HEC507267 327 bp RNA linear VRL 08-SEP-2002
LOCUS Hepatitis C virus partial gene for NS5B protein, isolate KGV244.
DEFINITION AJ507267 GI:22799051
ACCESSION
VERSION NS5B protein.
KEYWORDS Hepatitis C virus
SOURCE Hepatitis C virus
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepciviruses.

REFERENCE 1
AUTHORS Shustov,A.V., Gavrilova,I.V. and Netesov,S.V.
TITLE Genetic variability of hepatitis C virus in Siberia
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 327)
AUTHORS Shustov,A.V.
TITLE Direct Submission
JOURNAL Submitted (01-SEP-2002) Shustov A. V., Inst. Molecular Biology,
State Research Center of Virology and Biotechnology VECTOR, 630559,
Koltsovo, Novosibirsk region, RUSSIA
LOCATION/Qualifiers

FEATURES
source 1..327
/organism="Hepatitis C virus"
/mol_type="genomic RNA"
/isolate="KGV244"
/db_xref="taxon:11103"
<1..>327
/codon_start=1
/product="NS5B protein"
/protein_id="CAD45268.1"
/db_xref="GI:22799052"
/translation="EEETVCCDLEPEARKVTSITERYCGGPMFNSKGAQCGYRRC
RASGVLPSTFSGNTICYIKATMAAKAGLRNDFVCGDDLVVAESDGVDEGALRL
AFTERAMT"
CDS
BASE COUNT 68 a 85 c 105 g 69 t
ORIGIN

Query Match 0.0%; Score 20; DB 1; Length 327;
Best Local Similarity 100.0%; Pred. No. 8.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 86659 ACCGGCTGCGAAGCCGCAG 86678
|||||
Db 195 ACCGGCTGCGAAGCCGCAG 214

RESULT 30
AF506542 329 bp RNA linear VRL 04-JUN-2002
LOCUS Hepatitis C virus isolate KGV231 nonfunctional NS5B gene, partial
DEFINITION AF506542
ACCESSION sequence.
VERSION AF506542
KEYWORDS AF506542.1 GI:21321444
SOURCE Hepatitis C virus
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepciviruses.
REFERENCE 1 (bases 1 to 329)
AUTHORS Shustov,A.V., Gavrilova,I.V. and Netesov,S.V.
TITLE Genetic variability of hepatitis C virus in Western Siberia
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 329)
AUTHORS Shustov,A.V., Gavrilova,I.V. and Netesov,S.V.
TITLE Direct Submission

JOURNAL Submitted (26-APR-2002) Inst. Molecular Biology, State Research
Center 'Vector', SRC VB 'Vector', Koltsovo, Novosibirskaya obl.
630559, Russia
FEATURES
source 1..329
Location/Qualifiers
/organism="Hepatitis C virus"
/mol_type="genomic RNA"
/isolate="KGV231"
/db_xref="taxon:11103"
/country="Russia"
<1..>329
/note="nonfunctional NS5B protein due to mutation;
polyprotein precursor"

BASE COUNT 70 a 87 c 103 g 69 t
ORIGIN

Query Match 0.0%; Score 20; DB 1; Length 329;
Best Local Similarity 100.0%; Pred. No. 8.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 86659 ACCGGCTGCGAAGCCGCAG 86678
|||||
Db 190 ACCGGCTGCGAAGCCGCAG 209

RESULT 31
AF506546 329 bp RNA linear VRL 04-JUN-2002
LOCUS Hepatitis C virus isolate RIG450 nonfunctional NS5B gene, partial
DEFINITION AF506546
ACCESSION AF506546
VERSION AF506546.1 GI:21321450
KEYWORDS Hepatitis C virus
SOURCE Hepatitis C virus
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepciviruses.
REFERENCE 1 (bases 1 to 329)
AUTHORS Shustov,A.V., Gavrilova,I.V. and Netesov,S.V.
TITLE Genetic variability of hepatitis C virus in Western Siberia
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 329)
AUTHORS Shustov,A.V., Gavrilova,I.V. and Netesov,S.V.
TITLE Direct Submission
JOURNAL Submitted (26-APR-2002) Inst. Molecular Biology, State Research
Center 'Vector', SRC VB 'Vector', Koltsovo, Novosibirskaya obl.
630559, Russia
LOCATION/Qualifiers

FEATURES
source 1..329
/organism="Hepatitis C virus"
/mol_type="genomic RNA"
/isolate="RIG450"
/db_xref="taxon:11103"
/country="Russia"
<1..>329
/note="nonfunctional NS5B protein due to mutation;
polyprotein precursor"

misc-feature
BASE COUNT 71 a 86 c 105 g 67 t
ORIGIN

Query Match 0.0%; Score 20; DB 1; Length 329;
Best Local Similarity 100.0%; Pred. No. 8.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 86659 ACCGGCTGCGAAGCCGCAG 86678
|||||
Db 191 ACCGGCTGCGAAGCCGCAG 210

RESULT 32
AY257434 332 bp RNA linear VRL 14-MAY-2003
LOCUS Hepatitis C virus isolate Mar14 NS5b (NS5b) gene, partial cds.
DEFINITION

ACCESSION AV257434
VERSION AV257434.1 GI:30720337
KEYWORDS
SOURCE Hepatitis C virus
ORGANISM Hepatitis C virus
VIRUSES: ssRNA positive-strand viruses, no DNA stage: Flaviviridae;
Hepacivirus.

REFERENCE
AUTHORS 1 (bases 1 to 332)
Martial,J., Morice,Y., Abel,S., Cable,A., Rat,C., Lombard,F.,
Edouard,A., Pierre-Louis,S., Garsaud,P., Bera,O., Chout,R.,
Gordien,E., Dery,P. and Cesaire,R.
Hepatitis C virus (HCV) genotypes in the Caribbean island of
Martinique: evidence for a large radiation of HCV-2 and for a
recent introduction from Europe of HCV-4
Unpublished

JOURNAL 2 (bases 1 to 332)
REFERENCE
AUTHORS Martial,J., Morice,Y., Abel,S., Cable,A., Rat,C., Lombard,F.,
Edouard,A., Pierre-Louis,S., Garsaud,P., Bera,O., Chout,R.,
Gordien,E., Dery,P. and Cesaire,R.
Direct Submission
Submitted (17-MAR-2003) Laboratoire de Virologie-Immunologie,
Centre Hospitalier Universitaire de Fort-de-France, Hopital
Pierre-Zobda-Oultman, Fort-de-France, Martinique 97261, France

FEATURES
source
1..332
Location/Qualifiers
/organism="Hepatitis C virus"
/viation
/mol_type="genomic RNA"
/isolate="Martia"
/db_xref="taxon:11103"
/country="Martinique"
/note="type: 3a"
<1..>332
/gene="NS5b"
<1..>332
/gene="NS5b"
/codon_start=2
/product="NS5b"
/protein_id="AAP33856.1"
/db_xref="GI:30720338"
/translation="TVTEODIRVEEETIYOCNLEPPARKYISSLTERLYCGGPMFNK
GAOCYRCRASGVLPFSFGNTTCYIKATAAKAAGLRNPDPLVCGDDLVVAESDG
VDEDRALV"

BASE COUNT 77 a 86 c 102 g 67 t
ORIGIN

Query Match 0.0%; Score 20; DB 1; Length 332;
Best Local Similarity 100.0%; Pred. No. 8.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 86659 AGCGGCTGCGAGCGCCGAG 86678
|||||
Db 223 AGCGGCTGCGAGCGCCGAG 242

RESULT 33
AB081064 336 bp RNA linear VRL 06-AUG-2002
LOCUS
DEFINITION Hepatitis C virus gene for polypeptide (NS5B region), partial cds,
strain:037.
ACCESSION AB081064
VERSION AB081064.1 GI:22122150
KEYWORDS
SOURCE Hepatitis C virus
ORGANISM Hepatitis C virus
VIRUSES: ssRNA positive-strand viruses, no DNA stage: Flaviviridae;
Hepacivirus.

REFERENCE
AUTHORS 1
TITLE Kurbanov,F.M., Tanaka,Y., Orito,E., Mizokami,M. and Ruzhybakiev,R.M.
JOURNAL Molecular epidemiology of hepatitis C virus in Uzbekistan
REFERENCE 2 (bases 1 to 336)
Tanaka,Y., Kurbanov,F. and Mizokami,M.

TITLE Direct Submission
JOURNAL Submitted (06-MAR-2002) Yasunito Tanaka, Nagoya City University
Graduate School of Medical Sciences, Department of Clinical
Molecular Informative Medicine, Kawasumi, Mizuno, Nagoya 467-8601,
Japan (E-mail:ytanaka@med.nagoya-cu.ac.jp,
Tel:81-52-851-5511(ex.8292), Fax:81-52-842-0021)
Location/Qualifiers
1..336
/organism="Hepatitis C virus"
/mol_type="genomic RNA"
/strain="U37"
/db_xref="taxon:11103"
<1..>336
/note="NS5B"
/codon_start=2
/product="polyprotein"
/protein_id="BAC07218.1"
/db_xref="GI:22122151"
/translation="TVTEODIRVEEETIYOCNLEPPARKYISSLTERLYCGGPMFNK
GAOCYRCRASGVLPFSFGNTTCYIKATAAKAAGLRNPDPLVCGDDLVVAESDG
VDEDRALRV"

BASE COUNT 77 a 82 c 105 g 72 t
ORIGIN

Query Match 0.0%; Score 20; DB 1; Length 336;
Best Local Similarity 100.0%; Pred. No. 8.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 86659 AGCGGCTGCGAGCGCCGAG 86678
|||||
Db 223 AGCGGCTGCGAGCGCCGAG 242

RESULT 34
D14179 337 bp RNA linear VRL 03-FEB-1999
LOCUS
DEFINITION Hepatitis C virus genomic RNA for NS5, partial cds.
D14179
ACCESSION D14179.1 GI:1783186
VERSION
KEYWORDS NS5
SOURCE Hepatitis C virus
ORGANISM Hepatitis C virus
VIRUSES: ssRNA positive-strand viruses, no DNA stage: Flaviviridae;
Hepacivirus.

REFERENCE 1 (bases 1 to 337)
AUTHORS Okamoto,H.
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 337)
AUTHORS Okamoto,H.
TITLE Direct Submission
JOURNAL Submitted (25-JAN-1993) Hiroaki Okamoto, Jichi Medical School,
Immunology Division: Minamikawachi-machi, Kawachi-gun, Tochigi
329-04, Japan (E-mail:hokamoto@jichi.ac.jp,
Tel:0285-44-2111(ex.3354), Fax:0285-44-1357)
Location/Qualifiers
1..337
/organism="Hepatitis C virus"
/mol_type="genomic RNA"
/isolate="Mal-HM"
/db_xref="taxon:11103"
<1..>337
/codon_start=2
/product="NS5"
/protein_id="BAA03214.1"
/db_xref="GI:1783187"
/translation="TVTEODIRVEEETIYOCNLEPPARKYISSLTERLYCGGPMFNK
GAOCYRCRASGVLPFSFGNTTCYIKATAAKAAGLRNPDPLVCGDDLVVAESDG
VDEDRALRV"

BASE COUNT 75 a 88 c 106 g 68 t
ORIGIN

Query Match 0.0%; Score 20; DB 1; Length 337;
Best Local Similarity 100.0%; Pred. No. 8.1;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 86659 AGCGGCTGCGAAGCCGCGAG 86678
|||||
Db 223 AGCGGCTGCGAAGCCGCGAG 242

RESULT 35
HPCNS5A22 337 bp RNA linear VRL 03-FEB-1999
LOCUS Hepatitis C virus gene for NS5, partial cds, isolate HEM26.
DEFINITION D14214
ACCESSION D14214.1 GI:529638
VERSION NS5.
KEYWORDS Hepatitis C virus
SOURCE Hepatitis C virus
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.
1 (bases 1 to 337)
REFERENCE 1 Tokita, H. and Okamoto, H.
AUTHORS Unpublished
JOURNAL 2 (bases 1 to 337)
REFERENCE 2 (bases 1 to 337)
AUTHORS Okamoto, H.
TITLE Direct Submission
JOURNAL Submitted (25-JAN-1993) Hiroaki Okamoto, Jichi Medical School,
Immunology Division, Minamikawachi-machi, Kawachi-gun, Tochigi
329-04, Japan (E-mail: hokamoto@ichi.ac.jp,
Tel:0285-44-2111(ex.334), Fax:0285-44-1557)
Location/Qualifiers
1.337
FEATURES
source
/organism="Hepatitis C virus"
/mol_type="genomic RNA"
/isolate="HEM26"
/db_xref="taxon:11103"
<1..>337
/codon_start=2
/product="NS5"
/protein_id="BAA03242.1"
/db_xref="GI:529638"
/translation="TVTEQDIVEEEIYOCNLEPEARKYISLTERLYCGGPMENSK
GAOCGYRRCRASGVLPFSFGNTTCYIKATAAKAAGLRNPDFLVCGDDLVVAESDG
VDEDRALRA"

BASE COUNT 76 a 86 c 105 g 70 t

ORIGIN

Query Match 0.0%; Score 20; DB 1; Length 337;
Best Local Similarity 100.0%; Pred. No. 8.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 86659 AGCGGCTGCGAAGCCGCGAG 86678
|||||
Db 223 AGCGGCTGCGAAGCCGCGAG 242

RESULT 36
AF515972 339 bp RNA linear VRL 29-MAR-2003
LOCUS Hepatitis C virus isolate P8.Don non-structural protein NS5-B
DEFINITION (NS5-b) gene, partial cds.
ACCESSION AF515972
VERSION AF515972.1 GI:29365772
KEYWORDS Hepatitis C virus
SOURCE Hepatitis C virus
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.
1 (bases 1 to 339)
REFERENCE 1 Cantaloube, J.F., Bigini, P., Attoui, H., Gallian, P., de Micco, P. and
AUTHORS de Lamballerie, X.
TITLE Evolution of hepatitis C virus in blood donors and their respective
JOURNAL recipients
MEDLINE J. Gen. Virol. 84 (Pt 2), 441-446 (2003)
22447295

PUBMED 12560577
REFERENCE 2 (bases 1 to 339)
AUTHORS Cantaloube, J.F., de Micco, P. and de Lamballerie, X.
TITLE Direct Submission
JOURNAL Submitted (29-MAY-2002) Emerging Viruses Department, ERS
Alpes-Mediterranee, 149 Boulevard Baillie, Marseille 13005, France
Location/Qualifiers
1.339
FEATURES
source
/organism="Hepatitis C virus"
/virlon
/mol_type="genomic RNA"
/isolate="P8.Don"
/db_xref="taxon:11103"
/note="genotype: 3a"
<1..>339
/gene="NS5-B"
<1..>339
/product="non-structural protein NS5-B"
/protein_id="AA083279.1"
/db_xref="GI:29365773"
/translation="STVTEQDIVEEEIYOCNLEPEARKYISLTERLYCGGPMENSK
GAOCGYRRCRASGVLPFSFGNTTCYIKATAAKAAGLRNPDFLVCGDDLVVAESD
GVDEDRALRA"

BASE COUNT 77 a 88 c 104 g 70 t

ORIGIN

Query Match 0.0%; Score 20; DB 1; Length 339;
Best Local Similarity 100.0%; Pred. No. 8.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 86659 AGCGGCTGCGAAGCCGCGAG 86678
|||||
Db 225 AGCGGCTGCGAAGCCGCGAG 244

RESULT 37
HC061361 340 bp mRNA linear VRL 15-JUL-1996
LOCUS Hepatitis C virus nonstructural protein (ns5b) mRNA, partial cds.
DEFINITION U61361
ACCESSION U61361.1 GI:1420933
VERSION U61361.1 GI:1420933
KEYWORDS Hepatitis C virus
SOURCE Hepatitis C virus
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.
1 (bases 1 to 340)
REFERENCE 1 Stuyver, L., Wisse, A., van Arnhem, W., Hernandez, F. and Maertens, G.
AUTHORS Direct Submission
JOURNAL Submitted (20-JUN-1996) Nucleic Acid Chemistry, Innogenetics,
Industriepark 7, Box 4, Gent 9052, Belgium
Location/Qualifiers
1.340
FEATURES
source
/organism="Hepatitis C virus"
/mol_type="mRNA"
/db_xref="taxon:11103"
/note="type 3a sequence from French blood donor"
1.340
/gene="ns5b"
<1..>340
/gene="ns5b"
/codon_start=2
/product="nonstructural protein"
/protein_id="AAB03842.1"
/db_xref="GI:1420934"
/translation="STVTEQDIVEEEIYOCNLEPEARKYISLTERLYCGGPMENSK
GAOCGYRRCRASGVLPFSFGNTTCYIKATAAKAAGLRNPDFLVCGDDLVVAESD
GVDEDRALRA"

BASE COUNT 77 a 89 c 105 g 69 t

ORIGIN

Query Match 0.0%; Score 20; DB 1; Length 340;
Best Local Similarity 100.0%; Pred. No. 8.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 86659 AGCGGCTCGAAGCGCCGAG 86678
|||||
226 AGCGGCTCGAAGCGCCGAG 245

RESULT 38
LOCUS HPC1 340 bp RNA linear VRL 23-JUN-1999
DEFINITION Hepatitis C virus (HCV) T-1(HCV-Ta) gene, partial sequence.
ACCESSION D10078
VERSION D10078.1 GI:221678
KEYWORDS T-1(HCV-Ta).
SOURCE Hepatitis C virus
ORGANISM Hepatitis C virus
VIRUSES: ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepcivirus.
REFERENCE 1 (bases 1 to 340)
Mori, S., Kato, N., Yagyu, A., Tanaka, T., Ikeda, Y., Petchclai, B., Chiewslip, P., Kurimura, T. and Shimotohno, K.
A new type of hepatitis C virus in patients in Thailand
JOURNAL Blochem. Biophys. Res. Commun. 183 (1), 334-342 (1992)
MEDLINE 92181465
PUBMED 1311926
COMMENT Data kindly submitted in computer readable form by: Shigenisa Mori

FEATURES
source National Cancer Center
Research Institute
5-1-1 Tsukiji, Chuo-ku
Tokyo 104
Japan
Phone: 03-3542-2511 x4702
Fax: 813-3545-3567.
Location/Qualifiers
1..340
/organism="Hepatitis C virus"
/mol_type="genomic RNA"
/strain="T1"
/db_xref="taxon:11103"
1..340
/gene="T-1(HCV-Ta)"
<1..>340
/codon_start=2
/protein_id="BA00972.1"
/db_xref="GI:221678"
/translation="STVTEODIRVEEIIYCCNLEPEARKVISSLTERLYCGP
MNSKAGCGYRCRAGSVLPFSFGNTITCYIKATAAKAAGLRNPDLVCGDDLVVAESD
GVDEEDRALRA"

BASE COUNT 76 a 92 c 106 g 66 t

ORIGIN

Query Match 0.0%; Score 20; DB 1; Length 340;
Best Local Similarity 100.0%; Pred. No. 8.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 86659 AGCGGCTCGAAGCGCCGAG 86678
|||||
226 AGCGGCTCGAAGCGCCGAG 245

RESULT 39
LOCUS AF506608 378 bp RNA linear VRL 04-JUN-2002
DEFINITION Hepatitis C virus isolate SGF65 polypeptide precursor gene, NSSB
region, partial cds.
ACCESSION AF506608
VERSION AF506608.1 GI:21321566
KEYWORDS Hepatitis C virus
SOURCE

ORGANISM Hepatitis C virus
VIRUSES: ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepcivirus.
REFERENCE 1 (bases 1 to 378)
Autors Shustov, A.V., Gavrilova, I.V. and Netesov, S.V.
Genetic variability of hepatitis C virus in Western Siberia
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 378)
Autors Shustov, A.V., Gavrilova, I.V. and Netesov, S.V.
Direct Submission
TITLE Submitted (26-APR-2002) Inst. Molecular Biology, State Research
JOURNAL Center 'Vector', SRC VB 'Vector', Koltsovo, Novosibirskaya obl.
630559, Russia
Location/Qualifiers
1..378
/organism="Hepatitis C virus"
/mol_type="genomic RNA"
/isolate="SGF65"
/db_xref="taxon:11103"
/country="Russia"
<1..>378
/codon_start=3
/product="polypeptide precursor"
/protein_id="AA047258.1"
/db_xref="GI:21321567"
/translation="CCFDSVTEODIRVEEIIYCCNLEPEARKVISSLTERLYCGP
MNSKAGCGYRCRAGSVLPFSFGNTITCYIKATAAKAAGLRNPDLVCGDDLVVA
AESDGVDEEDRALRAFTFAMTRY"
<1..>378
/product="NSSB"
mat_peptide 83 a 98 c 115 g 82 t

BASE COUNT 83 a 98 c 115 g 82 t

ORIGIN

Query Match 0.0%; Score 20; DB 1; Length 378;
Best Local Similarity 100.0%; Pred. No. 8.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 86659 AGCGGCTCGAAGCGCCGAG 86678
|||||
239 AGCGGCTCGAAGCGCCGAG 258

RESULT 40
LOCUS AF506582 391 bp RNA linear VRL 04-JUN-2002
DEFINITION Hepatitis C virus isolate RIG101 polypeptide precursor gene, NSSB
region, partial cds.
ACCESSION AF506582
VERSION AF506582.1 GI:21321517
KEYWORDS Hepatitis C virus
SOURCE Hepatitis C virus
ORGANISM Hepatitis C virus
VIRUSES: ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepcivirus.
REFERENCE 1 (bases 1 to 391)
Autors Shustov, A.V., Gavrilova, I.V. and Netesov, S.V.
Genetic variability of hepatitis C virus in Western Siberia
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 391)
Autors Shustov, A.V., Gavrilova, I.V. and Netesov, S.V.
Direct Submission
TITLE Submitted (26-APR-2002) Inst. Molecular Biology, State Research
JOURNAL Center 'Vector', SRC VB 'Vector', Koltsovo, Novosibirskaya obl.
630559, Russia
Location/Qualifiers
1..391
/organism="Hepatitis C virus"
/mol_type="genomic RNA"
/isolate="RIG101"
/db_xref="taxon:11103"
/country="Russia"
<1..>391
/codon_start=1

mat_peptide
BASE COUNT 85 a 100 c 118 g 88 t
ORIGIN

Query Match 0.0%; Score 20; DB 1; Length 391;
Best Local Similarity 100.0%; Pred. No. 8.2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 86659 AGCGGCTGCGAAGCCGCGAG 86678
|||||
Db 252 AGCGGCTGCGAAGCCGCGAG 271

RESULT 41
AF506586 392 bp RNA linear VRL 04-JUN-2002
LOCUS Hepatitis C virus isolate RI6132 polyprotein precursor gene, NS5B
DEFINITION region, partial cds.
ACCESSION AF506586 GI:21321525
VERSION AF506586.1 GI:21321525
KEYWORDS
SOURCE Hepatitis C virus
ORGANISM Hepatitis C virus
VIRUSES: ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepadnavirus.

REFERENCE 1 (bases 1 to 392)
AUTHORS Shustov,A.V., Gavrilova,I.V. and Netesov,S.V.
TITLE Genetic variability of hepatitis C virus in Western Siberia
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 392)
AUTHORS Shustov,A.V., Gavrilova,I.V. and Netesov,S.V.
TITLE Direct Submission
JOURNAL Submitted (26-APR-2002) Inst. Molecular Biology, State Research Center 'Vector', SRC VB 'Vector', Koltsovo, Novosibirskaya obl. 630559, Russia

FEATURES
Location/Qualifiers
source 1..392
/organism="Hepatitis C virus"
/mol_type="genomic RNA"
/isolate="RI6132"
/db_xref="taxon:11103"
/country="Russia"
<1..>392
/codon_start=1
/product="polyprotein precursor"
/protein_id="AA047239.1"
/db_xref="GI:21321526"
/translation="FSYDRCFSDTVTEODIRVEEETIYCCNLEPARKYISITERL YCGPMFNKSGACGYRCRACASVLPFSFNTITCYIKATAAKAAGLRNPDVLCGD DLVVAESDGVDDRALRAFTFAMTRY"
<1..>392
mat_peptide /product="NS5B"
BASE COUNT 84 a 101 c 119 g 88 t
ORIGIN

Query Match 0.0%; Score 20; DB 1; Length 392;
Best Local Similarity 100.0%; Pred. No. 8.2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 86659 AGCGGCTGCGAAGCCGCGAG 86678
|||||
Db 252 AGCGGCTGCGAAGCCGCGAG 271

RESULT 42
AY100081

LOCUS AY100081 678 bp RNA linear VRL 04-NOV-2002
DEFINITION Hepatitis C virus isolate L6 NS5B protein (NS5B) gene, partial cds.
ACCESSION AY100081
VERSION AY100081.1 GI:21065079
KEYWORDS
SOURCE Hepatitis C virus
ORGANISM Hepatitis C virus
VIRUSES: ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepadnavirus.

REFERENCE 1 (bases 1 to 678)
AUTHORS Cochran,A., Searle,B., Hardie,A., Robertson,R., Delahooke,T., Cameron,S., Tedder,R.S., Dushenko,G.M., De Lamballerie,X. and Simmonds,P.
TITLE A genetic analysis of hepatitis C virus transmission between injection drug users
JOURNAL J. Infect. Dis. 186 (9), 1212-1221 (2002)
MEDLINE 22289487
PUBMED 12402190

REFERENCE 2 (bases 1 to 678)
AUTHORS Cochran,A. and Simmonds,P.
TITLE Direct Submission
JOURNAL Submitted (25-APR-2002) Laboratory for Clinical and Molecular Virology, University of Edinburgh, Summerhall, Edinburgh, Scotland EH9 1QH, United Kingdom

FEATURES
Location/Qualifiers
source 1..678
/organism="Hepatitis C virus"
/mol_type="genomic RNA"
/isolate="L6"
/isolation_source="from serum of patient in risk group IDU from London, England, United Kingdom"
/db_xref="taxon:11103"
/country="United Kingdom"
/note="genotype: 3a"
<1..>678
/gene="NS5B"
<1..>678
/gene="NS5B"
/codon_start=2
/product="NS5B protein"
/protein_id="AA029008.1"
/db_xref="GI:21065080"
/translation="RVEEETIYCCNLEPARKYISITERLYCGPMFNKSGACGRCRASGLVLPFSFNTITCYIKATAAKAAGLRNPDVLCGDDLVVAESDGVDDRALRAFTFAMTRYSAAPGDAPQATVDLEITSCSNVSARDDKGRXYLRRDATTPLA RAAMETVRRHTPVNSMLGNITMYAPTIVRWMTHTFSSILQSOEILDRPDPFMYGAT YSVXPLX"

BASE COUNT 146 a 193 c 179 g 156 t 4 others
ORIGIN

Query Match 0.0%; Score 20; DB 1; Length 678;
Best Local Similarity 100.0%; Pred. No. 8.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 86659 AGCGGCTGCGAAGCCGCGAG 86678
|||||
Db 202 AGCGGCTGCGAAGCCGCGAG 221

RESULT 43
AF516375 681 bp RNA linear VRL 04-NOV-2002
LOCUS AF516375
DEFINITION Hepatitis C virus isolate 195 NS5B gene, partial cds.
ACCESSION AF516375
VERSION AF516375.1 GI:21591680
KEYWORDS
SOURCE Hepatitis C virus
ORGANISM Hepatitis C virus
VIRUSES: ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepadnavirus.

REFERENCE 1 (bases 1 to 681)
AUTHORS Cochran,A., Searle,B., Hardie,A., Robertson,R., Delahooke,T., Cameron,S., Tedder,R.S., Dushenko,G.M., De Lamballerie,X. and

TITLE
A Genetic Analysis of Hepatitis C Virus Transmission between
Injection Drug Users
JOURNAL
J. Infect. Dis. 186 (9), 1212-1221 (2002)
MEDLINE
22289487
PUBMED
12402190
REFERENCE
2 (bases 1 to 681)
AUTHORS
Cochrane, A. and Simmonds, P.
TITLE
Direct Submission
JOURNAL
Submitted (29-MAY-2002) Laboratory of Clinical and Molecular
Virology, University of Edinburgh, Summerhall, Edinburgh EH9 1QH,
UK

FEATURES
source
Location/Qualifiers
1..681
/organism="Hepatitis C virus"
/mol_type="genomic RNA"
/isolate="195"
/isolation_source="injecting drug user, Glasgow"
/db_xref="taxon:11103"
/country="United Kingdom"
/note="genotype: 3a"
<1..>681
/codon_start=2
/product="NS5B"
/protein_id="AA64176.1"
/db_xref="GI:21591681"
/translation="RVEEIIYQCCNLEPEARKVVISLTERLYCGGPMFNSKAGCGYR
RCRASGVLPISFGNTTCYIKATPAAKAGLRNDFLYCGDLYVAESDVEDRRA
LRAFTAMTRYSAPPGDAPQPTDLELTSSSVSAQDNKGRKRYLLTDAATPLA
RAAMETARHTPNSMILGNIMYAPTIWRYVMWMTHTFSSILSOEILDRPLDFEMGAT
YSVTPXDXP"

CDS
BASE COUNT
152 a 204 c 176 g 147 t 2 others
ORIGIN

Query Match
Best Local Similarity 100.0%; Score 20; DB 1; Length 681;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 86659 AGCGCTCGGAAGCCGCAG 86678
|||||
202 AGCGCTCGGAAGCCGCAG 221

RESULT 44
AF516377 682 bp RNA linear VRL 04-NOV-2002
LOCUS
DEFINITION
Hepatitis C virus isolate GWN513 NS5B gene, partial cds.
ACCESSION
AF516377
VERSION
AF516377.1 GI:21591684
KEYWORDS
Hepatitis C virus
SOURCE
Hepatitis C virus
ORGANISM
Hepatitis C virus
VIRUSES; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepadnavirus.
1 (bases 1 to 682)
Cochrane, A., Searle, B., Hardie, A., Robertson, R., Delahooke, T.,
Cameron, S., Tedder, R.S., Dushenko, G.M., De Lamballerie, X. and
Simmonds, P.
TITLE
A Genetic Analysis of Hepatitis C Virus Transmission between
Injection Drug Users
J. Infect. Dis. 186 (9), 1212-1221 (2002)
MEDLINE
22289487
PUBMED
12402190
REFERENCE
2 (bases 1 to 682)
AUTHORS
Cochrane, A. and Simmonds, P.
TITLE
Direct Submission
JOURNAL
Submitted (29-MAY-2002) Laboratory of Clinical and Molecular
Virology, University of Edinburgh, Summerhall, Edinburgh EH9 1QH,
UK

FEATURES
source
Location/Qualifiers
1..682
/organism="Hepatitis C virus"
/mol_type="genomic RNA"

/isolate="GWN513"
/isolation_source="injecting drug user, Glasgow"
/db_xref="taxon:11103"
/country="United Kingdom"
/note="genotype: 3a"
<1..>682
/codon_start=2
/product="NS5B"
/protein_id="AA64176.1"
/db_xref="GI:21591685"
/translation="RMEERIYQCCNLEPEARKVVISLTERLYCGGPMFNSKAGCGYR
RCRASGVLPISFGNTTCYIKATPAAKAGLRNDFLYCGDLYVAESDVEDRRA
LRAFTAMTRYSAPPGDAPQPTDLELTSSSVSAQDNKGRKRYLLTDAATPLA
RAAMETARHTPNSMILGNIMYAPTIWRYVMWMTHTFSSILSOEILDRPLDFEMGAT
YSVTPXDXP"

CDS
BASE COUNT
150 a 197 c 179 g 155 t 1 others
ORIGIN

Query Match
Best Local Similarity 100.0%; Score 20; DB 1; Length 682;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 86659 AGCGCTCGGAAGCCGCAG 86678
|||||
202 AGCGCTCGGAAGCCGCAG 221

RESULT 45
AY100067 683 bp RNA linear VRL 04-NOV-2002
LOCUS
DEFINITION
Hepatitis C virus isolate G12 NS5B protein (NS5B) gene, partial
cds.
ACCESSION
AY100067
VERSION
AY100067.1 GI:21065051
KEYWORDS
Hepatitis C virus
SOURCE
Hepatitis C virus
ORGANISM
Hepatitis C virus
VIRUSES; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepadnavirus.
1 (bases 1 to 683)
Cochrane, A., Searle, B., Hardie, A., Robertson, R., Delahooke, T.,
Cameron, S., Tedder, R.S., Dushenko, G.M., De Lamballerie, X. and
Simmonds, P.
TITLE
A Genetic Analysis of Hepatitis C Virus Transmission between
Injection Drug Users
J. Infect. Dis. 186 (9), 1212-1221 (2002)
MEDLINE
22289487
PUBMED
12402190
REFERENCE
2 (bases 1 to 683)
AUTHORS
Cochrane, A. and Simmonds, P.
TITLE
Direct Submission
JOURNAL
Submitted (25-APR-2002) Laboratory for Clinical and Molecular
Virology, University of Edinburgh, Summerhall, Edinburgh, Scotland
EH9 1QH, United Kingdom

FEATURES
source
Location/Qualifiers
1..683
/organism="Hepatitis C virus"
/mol_type="genomic RNA"
/isolate="G12"
/isolation_source="from serum of patient in risk group IDU
from Glasgow, Scotland, United Kingdom"
/db_xref="taxon:11103"
/country="United Kingdom"
/note="genotype: 3a"
<1..>683
/gene="NS5B"
/gene="NS5B"
/gene="NS5B"
/codon_start=2
/product="NS5B protein"
/protein_id="AA28994.1"
/db_xref="GI:21065052"
/translation="RVEEIIYQCCNLEPEARKVVISLTERLYCGGPMFNSKAGCGYR

RCRAGVLPISGNTITCYIKATAAKAGLRSPDPLVCGDDLWVAESDGVDEDERA
LRATFAMTRISAPPCDAPQPTDLELITSCSSNVSAVDNKGKRYIYLRDATTPLA
RAAMETARHTPVNSWLGNIIMTAPTIWVRWVMTTFESILOSQELDRPLDFEMYGAT
YSVTPDLDP
BASE COUNT 150 a 196 c 180 g 156 t 1 others
ORIGIN

Query Match 0.0%; Score 20; DB 1; Length 683;
Best Local Similarity 100.0%; Pred. No. 8.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 86659 AGCGGCTGCGAGCGCCGAG 86678
|||
Db 202 AGCGGCTGCGAGCGCCGAG 221

Search completed: September 30, 2003, 02:54:01
Job time : 33895 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 29, 2003, 10:19:43 ; Search time 6306 Seconds
(without alignments)
12337.108 Million cell updates/sec

Title: US-09-831-000-1_COPY_104900_133719

Perfect score: 28820
Sequence: 1 ccaactcacgtccgcgcga.....cggcaccgcgcacgatct 28820

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 2552756 seqs, 1349719017 residues

Word size : 0
Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : N_Geneseq_19Jun03.*

1: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT.*
2: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT.*
3: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT.*
4: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT.*
5: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT.*
6: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT.*
7: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT.*
8: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT.*
9: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT.*
10: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT.*
11: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT.*
12: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT.*
13: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT.*
14: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT.*
15: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT.*
16: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT.*
17: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT.*
18: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT.*
19: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT.*
20: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT.*
21: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT.*
22: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT.*
23: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.*
24: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*
25: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	28820	100.0	128139	24	AA164291	RRV genome nucleot
2	28820	100.0	133719	21	AA164291	Macaca mulatta rha
3	33	0.1	128139	24	AA164291	RRV genome nucleot
4	33	0.1	133719	21	AA164291	Macaca mulatta rha
5	28	0.1	3571	21	AA164291	Macaca mulatta rha
6	28	0.1	3571	21	AA164291	Macaca mulatta rha
7	28	0.1	3571	21	AA164291	Macaca mulatta rha
8	28	0.1	3571	21	AA164291	Macaca mulatta rha

C	9	28	0.1	3571	24	AA172444	Mouse zvegf3 codin
C	10	28	0.1	3571	25	ABX93182	DNA encoding mouse
C	11	27	0.1	2218	14	AA047929	Paired basic amino
C	12	27	0.1	4361	24	AA594758	Human DNA sequence
C	13	27	0.1	4403	14	AA047927	Paired basic amino
C	14	27	0.1	4403	24	ABN95905	Gene #2403 used to
C	15	26	0.1	3132	24	AA594759	Human DNA sequence
C	16	25	0.1	2870	24	ABV94750	Human pancreatic c
C	17	25	0.1	2876	18	AA797303	Human plasmidogen
C	18	25	0.1	2876	22	AA509460	Human cDNA encodin
C	19	25	0.1	2876	22	AAH02917	Human shear stress
C	20	25	0.1	2876	24	ABV77991	Hypoxia-regulated
C	21	25	0.1	2944	9	AAH80253	Insert of Lambda 3
C	22	25	0.1	3171	24	AA594905	Human DNA sequence
C	23	25	0.1	3172	25	ABX63842	Human cDNA #842 d1
C	24	25	0.1	3172	25	AA546568	Tumour suppressor
C	25	25	0.1	7309	24	ABK34011	Human DNA for stag
C	26	25	0.1	7309	24	ABK33817	Human immune syste
C	27	25	0.1	17509	24	ABN95599	Gene #2097 used to
C	28	23	0.1	2307	24	ABK32842	DNA encoding human
C	29	23	0.1	6816	25	ABX08754	Angiogenesis-assoc
C	30	23	0.1	7752	24	AB170224	Chemically treated
C	31	23	0.1	32207	20	AAV73805	KSHV LUR DNA (nucl
C	32	23	0.1	137507	19	AAV19941	KSHV long unique c
C	33	22	0.1	1044	24	ABK97604	Human prostate spe
C	34	22	0.1	3024	22	AAK90497	Human digestive sy
C	35	22	0.1	3024	22	AAK90501	Human digestive sy
C	36	22	0.1	4176	22	AA157831	Human polynucleoti
C	37	22	0.1	13334	22	ABAI5786	Human nervous syst
C	38	22	0.1	38997	24	ABAD36069	Human share YKT6 9
C	39	22	0.1	157875	24	ABK99972	Human CDPKL genom
C	40	22	0.1	254366	25	ABZ23704	Human phosphatase
C	41	22	0.1	1082138	21	AAE22305	Arabidopsis thalia
C	42	21	0.1	414	22	AAH42781	Nucleotide sequenc
C	43	21	0.1	597	24	ABO41636	Oligonucleotide fo
C	44	21	0.1	597	24	ABO41637	Oligonucleotide fo
C	45	21	0.1	607	22	AAK77708	Human immune/haema

ALIGNMENTS

RESULT 1	AA164291	standard; DNA: 128139 BP.
AC	AA164291:	
XX	22-APR-2002	(first entry)
DT	RRV genome nucleotide sequence.	
XX	RRV genome nucleotide sequence.	
XX	RRV, rhesus rhadinovirus; Japanese macaque virus; multiple sclerosis;	
KW	JMNV; cytostatic; antisthmatic; antiallergic; dermatological;	
KW	vulnerary; gene therapy; leucopenia; thrombocytopenia;	
KW	inflammatory disease; asthma; allergy; dermatitis; virus; ds.	
XX	Macaca mulatta rhadinovirus 17577.	
OS	Macaca mulatta rhadinovirus 17577.	
XX	Location/Qualifiers	
FH	Key	
FT	1353..2674	
FT	/tag= a	
FT	/product= "RRV R1"	
FT	complement (2692..3258)	
FT	/tag= b	
FT	/product= "dihydrofolate reductase"	
FT	/label= RRV_ORF2	
FT	/note= "has similarity to Kaposi's sarcoma-associated	
FT	virus (KSHV) open reading frame (ORF) 2"	
FT	3676..5613	
FT	/tag= c	
FT	/product= "complement binding protein"	
FT	/label= RRV_ORF4	

```

FT      /note="has similarity to KSHV ORF4"
FT CDS   /tag= d
FT      /product= "ssDNA binding protein"
FT      /label= RRV_ORF6
FT      /note="has similarity to KSHV ORF6"
FT      9468..11528
FT      /tag= e
FT      /product= "transport protein"
FT      /label= RRV_ORF7
FT      /note="has similarity to KSHV ORF7"
FT      11515..14004
FT CDS   /tag= f
FT      /product= "glycoprotein B"
FT      /label= RRV_ORF8
FT      /note="has similarity to KSHV ORF8"
FT      14122..17166
FT CDS   /tag= g
FT      /product= "DNA polymerase protein"
FT      /label= RRV_ORF9
FT      /note="has similarity to KSHV ORF9"
FT      17261..18511
FT      /tag= h
FT      /label= RRV_ORF10
FT      /note="has similarity to KSHV ORF10"
FT      18520..19749
FT CDS   /tag= i
FT      /label= RRV_ORF11
FT      /note="has similarity to KSHV ORF11"
FT      complement (19921..20544)
FT CDS   /tag= j
FT      /product= "RVV R2"
FT      /label= RRV_ORF
FT      /note="has similarity to KSHV interleukin (IL)-6 gene"
FT      complement (20777..21778)
FT CDS   /tag= k
FT      /product= "thymidylate synthase"
FT      /label= RRV_ORF70
FT      /note="has similarity to KSHV ORF70"
FT      complement (22245..22592)
FT CDS   /tag= l
FT      /product= "RVV R3"
FT      /note="has similarity to KSHV K4 viral MIP gene"
FT      26846..27409
FT CDS   /tag= m
FT      /product= "Bcl2-homologue"
FT      /label= RRV_ORF16
FT      /note="has similarity to KSHV ORF16"
FT      complement (27515..29125)
FT CDS   /tag= n
FT      /label= RRV_ORF17
FT      /note="has similarity to KSHV ORF17"
FT      28998..29897
FT CDS   /tag= o
FT      /label= RRV_ORF18
FT      /note="has similarity to KSHV ORF18"
FT      complement (29905..31548)
FT CDS   /tag= p
FT      /product= "tegument protein"
FT      /label= RRV_ORF19
FT      /note="has similarity to KSHV ORF19"
FT      complement (31043..32095)
FT CDS   /tag= q
FT      /label= RRV_ORF20
FT      /note="has similarity to KSHV ORF20"
FT      32094..33767
FT CDS   /tag= r
FT      /product= "thymidine kinase"
FT      /label= RRV_ORF21
FT      /note="has similarity to KSHV ORF21"
FT      33754..35868
FT CDS   /tag= s
FT      /product= "glycoprotein H"

```

```

FT      /label= RRV_ORF22
FT      /note="has similarity to KSHV ORF22"
FT CDS   complement (35865..37073)
FT      /tag= t
FT      /label= RRV_ORF23
FT      /note="has similarity to KSHV ORF23"
FT      complement (37123..39321)
FT CDS   /tag= u
FT      /label= RRV_ORF24
FT      /note="has similarity to KSHV ORF24"
FT      39323..44459
FT CDS   /tag= v
FT      /product= "major capsid protein"
FT      /label= RRV_ORF25
FT      /note="has similarity to KSHV ORF25"
FT      43491..44408
FT CDS   /tag= w
FT      /product= "capsid protein"
FT      /label= RRV_ORF26
FT      /note="has similarity to KSHV ORF26"
FT      44433..45242
FT CDS   /tag= x
FT      /label= RRV_ORF27
FT      /note="has similarity to KSHV ORF27"
FT      45408..45683
FT CDS   /tag= y
FT      /label= RRV_ORF28
FT      /note="has similarity to KSHV ORF28"
FT      complement (45733..46779)
FT CDS   /tag= z
FT      /label= RRV_ORF29b
FT      /note="has similarity to KSHV ORF29b"
FT      46905..47135
FT CDS   /tag= aa
FT      /label= RRV_ORF30
FT      /note="has similarity to KSHV ORF30"
FT      47093..47746
FT CDS   /tag= ab
FT      /label= RRV_ORF31
FT      /note="has similarity to KSHV ORF31"
FT      47683..49077
FT CDS   /tag= ac
FT      /label= RRV_ORF32
FT      /note="has similarity to KSHV ORF32"
FT      49049..50059
FT CDS   /tag= ad
FT      /label= RRV_ORF33
FT      /note="has similarity to KSHV ORF33"
FT      complement (49977..50960)
FT CDS   /tag= ae
FT      /label= RRV_ORF29a
FT      /note="has similarity to KSHV ORF29a"
FT      50959..51942
FT CDS   /tag= af
FT      /label= RRV_ORF34
FT      /note="has similarity to KSHV ORF34"
FT      51923..52372
FT CDS   /tag= ag
FT      /label= RRV_ORF35
FT      /note="has similarity to KSHV ORF35"
FT      52278..53585
FT CDS   /tag= ah
FT      /product= "kinase"
FT      /label= RRV_ORF36
FT      /note="has similarity to KSHV ORF36"
FT      53566..55008
FT CDS   /tag= ai
FT      /product= "alkaline exonuclease"
FT      /label= RRV_ORF37
FT      /note="has similarity to KSHV ORF37"
FT      54963..55172
FT CDS   /tag= aj
FT      /label= RRV_ORF38

```

FT	/note- "has similarity to KSHV ORF38"
FT	complement (55255..56391)
FT	/*tag- ak
FT	/product- "glycoprotein M"
FT	/label= RRV_ORF39
FT	/note- "has similarity to KSHV ORF39"
FT	56526..57932
FT	/*tag- al
FT	/product- "helicase/primase"
FT	/label= RRV_ORF40
FT	/note- "has similarity to KSHV ORF40"
FT	57917..58528
FT	/*tag- am
FT	/product- "helicase/primase"
FT	/label= RRV_ORF41
FT	/note- "has similarity to KSHV ORF41"
FT	complement (58525..59343)
FT	/*tag- an
FT	/label= RRV_ORF42
FT	/note- "has similarity to KSHV ORF42"
FT	complement (59297..61027)
FT	/*tag- ao
FT	/product- "capsid protein"
FT	/label= RRV_ORF43
FT	/note- "has similarity to KSHV ORF43"
FT	

Query Match	100.0%	Score 28820	DB 24	Length 128139
Best Local Similarity	100.0%	Pred. No. 0		
Matches 28820	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY 1	CCAACCTACCTCCCGGCGCACGAGAGAGCCCTCTGCACCGCACATCACATCAAC	60		
Db 99320	CCAACCTACCTCCCGGCGCACGAGAGAGCCCTCTGCACCGCACATCACTCAAC	99379		
QY 61	GTCCTAGAGCGCTTTGTTTCATTATGTTCCACCACCTAACCCGGTTCCGAGGCCCC	120		
Db 99380	GTCCTAGAGCGCTTTGTTTCATTATGTTCCACCACCTAACCCGGTTCCGAGGCCCC	99439		
QY 121	GGTCTGGAATTCGCAACACGAGCGCGGGGCGAGAGCGGCAACGTGGATGGACAGA	180		
Db 99440	GGTCTGGAATTCGCAACACGAGCGCGGGGCGAGAGCGGCAACGTGGATGGACAGA	99499		
QY 181	CAGTGGCGGACATCGCTCAGACGCTCCAAAGCTTCTCGACACGTAGACACACACC	240		
Db 99500	CAGTGGCGGACATCGCTCAGACGCTCCAAAGCTTCTCGACACGTAGACACACACC	99559		
QY 241	GCCACGCAACCGGGGCGGGGATTTAACACACTTGTGGCAATGGCTTTTACGCA	300		
Db 99560	GCCACGCAACCGGGGCGGGGATTTAACACACTTGTGGCAATGGCTTTTACGCA	99619		
QY 301	ATCATCAGGGGCGCTAGCAGAGCGGTGACGCTTCCCAAGTTAACGAGCACCGCGTCAT	360		
Db 99620	ATCATCAGGGGCGCTAGCAGAGCGGTGACGCTTCCCAAGTTAACGAGCACCGCGTCAT	99679		
QY 361	TTTTCAGAGAGATCGTTTACACACCGAGGAATGCACAACTGTGTCACCGCATGTG	420		
Db 99680	TTTTCAGAGAGATCGTTTACACACCGAGGAATGCACAACTGTGTCACCGCATGTG	99739		
QY 421	CCCAACCTGCGGGCGCAATCTTACGATTAAATCCCTACTCGGAAACCCCTAGACTAATG	480		
Db 99740	CCCAACCTGCGGGCGCAATCTTACGATTAAATCCCTACTCGGAAACCCCTAGACTAATG	99799		
QY 481	AGTCGTTTCTCCCGCTAATGTTTCAGGGGCTCCGCACTTAACGCTAGAGCGCCAGTGC	540		
Db 99800	AGTCGTTTCTCCCGCTAATGTTTCAGGGGCTCCGCACTTAACGCTAGAGCGCCAGTGC	99859		
QY 541	AAAAAGGCGCCACATTAACACCGCGCTCAGTTAGATGCTTGGCCAAAACAGAGCAATT	600		
Db 99860	AAAAAGGCGCCACATTAACACCGCGCTCAGTTAGATGCTTGGCCAAAACAGAGCAATT	99919		
QY 601	CGGTATTTCCGCGCATGCGACGTACGCGAACCTAGACAGACCTGTGGGACAGACG	660		
Db 99920	CGGTATTTCCGCGCATGCGACGTACGCGAACCTAGACAGACCTGTGGGACAGACG	99979		

QY	661	GAC	TTTTTGC	AAATCTGC	GATTAACA	ATCAAC	CCAGGCCA	GGGTGGCGCCGCTCAC	CTGG	720		
Db	99980	GAC	TTTTTGGCA	AAATCTGC	GATTAACA	ATCAAC	CCAGGCCA	GGGTGGCGCCGCTCAC	CTGG	1000399		
QY	721	GGCGTC	CACACATATG	AGCGGGCTGG	TTTTGGAC	CAACTGTGGGTC	CCACATTTAA	AAACCATG	780			
Db	100040	GGCGTC	CACACATATG	AGCGGGCTGG	TTTTGGAC	CAACTGTGGGTC	CCACATTTAA	AAACCATG	1000999			
QY	781	ACAGCGCG	CTAGAC	GCAGACGTA	CGTGA	CCCTAGT	GAGACCCCTTAC	ACCTGAC	CTTAC	840		
Db	100100	ACAGCGCG	CTAGAC	GCAGACGTA	CGTGA	CCCTAGT	GAGACCCCTTAC	ACCTGAC	CTTAC	1001599		
QY	841	GGCCCCGG	CGGTCCAA	CGCCGAGCG	AGAAAGAC	CAACCGAG	ACCCGGCCGCTG	ACAG	74C	900		
Db	100160	GGCCCCGG	CGGTCCAA	CGCCGAGCG	AGAAAGAC	CAACCGAG	ACCCGGCCGCTG	ACAG	74C	1002199		
QY	901	GGACAGCC	CCAGCGGTACT	GCATCTCGGG	CTCATC	AGCAGCGCGCGT	CCAGCGTTCA	AAAC	960			
Db	100220	GGACAGCC	CCAGCGGTACT	GCATCTCGGG	CTCATC	AGCAGCGCGCGT	CCAGCGTTCA	AAAC	1002799			
QY	961	ACACCGGTA	TCCGCTTTG	GAGCGGTGCT	CGAGCAT	GTGTTTC	ACGTACCG	GATCAGA	1020			
Db	100280	ACACCGGTA	TCCGCTTTG	GAGCGGTGCT	CGAGCAT	GTGTTTC	ACGTACCG	GATCAGA	1003399			
QY	1021	ATATTTTGG	CGCCCAAG	CCCTTTGG	CCAGCGCGGGCGCAT	GTGGGCGCTC	TC	1080				
Db	100340	ATATTTTGG	CGCCCAAG	CCCTTTGG	CCAGCGCGGGCGCAT	GTGGGCGCTC	TC	1003999				
QY	1081	ACACCCAT	CTCGGAATGCGT	CCCGCGAC	GTGAG	CGCCCTTCA	AAAGCCTGTATTA	CGCACCC	1140			
Db	100400	ACACCCAT	CTCGGAATGCGT	CCCGCGCGAC	GTGAG	CGCCCTTCA	AAAGCCTGTATTA	CGCACCC	1004599			
QY	1141	CGCAACCCG	GTCCCATTA	GAACGGTAC	CCCGCATCCCTC	ACCCGAGCAG	CGAGCGACAG	1200				
Db	100460	CGCAACCCG	GTCCCATTA	GAACGGTAC	CCCGCATCCCTC	ACCCGAGCAG	CGAGCGACAG	1005199				
QY	1201	GTCTTTCTG	AGACAG	GCACAGTGG	CTATCCTAC	CCGATTTCA	CACACAGCA	AGCGGCCG	1260			
Db	100520	GTCTTTCTG	AGACAG	GCACAGTGG	CTATCCTAC	CCGATTTCA	CACACAGCA	AGCGGCCG	1005799			
QY	1261	TCGTGAC	CTCCGCTTCTG	TGTCAT	AGACCCCTG	AAACCTG	CTAACGGC	ACGTAC	1320			
Db	100580	TCGTGAC	CTCCGCTTCTG	TGTCAT	AGACCCCTG	AAACCTG	CTAACGGC	ACGTAC	1006399			
QY	1321	TCACATGG	CGGCGCTG	CAAAATTTG	AGACAG	CAAGCGCTTTAC	GTGATG	CCGGAG	CACTAC	1380		
Db	100640	TCACATGG	CGGCGCTG	CAAAATTTG	AGACAG	CAAGCGCTTTAC	GTGATG	CCGGAG	CACTAC	1006999		
QY	1381	CCCCCAG	ACTGGCC	CAAAAAAG	CGTGTG	GTACATCA	AAACAG	CTCGTGA	CGCACTAC	1440		
Db	100700	CCCCCAG	ACTGGCC	CAAAAAAG	CGTGTG	GTACATCA	AAACAG	CTCGTGA	CGCACTAC	1007599		
QY	1441	CACGACG	AGATATG	TAACCTCTTTACT	AGCGTATCC	CGAGAACAG	GGGAGCCGG	CAAGG	1500			
Db	100760	CACGACG	AGATATG	TAACCTCTTTACT	AGCGTATCC	CGAGAACAG	GGGAGCCGG	CAAGG	1008199			
QY	1501	AGGAGTAT	CTTGC	AGCGGCTCC	GACAAAC	GTGCAC	ACCGGA	AAACCGGC	CAATCTCCG	1560		
Db	100820	AGGAGTAT	CTTGC	AGCGGCTCC	GACAAAC	GTGCAC	ACCGGA	AAACCGGC	CAATCTCCG	1008799		
QY	1561	GCATGGG	AAACGGGAT	TACCGATTA	TAAAC	GCAGAAAGAA	ACCGCCAA	AAAAA	ACTCTATTA	1620		
Db	100880	GCATGGG	AAACGGGAT	TACCGATTA	TAAAC	GCAGAAAGAA	ACCGCCAA	AAAAA	ACTCTATTA	1009399		
QY	1621	ATTCTCG	CGTCTTAA	AGCGGAGAT	ATCCAC	CGGTGGA	AAACAG	CAACCC	ACCAATTC	1680		
Db	100940	ATTCTCG	CGTCTTAA	AGCGGAGAT	ATCCAC	CGGTGGA	AAACAG	CAACCC	ACCAATTC	1009999		
QY	1681	CAAGGG	CAAGCGGTG	CCAAAC	AGCAAC	AGTAAC	CAAGCCGG	CGCTCA	AAATTA	CTTCA	1740	
Db	101000	CAAGGG	CAAGCGGTG	CCAAAC	AGCAAC	AGTAAC	CAAGCCGG	CGCTCA	AAATTA	CTTCA	1010599	

QY 1741 CAGCGTCAGGTAAACACCGTCACCGCCTCATCTTACCGGAAAAATTC 1800
| | | | |
Db 101060 CAGCGTCAGGTAAACACCGTCACCGCCTCATCTTACCGGAAAAATTC 101119
QY 1801 AACAGCAAAAGGCTGCTGACTAATATCTCAAAAGCTGGAAAGCGCCATTAATAACAG 1860
| | | | |
Db 101120 AACAGCAAAAGGCTGCTGACTAATATCTCAAAAGCTGGAAAGCGCCATTAATAACAG 101119
QY 1861 CCAGCCTCCGGCCAGGTCAACCGAAGGGAATCTTTGGAGGTATAAACCCGAGTG 1920
| | | | |
Db 101180 CCAGCCTCCGGCCAGGTCAACCGAAGGGAATCTTTGGAGGTATAAACCCGAGTG 101239
QY 1921 CTCACGGAACCCCGCAAAACCCCGAAGCGCGGTAGCTCTGCGCAACAGAGCAACC 1980
| | | | |
Db 101240 CTCACGGAACCCCGCAAAACCCCGAAGCGCGGTAGCTCTGCGCAACAGAGCAACC 101299
QY 1981 ACCAGCGTCCCAAGTACCGATTAAATCCACCGCTAGGCTTTTATAGGAGCCGC 2040
| | | | |
Db 101300 ACCAGCGTCCCAAGTACCGATTAAATCCACCGCTAGGCTTTTATAGGAGCCGC 101359
QY 2041 TCCAAACTCTCCGACCGCTGGAAGAGCCACGCGCCACACCCGACACATCACTAGTCG 2100
| | | | |
Db 101360 TCCAAACTCTCCGACCGCTGGAAGAGCCACGCGCCACACCCGACACATCACTAGTCG 101419
QY 2101 AAGATGATCGGGAATAATACGCGGAGTGCCTCGCGGCAACCCACACCTCGAAGAG 2160
| | | | |
Db 101420 AAGATGATCGGGAATAATACGCGGAGTGCCTCGCGGCAACCCACACCTCGAAGAG 101479
QY 2161 GGGCCACAGGAGCCTCAGTCAACACTCCAACCGGCGACACATAAACGTCCTCTAGC 2220
| | | | |
Db 101480 GGGCCACAGGAGCCTCAGTCAACACTCCAACCGGCGACACATAAACGTCCTCTAGC 101539
QY 2221 CAAGGTCAAAAAACAGTACACGGGGCGGAAATTCGGGCTTAAACAGCACTCCAGC 2280
| | | | |
Db 101540 CAAGGTCAAAAAACAGTACACGGGGCGGAAATTCGGGCTTAAACAGCACTCCAGC 101599
QY 2281 GCGCCCAACCAACCGCATCAAAACCGCGCATTCATPACAGCTCCCGAGAGGAGGCG 2340
| | | | |
Db 101600 GCGCCCAACCAACCGCATCAAAACCGCGCATTCATPACAGCTCCCGAGAGGAGGCG 101659
QY 2341 CGGTTGCTTACAGCAGCAATCGAGGTGGAATCGACCCCAACCGAGGAGGTAAACAGATCG 2400
| | | | |
Db 101660 CGGTTGCTTACAGCAGCAATCGAGGTGGAATCGACCCCAACCGAGGAGGTAAACAGATCG 101719
QY 2401 CCAAAAAACAGAGATGTGTCTCAGGGGGCGGAAACCGGAGAGCTCCAGGTGAGCCGCCG 2460
| | | | |
Db 101720 CCAAAAAACAGAGATGTGTCTCAGGGGGCGGAAACCGGAGAGCTCCAGGTGAGCCGCCG 101779
QY 2461 CTCGGTCCAAACCTAGAGATTCTACGACTGGAGACACCCCAAAATTCGCAAAAATATAACT 2520
| | | | |
Db 101780 CTCGGTCCAAACCTAGAGATTCTACGACTGGAGACACCCCAAAATTCGCAAAAATATAACT 101839
QY 2521 TCACCTACCGTCCCACTCCAGAGTCAACCCCAATCTCTCCCACTAATCTGGATACCC 2580
| | | | |
Db 101840 TCACCTACCGTCCCACTCCAGAGTCAACCCCAATCTCTCCCACTAATCTGGATACCC 101899
QY 2581 CTATCCAGGTCAACTTCAACACGAAAGAAATCAGACGAGCAAGATGTGTTAATGCGA 2640
| | | | |
Db 101900 CTATCCAGGTCAACTTCAACACGAAAGAAATCAGACGAGCAAGATGTGTTAATGCGA 101959
QY 2641 TTTATTCAAAGCTAGAGAAAACTTCAAGGCTGCTGAGGCTTATCCGAGGCTATT 2700
| | | | |
Db 101960 TTTATTCAAAGCTAGAGAAAACTTCAAGGCTGCTGAGGCTTATCCGAGGCTATT 102019
QY 2701 GCCAGATTAAGTTTATATCTGTAAACGCGCCATCTCATCTTCTTTTATTTATGAG 2760
| | | | |
Db 102020 GCCAGATTAAGTTTATATCTGTAAACGCGCCATCTCATCTTCTTTTATTTTGGAG 102079
QY 2761 ACAGAGCTTGTGTCCAGAGTAGTTCGCTGCTAGGTATTAAGAGTGCAGCCTATGC 2820
| | | | |
Db 102080 ACAGAGCTTGTGTCCAGAGTAGTTCGCTGCTAGGTATTAAGAGTGCAGCCTATGC 102139
QY 2821 CAGAAGAGCCCAAGCTCCCGGGTCCGCGGCAACCGGGCGGGGCCCATCGAGCCTATCA 2880
| | | | |

Db 102140 CAGAAGAGCCGACGCTCCGGGTCCGCGCACCGGGCGGGGCCATCGAGCCTATCA 102199
| | | | |
QY 2881 ATGAATGGGGCCCGCTGAGAGATCGTAGTAAGCTATTGACCCGAGGCTGAGAGCCACCG 2940
| | | | |
Db 102200 ATGAATGGGGCCCGCTGAGAGATCGTAGTAAGCTATTGACCCGAGGCTGAGAGCCACCG 102259
QY 2941 GGGCAACGCTCGGGGGCGCCGAGCCGAGCCGACAAACGCCGAGATCTAGAACTAG 3000
| | | | |
Db 102260 GGGCAACGCTCGGGGGCGCCGAGCCGAGCCGACAAACGCCGAGATCTAGAACTAG 102319
QY 3001 CGTCTTTTGGCGGAGGCGCCGGAGGAGTCTTGGCAGCAATTCATCTCTTTT 3060
| | | | |
Db 102320 CGTCTTTTGGCGGAGGCGCCGGAGGAGTCTTGGCAGCAATTCATCTCTTTT 102379
QY 3061 GCATATACATGTCGTATGATGTTTGGCGTTTAAAAACACAGATTAATACGTTTCGCA 3120
| | | | |
Db 102380 GCATATACATGTCGTATGATGTTTGGCGTTTAAAAACACAGATTAATACGTTTCGCA 102439
QY 3121 TGGCATATCTGGGGGAGACATGTCAACCTGGGGAAAGTTGTATCTGAGCAACACCG 3180
| | | | |
Db 102440 TGGCATATCTGGGGGAGACATGTCAACCTGGGGAAAGTTGTATCTGAGCAACACCG 102499
QY 3181 GGTGATTTGGGTAAATGCTGCTCAAGGCGTCCGAAAGATTTGCTCTTAACCCGCAAG 3240
| | | | |
Db 102500 GGTGATTTGGGTAAATGCTGCTCAAGGCGTCCGAAAGATTTGCTCTTAACCCGCAAG 102559
QY 3241 ACAGACATCTTTTAACTTCTATTAACATTTCCAGAGAGAGGAGATATAGCAGAGT 3300
| | | | |
Db 102560 ACAGACATCTTTTAACTTCTATTAACATTTCCAGAGAGAGGAGATATAGCAGAGT 102619
QY 3301 CAAATTAACAGCTCGGCCACACGCAAAATCTTATAGCCCGGTGGCGAGTCGGCGCA 3360
| | | | |
Db 102620 CAAATTAACAGCTCGGCCACACGCAAAATCTTATAGCCCGGTGGCGAGTCGGCGCA 102679
QY 3361 CGCCAAACAGGGGACACGACGAGCTAAACAGGAGTTCGCGTCTGATGCAATGTCGCG 3420
| | | | |
Db 102680 CGCCAAACAGGGGACACGACGAGCTAAACAGGAGTTCGCGTCTGATGCAATGTCGCG 102739
QY 3421 GTTGTGGGAGAGCAGCAGCAGCTAAATAGGAGTCTCAACACAGCTGATCTCGAATAGAGA 3480
| | | | |
Db 102740 GTTGTGGGAGAGCAGCAGCAGCTAAATAGGAGTCTCAACACAGCTGATCTCGAATAGAGA 102799
QY 3481 TATAACCCGATGCGATCCGCGCAATTAAGAGCAATTAAGCGCCGCTGTATGACCA 3540
| | | | |
Db 102800 TATAACCCGATGCGATCCGCGCAATTAAGAGCAATTAAGCGCCGCTGTATGACCA 102859
QY 3541 GATCGAAGCTGCTCTCTTTTGTGCGGACTGAAACACAGTGGTGGTGGAAAT 3600
| | | | |
Db 102860 GATCGAAGCTGCTCTCTTTTGTGCGGACTGAAACACAGTGGTGGTGGAAAT 102919
QY 3601 TACGGTTTCAAAATTTACCCCGTCCGAAATTTCAACAGTAAACCGGACTCGAGCACACAC 3660
| | | | |
Db 102920 TACGGTTTCAAAATTTACCCCGTCCGAAATTTCAACAGTAAACCGGACTCGAGCACACAC 102979
QY 3661 CACCCGCGAGCTGGAGAGGCTCTTCCAGTACGCTCGGCGCACACCGGGAGCAAC 3720
| | | | |
Db 102980 CACCCGCGAGCTGGAGAGGCTCTTCCAGTACGCTCGGCGCACACCGGGAGCAAC 103039
QY 3721 AGGTAGAGAGTACAGGAAACAGTACGTTATACGCAATACTTTTGAACCCAGTCCGCG 3780
| | | | |
Db 103040 AGGTAGAGAGTACAGGAAACAGTACGTTATACGCAATACTTTTGAACCCAGTCCGCG 103099
QY 3781 GGATATCTCCGTCGCTGCTGACTCCCTATGGGCAACACACAGGAGATGCTCAGCAG 3840
| | | | |
Db 103100 GGATATCTCCGTCGCTGCTGACTCCCTATGGGCAACACACAGGAGATGCTCAGCAG 103159
QY 3841 GGCCTTAACAGTACGCTCTCTGAAAGGGGCTTAAACGGGTTGCCGACAGGAGGTCGG 3900
| | | | |
Db 103160 GGCCTTAACAGTACGCTCTCTGAAAGGGGCTTAAACGGGTTGCCGACAGGAGGTCGG 103219
QY 3901 CGCCAGTTCGAGAGGAGGCGAGTCCCGGTCCGAGAGGGCCCGGGACATCTCATT 3960
| | | | |

Db 103220 CGCCAGTTCGCGACGAGCGCAGAGTCCCGCTCCGAGGCGCGGACACTCTGATTT 103279
QY 3961 CAGGTTAGTCCCGACAGCTGCGAAATGAGCGGAGACGTTCAAGTCGATCGAGACAAACC 4020
Db 103280 CAGGTTAGTCCCGACAGCTGCGAAATGAGCGGAGACGTTCAAGTCGATCGAGACAAACC 103339
QY 4021 GCCCGCTTCATTTCTTCCGCAAAAGCGGAGATCCACGCGTGTGTGCAAAAGAGT 4080
Db 103340 GCCCGCTTCATTTCTTCCGCAAAAGCGGAGATCCACGCGTGTGTGCAAAAGAGT 103399
QY 4081 AACGAGGGAAACCGCTGCGGACAGTTAAGGGTTTTGACACGAGACAAACAGCCCTCTG 4140
Db 103400 AACGAGGGAAACCGCTGCGGACAGTTAAGGGTTTTGACACGAGAACAGCCCTCTG 103459
QY 4141 AACGAGACAAACAGATACCGGAGCACAGCGCTCTGAGGAAAGCGCGTTAACTTAACC 4200
Db 103460 AACGAGACAAACAGATACCGGAGCACAGCGCTCTGAGGAAAGCGCGTTAACTTAACC 103519
QY 4201 TTGCTGCTGGGACAGCCCAAGCGGAGTACAGATACACCTCAGCACCGCAGCGCTACGCTC 4260
Db 103520 TTGCTGCTGGGACAGCCCAAGCGGAGTACAGATACACCTCAGCACCGCAGCGCTACGCTC 103579
QY 4261 TAAACAAGACCGCGCGATATCTGTCAGACCGCGATCTACGTCGCGCTTTTAAAGTGGGTT 4320
Db 103580 TAAACAAGACCGCGCGATATCTGTCAGACCGCGATCTACGTCGCGCTTTTAAAGTGGGTT 103639
QY 4321 ATCCGCGCTCCAGCGCGAGTATCTGTTACGAGGCGGTCTGAAGAGTGGGGAGAAAT 4380
Db 103640 ATCCGCGCTCCAGCGCGAGTATCTGTTACGAGGCGGTCTGAAGAGTGGGGAGAAAT 103699
QY 4381 TAAAGTGCAGAGCCCATTTTGGGGGTCGTCGCTCCAGGACACGAGCCCGTACGTACAAA 4440
Db 103700 TAAAGTGCAGAGCCCATTTTGGGGGTCGTCGCTCCAGGACACGAGCCCGTACGTACAAA 103759
QY 4441 ACACAGTACGATTCGCGGCGCTACTCGGATTTAGCGATAGAGGCGCGGAGATCTAAGCC 4500
Db 103760 ACACAGTACGATTCGCGGCGCTACTCGGATTTAGCGATAGAGGCGCGGAGATCTAAGCC 103819
QY 4501 CAGCGAGAAACCATCCAGACCAAGATGGGAGATGAAGAACCGGCGCATACAGGCGAC 4560
Db 103820 CAGCGAGAAACCATCCAGACCAAGATGGGAGATGAAGAACCGGCGCATACAGGCGAC 103879
QY 4561 TTGCTCTTCAGCCAGGTTAGGCAAGCGGCGCGAGCGCAATCCCAATTTTACCGATTGAA 4620
Db 103880 TTGCTCTTCAGCCAGGTTAGGCAAGCGGCGCGAGCGCAATCCCAATTTTACCGATTGAA 103939
QY 4621 TTGCTTAATTTGATATGCGCGCAAGCTCTCGCGCCCAATATCTTCAACTCCGACCCG 4680
Db 103940 TTGCTTAATTTGATATGCGCGCAAGCTCTCGCGCCCAATATCTTCAACTCCGACCCG 103999
QY 4681 AAGGCGGCGCACGAGCGCGCTTGCGCTCAACGCGACGAGCGCGTGGAGTGAACCGTCA 4740
Db 104000 AAGGCGGCGCACGAGCGCGCTTGCGCTCAACGCGACGAGCGCGTGGAGTGAACCGTCA 104059
QY 4741 GGGCAAAAACCGTTCTAAGAAAGGTTTTTAAACGTTTAAAGCGCTTTTGGAGTCAAGCA 4800
Db 104060 GGGCAAAAACCGTTCTAAGAAAGGTTTTTAAACGTTTAAAGCGCTTTTGGAGTCAAGCA 104119
QY 4801 AAAAAGTAAACCTGTGCGGTCTCGGTAAGTAAAGTGGCGCATATGACATGAGAGCTGT 4860
Db 104120 AAAAAGTAAACCTGTGCGGTCTCGGTAAGTAAAGTGGCGCATATGAGAGCTGT 104179
QY 4861 AAAGCTTTAGGTCTCGGAGAAACAGAGCTGCTTAAATTTATATAAATCGTCGCGC 4920
Db 104180 AAAGCTTTAGGTCTCGGAGAAACAGAGCTGCTTAAATTTATATAAATCGTCGCGC 104239
QY 4921 CCAGGACACGAGAGTCTCTCTCAAGATACAGTCCGATTTATAGGACGAGTTTTC 4980
Db 104240 CCAGGACACGAGAGTCTCTCTCAAGATACAGTCCGATTTATAGGACGAGTTTTC 104299
QY 4981 CAAACTGGGATCGCGGCTACGTCGCTTACCAAAAACATTTACGCTGGTGGCAAAAC 5040
Db 104300 CAAACTGGGATCGCGGCTACGTCGCTTACCAAAAACATTTACGCTGGTGGCAAAAC 104359

QY 5041 CGTTGTGATTAATTAACAAAACCGGGCAAAAGGGTAAAGGCGAGTCTGCTAGTTTGTGA 5100
Db 104360 CGTTGTGATTAATTAACAAAACCGGGCAAAAGGGTAAAGGCGAGTCTGCTAGTTTGTGA 104419
QY 5101 GCCAAAACCTTATACAAAACCTGAGATGATAGAGCAGCGCGTGTGACAGGCGCAGGTC 5160
Db 104420 GCCAAAACCTTATACAAAACCTGAGATGATAGAGCAGCGCGTGTGACAGGCGCAGGTC 104479
QY 5161 ACACGGGGACCGCGCGCTTTTACGATATAGGGAAGCCCGCTCTGACACTCTTCCAAAGT 5220
Db 104480 ACACGGGGACCGCGCGCTTTTACGATATAGGGAAGCCCGCTCTGACACTCTTCCAAAGT 104539
QY 5221 CCAGGAGATTCAGAGGGTCCAGGTAAAGAGACAACTAAATCCACAGCTCGTCAACTA 5280
Db 104540 CCAGGAGATTCAGAGGGTCCAGGTAAAGAGACAACTAAATCCACAGCTCGTCAACTA 104599
QY 5281 AACGTTTTCCGAACTATCGTTATAAAGATCTTTAGTGTCTGTGCGTGGCTCCGTTAA 5340
Db 104600 AACGTTTTCCGAACTATCGTTATAAAGATCTTTAGTGTCTGTGCGTGGCTCCGTTAA 104659
QY 5341 AAACCGGCTCGGCTTAACGATTTTGTGAATGACCTGTTTACGCGCTTACCTTGGCGT 5400
Db 104660 AAACCGGCTCGGCTTAACGATTTTGTGAATGACCTGTTTACGCGCTTACCTTGGCGT 104719
QY 5401 CCAGGACCATTCAGTGTCTCAGAGTGAAGTGAACCGCGTGTGAGACAGATGACAGAGAAAG 5460
Db 104720 CCAGGACCATTCAGTGTCTCAGAGTGAAGTGAACCGCGTGTGAGACAGATGACAGAGAAAG 104779
QY 5461 TTTTAAATTAATGACAGTAGTTAATGCGTTTGAAGCTGTGAATATATGTTGGGAAACATTA 5520
Db 104780 TTTTAAATTAATGACAGTAGTTAATGCGTTTGAAGCTGTGAATATATGTTGGGAAACATTA 104839
QY 5521 TTTTCAATGTCATCGGAGGAGGAGACTGGAACCGCAATTAATCTGACCCGAATCAAGT 5580
Db 104840 TTTTCAATGTCATCGGAGGAGGAGACTGGAACCGCAATTAATCTGACCCGAATCAAGT 104899
QY 5581 GAGACAGAGGTAAAGATGCTCAGCGCGGTGACCGCGTGAACAGCGACAGCCACCCCTT 5640
Db 104900 GAGACAGAGGTAAAGATGCTCAGCGCGGTGACCGCGTGAACAGCGACAGCCACCCCTT 104959
QY 5641 CAAATATTTTAAAGCTTTAAAGAGGCGCGCTTAAAGTGTGCAACTGAGTTTAAACATC 5700
Db 104960 CAAATATTTTAAAGCTTTAAAGAGGCGCGCTTAAAGTGTGCAACTGAGTTTAAACATC 105019
QY 5701 CTACCCATTAATGTTGTCGTCGCGTGAAGTGAAGACCCGATGAGACACTGCGCTCTGTG 5760
Db 105020 CTACCCATTAATGTTGTCGTCGCGTGAAGTGAAGACCCGATGAGACACTGCGCTCTGTG 105079
QY 5761 CGGGAGCTCGTAGAACAATCTTCTCCCGGTAACCGCGAGAGCTTTTAAAGCCG 5820
Db 105080 CGGGAGCTCGTAGAACAATCTTCTCCCGGTAACCGCGAGAGCTTTTAAAGCCG 105139
QY 5821 GTATTAATTCACACTCAGAGCTCTACAAACCGCGCTTATGTCAGAGGTGTAGCTTC 5880
Db 105140 GTATTAATTCACACTCAGAGCTCTACAAACCGCGCTTATGTCAGAGGTGTAGCTTC 105199
QY 5881 CTGTTCACTCTGTGTCGAGACTTTCGCAACCCCGCACTTTTCTTGAAGATAGGCGTGG 5940
Db 105200 CTGTTCACTCTGTGTCGAGACTTTCGCAACCCCGCACTTTTCTTGAAGATAGGCGTGG 105259
QY 5941 TTGTGCGTCACTCTGATATAGCGCCCGGATCATGAGAGGCTACCTCATGTGGTGGC 6000
Db 105260 TTGTGCGTCACTCTGATATAGCGCCCGGATCATGAGAGGCTACCTCATGTGGTGGC 105319
QY 6001 GACCTTTTGAAGTAAAGCAGTGTACTTCCCGCAATGCGTGAAGATGGGCGAGTATAC 6060
Db 105320 GACCTTTTGAAGTAAAGCAGTGTACTTCCCGCAATGCGTGAAGATGGGCGAGTATAC 105379
QY 6061 ACCGCCAAAGCATCTCTGGAATGAGGTCCAGTGCACCTTCTTCCGAACCCCGTGCCTTC 6120
Db 105380 ACCGCCAAAGCATCTCTGGAATGAGGTCCAGTGCACCTTCTTCCGAACCCCGTGCCTTC 105439

QY	6121	CGACCCATGACAGAGAACAAATTA	CTCCACACATCTCATTTAAATTTT	ACAAACCGAG	6180	
Db	105440	CGACCCATGACAGAGAACAAATTA	CTCCACACATCTCATTTAAATTTT	TACAAACCGAG	105499	
QY	6181	TTTATTAGGGGATGTGTAAGGACG	ATTCGCGGGATCGTCTGTTTAAACG	CTCAG	6240	
Db	105500	TTTATTAGGGGATGTGTAAGGACG	ATTCGCGGGATCGTCTGTTTAAACG	CTCAG	105559	
QY	6241	CCGCGACAGAAAGGAGACCCAC	CAACCTACCGTGTGCTGTTTCCAT	TGTGGCGCGGAG	6300	
Db	105560	CCGCGACAGAAAGGAGACCCAC	CAACCTACCGTGTGTTGTTCCG	TGTGGCGCGGAG	105619	
QY	6301	AGTCACACCACCGGATTAACCGCT	TACCCGAGACTGGAAGAGCGCTT	CAATCTCACG	6360	
Db	105620	AGTCACACCACCGGATTAACCGCT	TACCCGAGACTGGAAGAGCGCTT	CAATCTCACG	105679	
QY	6361	AACGCGAGGAAACCCACGCTCC	TCGCGGCTTTTGGCAACGCGGGC	ACAATCCGAG	6420	
Db	105680	AACGCGAGGAAACCCACGCTCC	TCGCGGCTTTTGGCAACGCGGGC	ACAATCCGAG	105739	
QY	6421	CTTTTGGCTCGACACACAAAGG	ACAGATATACCAATTTTCAACAC	CGCTCCGCTTCCCAAC	6480	
Db	105740	CTTTTGGCTCGACACACAAAGG	ACAGATATACCAATTTTCAACAC	CGCTCCGCTTCCCAAC	105799	
QY	6481	CCAGAAATGCTGACCAATACAGG	GGCCCTCGCTGATGACCCAAAC	GGCTCAACCTAAAA	6540	
Db	105800	CCAGAAATGCTGACCAATACAGG	GGCCCTCGCTGATGACCCAAAC	GGCTCAACCTAAAA	105859	
QY	6541	ACAAAAAACACACCGCATCCAT	TATGGCTTATGAGATGTCGG	CGGCACACCGGAC	6600	
Db	105860	ACAAAAAACACACCGCATCCAT	TATGGCTTATGAGATGTCGG	CGGCACACCGGAC	105919	
QY	6601	GCCGGTCCGGTCTGAAAGATTC	GCGTGGCGCATTTCTGGAAGAC	TGGAAGAAACAACGTT	6660	
Db	105920	GCCGGTCCGGTCTGAAAGATTC	GCGTGGCGCATTTCTGGAAGAC	TGGAAGAAACAACGTT	105979	
QY	6661	AAAGTCGTCAATCGATATCGTAC	TACTCTAAACGATCCGGACTAC	TGTACACGTCGC	6720	
Db	105980	AAAGTCGTCAATCGATATCGTAC	TACTCTAAACGATCCGGACTAC	TGTACACGTCGC	106039	
QY	6721	GACGAAACATGCGCGGCGCTA	TTTAAAGGCTCTGGGCAACA	GAAGAAATCCACAAGCATTT	6780	
Db	106040	GACGAAACATGCGCGGCGCTA	TTTAAAGGCTCTGGGCAACA	GAAGAAATCCACAAGCATTT	106099	
QY	6781	TTTTTGCGACCCGGTGTGCTCT	GTAACAGTACTGCACTGTCC	CGCGGCTTTTATTAA	6840	
Db	106100	TTTTTGCGACCCGGTGTGCTCT	GTAACAGTACTGCACTGTCC	CGCGGCTTTTATTAA	106159	
QY	6841	TGCCCACTCCCGAAAGATAT	TAGAGCTCAAAAGCTCGTCT	GGAACCGGAGAGTTCCTA	6900	
Db	106160	TGCCCACTCCCGAAAGATAT	TAGAGCTCAAAAGCTCGTCT	GGAACCGGAGAGTTCCTA	106219	
QY	6901	GACGTCAACAGAAATTTT	GACTGGCAGACCTTACAGAC	CCCTGGCGCTCTTTAAAGGG	6960	
Db	106220	GACGTCAACAGAAATTTT	GACTGGCAGACCTTACAGAC	CCCTGGCGCTCTTTAAAGGG	106279	
QY	6961	TCTCAACTGGCCAAATATCG	CAAAAAACAAGTCTCGAGAT	TAATCCGTGAACCTCGGATTT	7020	
Db	106280	TCTCAACTGGCCAAATATCG	CAAAAAACAAGTCTCGAGAT	TAATCCGTGAACCTCGGATTT	106339	
QY	7021	CAACTGGCTGACACACATTC	CAATCAACCAACCGCTTTCA	AACTCCAACTATACATT	7080	
Db	106340	CAACTGGCTGACACACATTC	CAATCAACCAACCGCTTTCA	AACTCCAACTATACATT	106399	
QY	7081	TAACTTTAGAAAGCCAC	CAGACATGGCAAAACAGCC	CAGAAAGTCGATTTGGCGCTCG	7140	
Db	106400	TAACTTTAGAAAGCCAC	CAGACATGGCAAAACAGCC	CAGAAAGTCGATTTGGCGCTCG	106459	
QY	7141	GCGCCGTACGACACTAG	CGTCAGCGACCGGACCCCA	GTCCACGCGACCGGCATCC	7200	
Db	106460	GCGCCGTACGACACTAG	CGTCAGCGACCGGACCCCA	GTCCACGCGACCGGCATCC	106519	
QY	7201	AGGCACGGCAGCTGCA	AAAAAGCAATTCATGCA	GTGAAAAAGTTAGTTCA	GACACGCGAG	7260

Db	106520	AGGCACGGACGTGCAAAAAGCGAAATCATGACAGTGGAAAAAGTTAGTTTCAGACACGCAG	106579
QY	7261	TTTTTTTTCGCCCTTAACGCGCGCCACGAGCTGGGGGTGGACTTTTAAAGAGAAATGGGG	7320
Db	106580	TTTTTTTTTCGCCCTTAACGCGCGCCACGAGCTGGGGGTGGACTTTTAAAGAGAAATGGGG	106639
QY	7321	ACCCGGATATGCACTCAAAAGTCGGTATATGTGGCTTAACCTTAANAACCATCGCCCCG	7380
Db	106640	ACCCGGATATGCACTCAAAAGTCGGTATATGTGGCTTAACCTTAANAACCATCGCCCCG	106699
QY	7381	GGTGGGTGGTCTCTCTCATCATCATTTCCGACACTGTCATAAATGGGGTTCAACTCTTGG	7440
Db	106700	GGTGGGTGGTCTCTCTCATCATCATTTCCGACACTGTCATAAATGGGGTTCAACTCTTGG	106759
QY	7441	TGCTGCACGCCAAGTACAGAGTACAGGGGTGTCTCTGACGCAAAACCGCTCGGCGAAGT	7500
Db	106760	TGCTGCACGCCAAGTACAGAGTACAGGGGTGTCTCTGACGCAAAACCGCTCGGCGAAGT	106819
QY	7501	TCCGCCAGGAAAAAGCAGCGAGCTGTGTTCAGTGGCGTTAACTTTTACCAACACGCCGAA	7560
Db	106820	TCCGCCAGGAAAAAGCAGCGAGCTGTGTTCAGTGGCGTTAACTTTTACCAACACGCCGAA	106879
QY	7561	AAGGTCTGTCACACACAGGGGCTTTTACCTGTCTCTGCTCAGCCACTTCATGGAAATCGTT	7620
Db	106880	AAGGTCTGTCACACACAGGGGCTTTTACCTGTCTCTGCTCAGCCACTTCATGGAAATCGTT	106939
QY	7621	AGGAAAAGCTTACGCAACCCGGGTGCTCTACGCCACCTTATGCTTAANAACCTTTGGC	7680
Db	106940	AGGAAAAGCTTACGCAACCCGGGTGCTCTACGCCACCTTATGCTTAANAACCTTTGGC	106999
QY	7681	CACGATCCTTTACCTATTTTTCACAGTCGATGCCGATGAGAGACTCGCACTCTGGCGGTG	7740
Db	107000	CACGATCCTTTACCTATTTTTCACAGTCGATGCCGATGAGAGACTCGCACTCTGGCGGTG	107059
QY	7741	TTTCCACTAGAGACCTTACCTCTGGGGGAAACCAAGTCGCCACTCATTTATGACAACCTT	7800
Db	107060	TTTCCACTAGAGACCTTACCTCTGGGGGAAACCAAGTCGCCACTCATTTATGACAACCTT	107119
QY	7801	CCAAATTTATGACATTAACGGTGGAGTCGATCGATCAAGCAAAACGTATATATGAAGTTTACACC	7860
Db	107120	CCAAATTTATGACATTAACGGTGGAGTCGATCGATCAAGCAAAACGTATATATGAAGTTTACACC	107179
QY	7861	TCGCGACCGGACACGCAACCGTGAAGGTTCTCTTCACAGCAATTTGCGAGGCGCGTGCC	7920
Db	107180	TCGCGACCGGACACGCAACCGTGAAGGTTCTCTTCACAGCAATTTGCGAGGCGCGTGCC	107239
QY	7921	ACCTTAGACTGCACCGGAGAGTTTGGAGAAAGAAATTCAAAAGGGCGACGGCCATCATTAAC	7980
Db	107240	ACCTTAGACTGCACCGGAGAGTTTGGAGAAAGAAATTCAAAAGGGCGACGGCCATCATTAAC	107299
QY	7981	TCCCAGGGGCTTTTGTAACTTTCCTCTAGACGAAACAGATGTAAATTCACATTTCAAT	8040
Db	107300	TCCCAGGGGCTTTTGTAACTTTCCTCTAGACGAAACAGATGTAAATTCACATTTCAAT	107359
QY	8041	GTTAAGTTTTTGTGTTGAACATATACCAATTAANAACCTTATGTTTACAGAAATTGAA	8100
Db	107360	GTTAAGTTTTTGTGTTGAACATATACCAATTAANAACCTTATGTTTACAGAAATTGAA	107419
QY	8101	GAGCGTTCAATTTTACCTAATAACATAGAAAAAACCCGCGTAACCTAATACTAATGCGA	8160
Db	107420	GAGCGTTCAATTTTACCTAATAACATAGAAAAAACCCGCGTAACCTAATACTAATGCGA	107479
QY	8161	TATTTGGATGGGATCCCTTAGAGCAATGAGCTGGCGCGGTATTAATTGACGGGANAAC	8220
Db	107480	TATTTGGATGGGATCCCTTAGAGCAATGAGCTGGCGCGGTATTAATTGACGGGANAAC	107539
QY	8221	ACGTTAACTGCTCTCCAGCAATCGCAAACTCCGCGTTTTTAAAGACCATTCGACGCCGTTA	8280
Db	107540	ACGTTAACTGCTCTCCAGCAATCGCAAACTCCGCGTTTTTAAAGACCATTCGACGCCGTTA	107599
QY	8281	ATAATTGCAGTAAACTGCGAAAGGCGTACATCGCAGTAGTGAATTTACGATGTGCGACA	8340

Db 107600 ATAAATGGCAGTAAACTGCGAAAAAGGCGGTACATCGCAGTAGTGATTTTACGATGTGCACA 107659.
QY 8341 CCTTCCGCGGTTTACCAGCAACAAAGCGGGTACACGAGCAGCTAAATGCGCCGG 8400
Db 107660 CCTTCCGCGGTTTACCAGCAACAAAGCGGGTACACGAGCAGCTAAATGCGCCGG 107719
QY 8401 CCTTTATGCCAAGTACAAAAGGAGCGGGCTGTACGTTACGAGAACACACTGTGAT 8460
Db 107720 CCTTTATGCCAAGTACAAAAGGAGCGGGCTGTACGTTACGAGAACACACTGTGAT 107779
QY 8461 CGCAANTACAAATAGTGTGTGTGTACCGGCAACCTGCCAAATCCCTAAATGATGACAT 8520
Db 107780 CGCAAAATACAAATAGTGTGTGTGTACCGGCAACCTGCCAAATCCCTAAATGATGACAT 107839
QY 8521 AGTCCCTCAAAATCTAGAACGAACTTCCAAAAATGCGGCAATTAACACACCCCTTGACAT 8580
Db 107840 AGTCCCTCAAAATCTAGAACGAACTTCCAAAAATGCGGCAATTAACACACCCCTTGACAT 107899
QY 8581 TAATGCACATCGTAAAGAGAGCGGAATCCAAAGACAGCGCCGATCTTAAGACCGAGGCA 8640
Db 107900 TAATGCACATCGTAAAGAGAGCGGAATCCAAAGACAGCGCCGATCTTAAGACCGAGGCA 107959
QY 8641 CGTGCTTTGGGTTCCGGGGGCGGTACGATGGAATGATCATACCAAGTATCCCATCAAC 8700
Db 107960 CGTGCTTTGGGTTCCGGGGGCGGTACGATGGAATGATCATACCAAGTATCCCATCAAC 108019
QY 8701 TGTTCACAAAGCGTAAAGATATCGGTTTACAAATTAACAAATTAAGTGGAGAGAT 8760
Db 108020 TGTTCACAAAGCGTAAAGATATCGGTTTACAAATTAACAAATTAAGTGGAGAGAT 108079
QY 8761 TACATTCGACATACAGCGGAGCCCAAAAAACACCCCAACGCAAAACAACTGAGAGACT 8820
Db 108080 TACATTCGACATACAGCGGAGCCCAAAAAACACCCCAACGCAAAACAACTGAGAGACT 108139
QY 8821 TGTCTTGGGTCCTTCCACGTCGCAATGAGATTTCTGTGACCGTGTCTCTTAACCC 8880
Db 108140 TGTCTTGGGTCCTTCCACGTCGCAATGAGATTTCTGTGACCGTGTCTCTTAACCC 108199
QY 8881 GTTACAGTTGTGTTTATGAGTACGTAACACACCAATCTAGAAATGCTAACAGTGCACC 8940
Db 108200 GTTACAGTTGTGTTTATGAGTACGTAACACACCAATCTAGAAATGCTAACAGTGCACC 108259
QY 8941 GCGCTTAGGCGCGTTGTGCACCTAAGTGTGACAGTTACTACTTATTTTAAACAG 9000
Db 108260 GCGCTTAGGCGCGTTGTGCACCTAAGTGTGACAGTTACTACTTATTTTAAACAG 108319
QY 9001 TAGCATACCAATGCAATTAATGTGACCTAAACCCAGTTAGTCTTTTATGAGTGCAGC 9060
Db 108320 TAGCATACCAATGCAATTAATGTGACCTAAACCCAGTTAGTCTTTTATGAGTGCAGC 108379
QY 9061 CCATAGTCTTCAATGAGAGAACCATTCATCTCCGTCAACGGCGTGCAGTTACCGTTGT 9120
Db 108380 CCATAGTCTTCAATGAGAGAACCATTCATCTCCGTCAACGGCGTGCAGTTACCGTTGT 108439
QY 9121 TATTCGCGGCAAAAGAGCTCGGGGAAAAAAGAGCAACATATCGTCACTTTAAACAAC 9180
Db 108440 TATTCGCGGCAAAAGAGCTCGGGGAAAAAAGAGCAACATATCGTCACTTTAAACAAC 108499
QY 9181 TCAATTTCTAAATCTCACCCACTGTGTAACAAAAACATTCGCACTTAAGTGTATGAC 9240
Db 108500 TCAATTTCTAAATCTCACCCACTGTGTAACAAAAACATTCGCACTTAAGTGTATGAC 108559
QY 9241 CGAATATAACAACAGAGTTTAAACACAGCTGCGGTAGTAAACCCCACTTGCACAG 9300
Db 108560 CGAATATAACAACAGAGTTTAAACACAGCTGCGGTAGTAAACCCCACTTGCACAG 108619
QY 9301 CGTGCGCGGTCTAAGTGTTTTAAATTTACATTTGCGTTTACACACGAGCAGATAT 9360
Db 108620 CGTGCGCGGTCTAAGTGTTTTAAATTTACATTTGCGTTTACACACGAGCAGATAT 108679
QY 9361 CTCAGAGGCGCGGTAAAGAGGATATACATTTCCCTTAACACGAGGAACGCGCGTGCAC 9420
Db 108680 CTCAGAGGCGCGGTAAAGAGGATATACATTTCCCTTAACACGAGGAACGCGCGTGCAC 108739

QY 9421 GCGCCTTCCCAATACAAACAGGAGCTACAAAGCTAGTGTAAATATATCAATTAATA 9480
Db 108740 GCGCCTTCCCAATACAAACAGGAGCTACAAAGCTAGTGTAAATATATCAATTAATA 108799
QY 9481 AAACGACAGAAACCTTATAGTGTGCGCAAAACCTAGCAAAAGTACCTAGAGCTTCCCT 9540
Db 108800 AAACGACAGAAACCTTATAGTGTGCGCAAAACCTAGCAAAAGTACCTAGAGCTTCCCT 108859
QY 9541 ATACTTCAAAAAACGCGGTATTTTGTACACCTAGTAACTAAACCCCGTAAGAT 9600
Db 108860 ATACTTCAAAAAACGCGGTATTTTGTACACCTAGTAACTAAACCCCGTAAGAT 108919
QY 9601 TATTCGCCGTTTATCAAAATGGAATAATTAAGCTTTGCTTTAAATCTGCTTAACCAAG 9660
Db 108920 TATTCGCCGTTTATCAAAATGGAATAATTAAGCTTTGCTTTAAATCTGCTTAACCAAG 108979
QY 9661 GGCACCTAATTTTCCAGTTTGGACTCGGACCTTAACGCTTAACGTTAAATTAATAT 9720
Db 108980 GGCACCTAATTTTCCAGTTTGGACTCGGACCTTAACGCTTAACGTTAAATTAATAT 109039
QY 9721 GCAAAAGCACATATTTTGTGTACACCTCAAAACCTACAGTAAAGTTAATACG 9780
Db 109040 GCAAAAGCACATATTTTGTGTACACCTCAAAACCTACAGTAAAGTTAATACG 109099
QY 9781 GCGACTTTGGGAGCAATCACTGTCTGCGCAAAACCTGTTAAATTAACACAAACAG 9840
Db 109100 GCGACTTTGGGAGCAATCACTGTCTGCGCAAAACCTGTTAAATTAACACAAACAG 109159
QY 9841 GAGCGGACTAATAACGAGCTAATGCTCATCGGGGCGCTGTTGAAGAAAGTGTGTGCA 9900
Db 109160 GAGCGGACTAATAACGAGCTAATGCTCATCGGGGCGCTGTTGAAGAAAGTGTGTGCA 109219
QY 9901 ATGCATTTGGGAGTCTAAAAAGAAATCCTGCTGCTAACAGGAAATGCTTAATGTC 9960
Db 109220 ATGCATTTGGGAGTCTAAAAAGAAATCCTGCTGCTAACAGGAAATGCTTAATGTC 109279
QY 9961 CCTACAGCATCAACAATTTGTAACATTAACGTAACGCGCGTGGGTTGCTGTGTG 10020
Db 109280 CCTACAGCATCAACAATTTGTAACATTAACGTAACGCGCGTGGGTTGCTGTGTG 100339
QY 10021 AAATGCTTGGTCAACTGTTACATGAGGCGGATGTAATGTGTGCTTGTGCACAGG 10080
Db 109340 AAATGCTTGGTCAACTGTTACATGAGGCGGATGTAATGTGTGCTTGTGCACAGG 100399
QY 10081 GTGGGGTGCAGTCCCGGCTGGGGTGCAGATCCCGGCTGGGGTGCAGTCCCGGCTG 10140
Db 109400 GTGGGGTGCAGTCCCGGCTGGGGTGCAGATCCCGGCTGGGGTGCAGTCCCGGCTG 109459
QY 10141 GGTGCAGGTCCCGGCTGGGGTGCAGATCCCGGCTGGGGTGCAGTCCCGGCTGGGG 10200
Db 109460 GGTGCAGGTCCCGGCTGGGGTGCAGATCCCGGCTGGGGTGCAGTCCCGGCTGGGG 109519
QY 10201 TGCAGATCCCGGCTGGGGTGCAGTCCCGGCTGGGGTGCAGTCCCGGCTGGGGTGC 10260
Db 109520 TGCAGATCCCGGCTGGGGTGCAGTCCCGGCTGGGGTGCAGTCCCGGCTGGGGTGC 109579
QY 10261 AAGTCCCGGCTGGGGTGCAGTCCCGGCTGGGGTGCAGTCCCGGCTGGGGTGCAG 10320
Db 109580 AAGTCCCGGCTGGGGTGCAGTCCCGGCTGGGGTGCAGTCCCGGCTGGGGTGCAG 109639
QY 10321 TCCCGGCTGGGGTGCAGTCCCGGCTGGGGTGCAGTCCCGGCTGGGGTGCAGTCC 10380
Db 109640 TCCCGGCTGGGGTGCAGTCCCGGCTGGGGTGCAGTCCCGGCTGGGGTGCAGTCC 109699
QY 10381 CCGGCTGGGGTGCAGTCCCGGCTGGGGTGCAGTCCCGGCTGGGGTGCAGTCCCGC 10440
Db 109700 CCGGCTGGGGTGCAGTCCCGGCTGGGGTGCAGTCCCGGCTGGGGTGCAGTCCCGC 109759
QY 10441 GGTGGGGTGCAGTCCCGGCTGGGGTGCAGTCCCGGCTGGGGTGCAGTCCCGGCTGG 10500
Db 109760 GGTGGGGTGCAGTCCCGGCTGGGGTGCAGTCCCGGCTGGGGTGCAGTCCCGGCTGG 109819

Dh 111980 GTAAACAAACCCAACTCGGGGATTTGGCTGCTGTTTGGGCAACGACGCAAAATTC 112039
Qy 12721 CTTGATGACAGGGGAGCTGGCCAAATGTTTGACGAGCATTTTGTATTTGACAGAGCGCG 12780
Dh 112040 CTTGATTTGACAGGGGAGCTGGCCAAATGTTTGGCAGCATTTTGTATTTGACAGAGCGCG 112099
Qy 12781 GCCAATGCAACCGAGAACTCGGACGAGCAAGCAAAAGACAGACGCGCGCGCAATG 12840
Dh 112100 GCCAATGCAACCGAGAACTCGGACGAGCAAGCAAAAGACAGACGCGCGCGCAATG 112159
Qy 12841 GCGCGCGGGGTTAGTTTGTATGACGCTTGCGCGCCATGGGAAACGTCCTGCGCGC 12900
Dh 112160 GCGCGCGGGGTTAGTTTGTATGACGCTTGCGCGCCATGGGAAACGTCCTGCGCGC 112219
Qy 12901 GCGCGCGGGGTTAGTTTGTATGACGCTTGCGCGCCATGGGAGGCGCGGTTGCGAC 12960
Dh 112220 GCGCGCGGGGTTAGTTTGTATGAGGATTTACGGCCGTAACATGCTGGCGCGGTGCGAC 112279
Qy 12961 GCGCGCGGAACCCCGCGCGGTTTGGCGTGACCTGCGCGCAACCCCGCGCGCTCATG 13020
Dh 112280 GCGCGCGGAACCCCGCGCGGTTTGGCGTGACCTGCGCGCAACCCCGCGCGCTCATG 112339
Qy 13021 GCGACCATGGGTGATGGGACCGCGCGCAACATTTTGTGCTACCGCGGAGACCCC 13080
Dh 112340 GCGACCATGGGTGATGGGACCGCGCGCAACATTTTGTGCTACCGCGGAGACCCC 112399
Qy 13081 GCGCGCAAGAGCGCGGATGGGTAGCGGCGGACCATGGAACATTTTTCATTAACCC 13140
Dh 112400 GCGCGCAAGAGCGCGGATGGGTAGCGGCGGACCATGGAACATTTTTCATTAACCC 112459
Qy 13141 CAGTGTACCCCGCGCGGCAAAATCTGGGGCCCATGTGTGCGCGCGCGCGCGCGCGCGC 13200
Dh 112460 CAGTGTACCCCGCGCGGCAAAATCTGGGGCCCATGTGTGCGCGCGCGCGCGCGCGC 112519
Qy 13201 ATTTCCACAGGTTTGTCTATGGGACCGAGCGGTCCCGGTGTATTTTCACTGACCC 13260
Dh 112520 ATTTCCACAGGTTTGTCTATGGGACCGAGCGGTCCCGGTGTATTTTCACTGACCC 112579
Qy 13261 TCGGATGACCGGGGCGAGCTTTTGTGACCATGTGTCCGGAATTTCCCATGAGTACATGT 13320
Dh 112580 TCGGATGACCGGGGCGAGCTTTTGTGACCATGTGTCCGGAATTTCCCATGAGTACATGT 112639
Qy 13321 TTTGGTACCCCGCGCGGACCCCGGGGCGCAAAAGCGCGCCCATGGGACCGGACGAC 13380
Dh 112840 TTTGGTACCCCGCGCGGACCCCGGGGCGCAAAAGCGCGCCCATGGGACCGGACGAC 112699
Qy 13381 CATGTGACATCTTTCACTGACGACCGCGGGGACCCCGCGCGCGCGCGCGCGCGG 13440
Dh 112700 CATGTGACATCTTTCACTGACGACCGCGGGGACCCCGCGCGCGCGCGCGCGG 112759
Qy 13441 GGTGATATGTTCTGATGACCGCGCTTACGTTTGTGACGGGTGTACAGGGAACATATCT 13500
Dh 112760 GGTGATATGTTCTGATGACCGCGCTTACGTTTGTGACGGGTGTACAGGGAACATATCT 112819
Qy 13501 CCGCGGCTCCGAGCCCGGGGCGCGGACCGGATTGGATTATTAAGTTACGTTAGGG 13560
Dh 112820 CCGCGGCTCCGAGCCCGGGGCGCGGACCGGATTGGATTATTAAGTTACGTTAGGG 112879
Qy 13561 ATTTAATTTTAACTCACTACCCCTTAACTGTGCGGCTGCGGCGGACGCTGACGCC 13620
Dh 112880 ATTTAATTTTAACTCACTACCCCTTAACTGTGCGGCTGCGGCGGACGCTGACGCC 112939
Qy 13621 GGGGGGTTGACCCATTGACCGCATCTGCGGTGGCGGGGACGAGCGCGCGGCAAGG 13680
Dh 112940 GGGGGGTTGACCCATTGACCGCATCTGCGGTGGCGGGGACGAGCGCGCGGCAAGG 112999
Qy 13681 TGGGATGCGGGGTTGACCCACCGCTGGGGAAGAACCCCTCCCTGCTGCTTCTGCGC 13740
Dh 113000 TGGGATGCGGGGTTGACCCACCGCTGGGGAAGAACCCCTCCCTGCTGCTTCTGCGC 113059
Qy 13741 TGGGATGCGGGGTTGACCCACCGCTGGGGAAGAACCCCTCCCTGCTGCTTCTGCGC 13800
Dh 113060 TGGGATGCGGGGTTGACCCACCGCTGGGGAAGAACCCCTCCCTGCTGCTTCTGCGC 113119

Qy 13801 TAGACAGAGAGTGCCTCCGCAAGACATGACGAGGGTTGCGGTGCGGTGACGAGCGCG 13860
Dh 113120 TAGACAGAGAGTGCCTCCGCAAGACATGACGAGGGTTGCGGTGCGGTGACGAGCGCG 113179
Qy 13861 CCGCTTGCCTGCTGAGGTGTGCGCGGTGGGCGGTATGACCCCGCAACGCGAGGGCGG 13920
Dh 113180 CCGCTTGCCTGCTGAGGTGTGCGCGGTGGGCGGTATGACCCCGCAACGCGAGGGCGG 113239
Qy 13921 CTTGGCGGGAATTTTCCCGCAACCGCGCGCGGCTTGGGGGGCGGCTTCTCCGCCA 13980
Dh 113240 CTTGGCGGGAATTTTCCCGCAACCGCGCGCGGCTTGGGGGGCGGCTTCTCCGCCA 113299
Qy 13981 ACAGCCCTAATTTGTTTAAAGTTTAAAGTCTGCTGTTTGTGACAGCG 14040
Dh 113300 ACAGCCCTAATTTGTTTAAAGTTTAAAGTCTGCTGTTTGTGACAGCG 113359
Qy 14041 CTTAAGGCTTGCACCTGTTGCGAGATCCCGCTGCGCATGCGCGCCCTCTGCGCTCG 14100
Dh 113360 CTTAAGGCTTGCACCTGTTGCGAGATCCCGCTGCGCATGCGCGCCCTCTGCGCTCG 113419
Qy 14101 GTGACGCTGCGGAGCGTGCACCTGTTGTTGTGTATCCCATGTGCGCATCCGCCA 14160
Dh 113420 GTGACGCTGCGGAGCGTGCACCTGTTGTTGTGTATCCCATGTGCGCATCCGCCA 113479
Qy 14161 TCTTATTTCCCGACAGGCAACATAAACGTACAGCTGTTGTAAAGAAATTAATGCTTTT 14220
Dh 113480 TCTTATTTCCCGACAGGCAACATAAACGTACAGCTGTTGTAAAGAAATTAATGCTTTT 113539
Qy 14221 TTTATTTTCTTAAACCCCGCAACCGCGATACAGTCTCTGCGCTTTCACCGCTGTTTGT 14280
Dh 113540 TTTATTTTCTTAAACCCCGCAACCGCGATACAGTCTCTGCGCTTTCACCGCTGTTTGT 113599
Qy 14281 TACAGCGCCCTTGTGGGGCGCGGACCGGCTTAAACCGGCTGTGCGGCGCACAGACT 14340
Dh 113600 TACAGCGCCCTTGTGGGGCGCGGACCGGCTTAAACCGGCTGTGCGGCGCACAGACT 113659
Qy 14341 TGGCAGCTGCGGCTGAGAGCGGCTTGCACAGGTCCTTAAACATGTAGTTTGAAG 14400
Dh 113660 TGGCAGCTGCGGCTGAGAGCGGCTTGCACAGGTCCTTAAACATGTAGTTTGAAG 113719
Qy 14401 GGTGTACCAAGGCGCGCTTTTTCATTTGTGAGAGCCACGAAAAAGGTGGGTGACTGGT 14460
Dh 113720 GGTGTACCAAGGCGCGCTTTTTCATTTGTGAGAGCCACGAAAAAGGTGGGTGACTGGT 113779
Qy 14461 TGGCGCTGCGACCAAGCTGTGCGCGCTTAAACAACTAATTTTTCAGCTCCCTTCTG 14520
Dh 113780 TGGCGCTGCGACCAAGCTGTGCGCGCTTAAACAACTAATTTTTCAGCTCCCTTCTG 113839
Qy 14521 AGACCTGCGGCTCAATGAGAGCATACAGGTGTTGTATGACTAAATTAATGAGGCTGG 14580
Dh 113840 AGACCTGCGGCTCAATGAGAGCATACAGGTGTTGTATGAGCTAAATTAATGAGGCTGG 113899
Qy 14581 ACCGAGCTCTGCAATAAATCCACGCTTGTAGTAAAAAAGGTGGAGCACAGTCCA 14640
Dh 113900 ACCGAGCTCTGCAATAAATCCACGCTTGTAGTAAAAAAGGTGGAGCACAGTCCA 113959
Qy 14641 ATGCGCCAAAGAGAAACAGGCGCTCCAGCAACCGGGAAGGGAATACCGGCTTCTCAG 14700
Dh 113960 ATGCGCCAAAGAGAAACAGGCGCTCCAGCAACCGGGAAGGGAATACCGGCTTCTCAG 114019
Qy 14701 TTTAGGGGACAGCGCGTTTTCAAACCCCTGGGCGTATCTGCGAGCGCGCGGCTCAA 14760
Dh 114020 TTTAGGGGACAGCGCGTTTTCAAACCCCTGGGCGTATCTGCGAGCGCGCGGCTCAA 114079
Qy 14761 AAAGCACAAGCAGCGCTCTCTGCTGCTGCTCTAGGTGCGACCGAAGTCCATACCC 14820
Dh 114080 AAAGCACAAGCAGCGCTCTCTGCTGCTGCTCTAGGTGCGACCGAAGTCCATACCC 114139
Qy 14821 GCTTATGCGGGAATATGGGTGCGGTGGGCGGCTGCGGACACCTTCTTACCTACACTA 14880
Dh 114140 GCTTATGCGGGAATATGGGTGCGGTGGGCGGCTGCGGACACCTTCTTACCTACACTA 114199

QY 14881 GAGCGTTGATTAATACGACGACCGCGGCTTACTTAAATGTCGTCGTAAT 14940
|||||
Db 114200 GAGCGTTGATTAATACGACGACCGCGGCTTACTTAAATGTCGTCGTAAT 114259
|||||
QY 14941 TCCCGAAGGTGGTGGCAACCGACTCGGGGCGCGCGGAGGTTGCGGCGGAACGCCG 15000
|||||
Db 114260 TCCCGAAGGTGGTGGCAACCGACTCGGGGCGCGCGGAGGTTGCGGCGGAACGCCG 114319
|||||
QY 15001 ACGGCTCCGCCAATCTGGCCGGAGGCGAGCGGACCGAGGCTAAACAGCGCGCAG 15060
|||||
Db 114320 ACGGCTCCGCCAATCTGGCCGGAGGCGAGCGGACCGAGGCTAAACAGCGCGCAG 114379
|||||
QY 15061 GCGCGCGCCACGACGAGGAGCGGCGACACCGCGGTCGCGGTTGACGATGGCTTGTGA 15120
|||||
Db 114380 GCGCGCGCCACGACGAGGAGCGGCGACACCGCGGTCGCGGTTGACGATGGCTTGTGA 114439
|||||
QY 15121 ACAGACTCCACCACTGGCTGTGAAGGCAAGAGCTGCTTTTGAAGCGCGCTTTTA 15180
|||||
Db 114440 ACAGACTCCACCACTGGCTGTGAAGGCAAGAGCTGCTTTTGAAGCGCGCTTTTA 114499
|||||
QY 15181 AACAGGTTGGCCCGATGCGTCGTTGGTAAGACGCGCTTATGTTCCACCTTAAAGCC 15240
|||||
Db 114500 AACAGGTTGGCCCGATGCGTCGTTGGTAAGACGCGCTTATGTTCCACCTTAAAGCC 114559
|||||
QY 15241 TTAAGGATTGATTTTCTGTTTCACTAAATCCGCGACGGAATAATCTCCGCGCGCA 15300
|||||
Db 114560 TTAAGGATTGATTTTCTGTTTCACTAAATCCGCGACGGAATAATCTCCGCGCGCA 114619
|||||
QY 15301 AAGCATMAAAGCGCGCTTGAAGAGATTCAAGTCTTATCTTGGCGCTAAATAAGA 15360
|||||
Db 114620 AAGCATMAAAGCGCGCTTGAAGAGATTCAAGTCTTATCTTGGCGCTAAATAAGA 114679
|||||
QY 15361 CAGCGGCGCCCGACCTTGAAACCGCCGACGCGGAGTGTGCGACACTGTAGATAGCA 15420
|||||
Db 114680 CAGCGGCGCCCGACCTTGAAACCGCCGACGCGGAGTGTGCGACACTGTAGATAGCA 114739
|||||
QY 15421 TCCAGAACTAAGCGGCGAGTGGGAAAGGCTAGACTCCGCGGTTGGCGCCGCGAACA 15480
|||||
Db 114740 TCCAGAACTAAGCGGCGAGTGGGAAAGGCTAGACTCCGCGGTTGGCGCCGCGAACA 114799
|||||
QY 15481 GAGCGCATCAGCTCCCGCAAGATACCTGCATGCCACCGTCACCTCCGTTTGTATGCTC 15540
|||||
Db 114800 GAGCGCATCAGCTCCCGCAAGATACCTGCATGCCACCGTCACCTCCGTTTGTATGCTC 114859
|||||
QY 15541 CCATAGCAGCGCGTGTATTTACAAAGAGACGCTTCTGGGCCAGAGGTTAGAGAGGCC 15600
|||||
Db 114860 CCATAGCAGCGCGTGTATTTACAAAGAGACGCTTCTGGGCCAGAGGTTAGAGAGGCC 114919
|||||
QY 15601 CGGTCTGTACAGGACGCGGTCGAATGTCGCGGTGGGACATGGGCAACAGAGCCATT 15660
|||||
Db 114920 CGGTCTGTACAGGACGCGGTCGAATGTCGCGGTGGGACATGGGCAACAGAGCCATT 114979
|||||
QY 15661 GTCAAGGCAAGGTAAAGAAAGCATATAGTCTTACCTCGGCTCAGGAGGCTTAAATAC 15720
|||||
Db 114980 GTCAAGGCAAGGTAAAGAAAGCATATAGTCTTACCTCGGCTCAGGAGGCTTAAATAC 115039
|||||
QY 15721 GAACGTCCGCGTTTACACACAATCTTCTTGGGCTTATGTCCGCTCACACTGTGCCA 15780
|||||
Db 115040 GAACGTCCGCGTTTACACACAATCTTCTTGGGCTTATGTCCGCTCACACTGTGCCA 115099
|||||
QY 15781 TGTCTTGTGAGTTCAGGCGCTGCTTTCGCGAAAGCGGCGAGTACAGTACAGCGGA 15840
|||||
Db 115100 TGTCTTGTGAGTTCAGGCGCTGCTTTCGCGAAAGCGGCGAGTACAGTACAGCGGA 115159
|||||
QY 15841 AGCGGCTGTTCATTTAAGTGTAGTACAGGCGGCGCAATTTGCCAACGATGACGCGTTT 15900
|||||
Db 115160 AGCGGCTGTTCATTTAAGTGTAGTACAGGCGGCGCAATTTGCCAACGATGACGCGTTT 115219
|||||
QY 15901 CCTGCACTCTGGGTTTTCACCTGGCAAGCGCACTGGTTCTTGGCAGCGCGCGGTGGG 15960
|||||
Db 115220 CCTGCACTCTGGGTTTTCACCTGGCAAGCGCACTGGTTCTTGGCAGCGCGCGGTGGG 115279
|||||
QY 15961 ATTTTGTAGTCTGAATTTGGCAGTCTCTGTCCATGGCCTATGCTGGCTGGAGTGTG 16020
|||||

Db 115280 ATTTTGTAGTCTGAATTTGGCAGTCTCTGTCCATGGCCTATGCTGGCTGGAGTGTG 115339
|||||
QY 16021 GGGGGCGGATGGGTGATGTGCTTCCACGCGGCGAGCGGCTTTTACGAGCTTGGCGGT 16080
|||||
Db 115340 GGGGGCGGATGGGTGATGTGCTTCCACGCGGCGAGCGGCTTTTACGAGCTTGGCGGT 115399
|||||
QY 16081 TCCGCGCTTTGACACACACCGTAAATGCAAAAAAGCGGAGATGACGGACGTCCAGTGC 16140
|||||
Db 115400 TCCGCGCTTTGACACACACCGTAAATGCAAAAAAGCGGAGATGACGGACGTCCAGTGC 115459
|||||
QY 16141 GTCCGCGCAAAACCGGACGCTGATGCTTAAAGCGGGAATGTAGACACTGTCGACG 16200
|||||
Db 115460 GTCCGCGCAAAACCGGACGCTGATGCTTAAAGCGGGAATGTAGACACTGTCGACG 115519
|||||
QY 16201 GCGATACAGTAAAGTAAAGGCTGAGTTAAACAAAGATGACCTCGTGACACAGCGCGCG 16260
|||||
Db 115520 GCGATACAGTAAAGTAAAGGCTGAGTTAAACAAAGATGACCTCGTGACACAGCGCGCG 115579
|||||
QY 16261 CCGAGGGGGGTGATCCTGGGTCCCAATACCTGACGATMAAATCTTCTGTGGCGGTA 16320
|||||
Db 115580 CCGAGGGGGGTGATCCTGGGTCCCAATACCTGACGATMAAATCTTCTGTGGCGGTA 115639
|||||
QY 16321 TTTTCTGGGTACCTCTTCTGTAGTAAAGGATACGTTAGGGAATGGGATGCGGCGG 16380
|||||
Db 115640 TTTTCTGGGTACCTCTTCTGTAGTAAAGGATACGTTAGGGAATGGGATGCGGCGG 115699
|||||
QY 16381 GCGCGGGGGGCGCGGGGGGCGCGCTGCTGCTGCTCCGCTCTTCTGCTCTG 16440
|||||
Db 115700 GCGCGGGGGGCGCGGGGGGCGCGGTTGCTGCTGCTCCGCTCTTCTGCTCTG 115759
|||||
QY 16441 TTGTCTTTTACAGAGCTTCTCTCTGTGGGAGTTGTACTGTGATCTGACGATGAAACA 16500
|||||
Db 115760 TTGTCTTTTACAGAGCTTCTCTCTGTGGGAGTTGTACTGTGATCTGACGATGAAACA 115819
|||||
QY 16501 AGGAATCTCTCCGCGACGCGGTGGTGGACCCCAACCCCTACGCTGTACGAGTGGAGTG 16560
|||||
Db 115820 AGGAATCTCTCCGCGACGCGGTGGTGGACCCCAACCCCTACGCTGTACGAGTGGAGTG 115879
|||||
QY 16561 ATGGCCAGGAAACGGGGGTCCTGGCCGAGACGCGCCGTTGGGTGCTGTGTGCTCAC 16620
|||||
Db 115880 ATGGCCAGGAAACGGGGGTCCTGGCCGAGACGCGCCGTTGGGTGCTGTGTGCTCAC 115939
|||||
QY 16621 CGCTCTTTCGCTGTTAAGGGATGAGGCGCTGTTGAGCGCTTGGCGATTGGGCTGCCG 16680
|||||
Db 115940 CGCTCTTTCGCTGTTAAGGGATGAGGCGCTGTTGAGCGCTTGGCGATTGGGCTGCCG 115999
|||||
QY 16681 TGAATCGGGCGGGGATTTGGAGAGGGGCGAGACGTCGCGCTTGGCGATTGTGCGGTC 16740
|||||
Db 116000 TGAATCGGGCGGGGATTTGGAGAGGGGCGAGACGTCGCGCTTGGCGATTGTGCGGTC 116059
|||||
QY 16741 AGGTGAGTGGGAGGGGGAAGGACGTCGAGGCTTACGCGGCTTACGATGAGTCTGTGTC 16800
|||||
Db 116060 AGGTGAGTGGGAGGGGGAAGGACGTCGAGGCTTACGCGGCTTACGATGAGTCTGTGTC 116119
|||||
QY 16801 CGATGCTTCAAAACGACGAAAGCTGCTGATTTGGGCGATGATTTATGCGAGACGCGCG 16860
|||||
Db 116120 CGATGCTTCAAAACGACGAAAGCTGCTGATTTGGGCGATGATTTATGCGAGACGCGCG 116179
|||||
QY 16861 TGCAGGTGAGTGGGGGCGGGGTTGACGAGGGGTTAGTGGGGGGGGAATGCGATCGGG 16920
|||||
Db 116180 TGCAGGTGAGTGGGGGCGGGGTTGACGAGGGGTTAGTGGGGGGGGAATGCGATCGGG 116239
|||||
QY 16921 GGATGCGGGGAGACCTTGAAGTGTGTTTGAAGTGAAGGCTTGAAGCTTAACACGCGCG 16980
|||||
Db 116240 GGATGCGGGGAGACCTTGAAGTGTGTTTGAAGTGAAGGCTTGAAGCTTAACACGCGCG 116299
|||||
QY 16981 AGACCGCTTTGGCGAGCGGCTTGGAGATCCCAACAGATGACGACTCAGACCTGTACCC 17040
|||||
Db 116300 AGACCGCTTTGGCGAGCGGCTTGGAGATCCCAACAGATGACGACTCAGACCTGTACCC 116359
|||||
QY 17041 TGAATGGCAGCCCTTGGGATGACCCGTCGATTCGAGTTCGGGCGTTTGGTGTGCGATCC 17100
|||||

Dh 116360 TGATGGGACCCCTTGGGATGACCCGTCGCTGATTCGGTGGCCGCTTCCGCTGCCATCC 116419
Qy 17101 GTGCCCCCTTGTTCGACACCCGCCACCTTGCGGCCCTGATGTTGTGGAGCGGGGGCGC 17160
Dh 116420 GTGCCCCCTTGTTCGACACCCGCCACCTTGCGGCCCTGATGTTGTGGAGCGGGGGCGC 116479
Qy 17161 GGGTGGCGGGCGGTGGCGGGCCGTCGACGCCCTCGCGGCCCTCCCGGCTGTCTCT 17220
Dh 116480 GGGTGGCGGGCGGTGGCGGGCCGTCGACGCCCTCGCGGCCCTCCCGGCTGTCTCT 116539
Qy 17221 AGTGGCCCCGCTCTTCCGCAATGTCCTTCGACGAGACTTCGCAACCCGCTGTCCGATAC 17280
Dh 116540 AGTGGCCCCGCTCTTCCGCAATGTCCTTCGACGAGACTTCGCAACCCGCTGTCCGATAC 116599
Qy 17281 TATGCGCGGAAGATGTTGCGGGCTGCCCCACATGTGCGGGATTACTGCGGTAAAC 17340
Dh 116600 TATGCGCGGAAGATGTTGCGGGCTGCCCCACATGTGCGGGATTACTGCGGTAAAC 116659
Qy 17341 GGCAGATTAAATAGATTGCCCTTTCACAGACCCGCGACCACTGAGCGCGCGACGAGA 17400
Dh 116660 GGCAGATTAAATAGATTGCCCTTTCACAGACCCGCGACCACTGAGCGCGCGACGAGA 116719
Qy 17401 ACCTATGTTAGTGCATGTCGATATGTCGCCGTAGTGGCGGGCTATTTTGAATCCGTC 17460
Dh 116720 ACCTATGTTAGTGCATGTCGATATGTCGCCGTAGTGGCGGGCTATTTTGAATCCGTC 116779
Qy 17461 GCGCAGCATTTGACCGTTAGTGGCGAGAGCGCGCTTAAACCGCAGCAGCAGCAGCAG 17520
Dh 116780 GCGCAGCATTTGACCGTTAGTGGCGAGAGCGCGCTTAAACCGCAGCAGCAGCAGCAG 116839
Qy 17521 CGGTTTTAGTTTCTTACTATTAACGTTTAAATCCGTGGCCGATATTGGGTGGCAG 17580
Dh 116840 CGGTTTTAGTTTCTTACTATTAACGTTTAAATCCGTGGCCGATATTGGGTGGCAG 116899
Qy 17581 TGTGTATGTACGCGCGCGCGCGGCCCTTACTGTCGCGCGGAGAACCGCGGAATCT 17640
Dh 116900 TGTGTATGTACGCGCGCGCGCGGCCCTTACTGTCGCGCGGAGAACCGCGGAATCT 116959
Qy 17641 GTTCCGCGCGGAGCGCGCGCGCGCTCCGCAAAACAGCGCGCTTGAATTTCCGCGCGG 17700
Dh 116960 GTTCCGCGCGGAGCGCGCGCGCGCTCCGCAAAACAGCGCGCTTGAATTTCCGCGCGG 117019
Qy 17701 CTGGGGCTTGGTGCATGATTCACACAGATGCGATGATGGCGGTGGTGCACGTC 17760
Dh 117020 CTGGGGCTTGGTGCATGATTCACACAGATGCGATGATGGCGGTGGTGCACGTC 117079
Qy 17761 ACTGTAAACCCGTAATCTGGAATCTGTCCGCGCGCGGTGAGCGCGGCCCTAA 17820
Dh 117080 ACTGTAAACCCGTAATCTGGAATCTGTCCGCGCGCGGTGAGCGCGGCCCTAA 117139
Qy 17821 GCGTTATAGTCTGTCGAGGATCTGAAACTCGAAAGCTGGCATATTAACCCAGTAT 17880
Dh 117140 GCGTTATAGTCTGTCGAGGATCTGAAACTCGAAAGCTGGCATATTAACCCAGTAT 117199
Qy 17881 GGCCTGCGTGTGCGTGGCAACTTTTGAAGAAATTTATTTGCCCGCGGGTGTAAACA 17940
Dh 117200 GGCCTGCGTGTGCGTGGCAACTTTTGAAGAAATTTATTTGCCCGCGGGTGTAAACA 117259
Qy 17941 CCAACACGAGCCGCTTTTCAATATATGTCGGAGAGATTAACATTAACGTCGTCGCG 18000
Dh 117260 CCAACACGAGCCGCTTTTCAATATATGTCGGAGAGATTAACATTAACGTCGTCGCG 117319
Qy 18001 CGAGCTTGGCAGCGTTCGATGCGCTCTTCAAGAGCACTATGCGGGTCCCGCTGCAC 18060
Dh 117320 CGAGCTTGGCAGCGTTCGATGCGCTCTTCAAGAGCACTATGCGGGTCCCGCTGCAC 117379
Qy 18061 CTACCGGCTCCCTGGGGTGGCTGTAAACAGACACCCACAGAGCTTCTATCTTACCTGCG 18120
Dh 117380 CTACCGGCTCCCTGGGGTGGCTGTAAACAGACACCCACAGAGCTTCTATCTTACCTGCG 117439
Qy 18121 AAAAAGAGGAATGCGCTAGTCCGCTTAAAGTGGGCAATATATGTTCCGAAGCGGGCAGG 18180
Dh 117440 AAAAAGAGGAATGCGCTAGTCCGCTTAAAGTGGGCAATATATGTTCCGAAGCGGGCAGG 117499

Qy 18181 TGTTCAGCCCCCTTGGCGGTAGGGTTGACATTTCCGAACACAGTTGACGAGAA 18240
Dh 117500 TGTTCAGCCCCCTTGGCGGTAGGGTTGACATTTCCGAACACAGTTGACGAGAA 117559
Qy 18241 CCTGAAGTTTTTAAATGACACCTCGAGAGCAGAGGGGTGCTACCTGTATCTTTAAAC 18300
Dh 117560 CCTGAAGTTTTTAAATGACACCTCGAGAGCAGAGGGGTGCTACCTGTATCTTTAAAC 117619
Qy 18301 CGTTGGAGTGGGAACCTGTCGGGAACCGCTGCTGAGCGTTAGTCCCGCTGACCA 18360
Dh 117620 CGTTGGAGTGGGAACCTGTCGGGAACCGCTGCTGAGCGTTAGTCCCGCTGACCA 117679
Qy 18361 TGTCCGTCAGTTTTTACCCTCCGATTAACCCGAGCAGCTGCTGTCGGGCGGAGCCA 18420
Dh 117680 TGTCCGTCAGTTTTTACCCTCCGATTAACCCGAGCAGCTGCTGTCGGGCGGAGCCA 117739
Qy 18421 GTCCCGACCGTGGTCACTGACCGCGGTGCCCGGAGCTGTGCAGCAGCCTGAG 18480
Dh 117740 GTCCCGACCGTGGTCACTGACCGCGGTGCCCGGAGCTGTGCAGCAGCCTGAG 117799
Qy 18481 TGTTCGCCCGCCCAAGGAACAACCTGTTGGGTGGGTGCGTGAAGTACGTCGGTGG 18540
Dh 117800 TGTTCGCCCGCCCAAGGAACAACCTGTTGGGTGGGTGCGTGAAGTACGTCGGTGG 117859
Qy 18541 ACCCGAAGACCTTGAGAACGCGACGTGCTGCTACTCATATATAGCGGGTTTGGCCGCG 18600
Dh 117860 ACCCGAAGACCTTGAGAACGCGACGTGCTGCTACTCATATATAGCGGGTTTGGCCGCG 117919
Qy 18601 CGCGGCCCTTGAGACCCCGGTGTTTGGATCCCTGGAAGGAGCAGCAGCAGCAGTGG 18660
Dh 117920 CGCGGCCCTTGAGACCCCGGTGTTTGGATCCCTGGAAGGAGCAGCAGCAGCAGTGG 117979
Qy 18661 GTGTGGTGGAGCGCGCGCTTTAGGCAATTTTAAAGCGGTTTTTGTGATAGGT 18720
Dh 117980 GTGTGGTGGAGCGCGCGCTTTAGGCAATTTTAAAGCGGTTTTTGTGATAGGT 118039
Qy 18721 CTATGTAGCGCGGTGTCGCCCTGTCATGTTTGTTCGCCAGTGTGTCATG 18780
Dh 118040 CTATGTAGCGCGGTGTCGCCCTGTCATGTTTGTTCGCCAGTGTGTCATG 118099
Qy 18781 ACAAAATTAATTTGAGCGTGGCTTTTAAAGGTGTTTCTTGTGCGAGCTTCTGTGTA 18840
Dh 118100 ACAAAATTAATTTGAGCGTGGCTTTTAAAGGTGTTTCTTGTGCGAGCTTCTGTGTA 118159
Qy 18841 ACTGCATACACCGGGGTGTGCGCAGAAACCGCGCTCCCTTATGTCGCGCTGC 18900
Dh 118160 ACTGCATACACCGGGGTGTGCGCAGAAACCGCGCTCCCTTATGTCGCGCTGC 118219
Qy 18901 CCAGAGCGAAAGTGAATGTTCTGCGGCGTTTTGGCGTTGAGAGATCGGGCGATGT 18960
Dh 118220 CCAGAGCGAAAGTGAATGTTCTGCGGCGTTTTGGCGTTGAGAGATCGGGCGATGT 118279
Qy 18961 TGCCGTAAGCGCGCTGCAAAAGCTCACCCGCTCTGTTTTTTTCTTTTGTGACAGAA 19020
Dh 118280 TGCCGTAAGCGCGCTGCAAAAGCTCACCCGCTCTGTTTTTTTCTTTTGTGACAGAA 118339
Qy 19021 CAACATGAGCGCTTGAACAATTAACCTTAACCTGCTGATGATTTTCTGTAACTATTC 19080
Dh 118340 CAACATGAGCGCTTGAACAATTAACCTTAACCTGCTGATGATTTTCTGTAACTATTC 118399
Qy 19081 GAATAGCTACAGTATGATGACGACAATATGCTTACACCTTAGACAGAGATCCAGCT 19140
Dh 118400 GAATAGCTACAGTATGATGACGACAATATGCTTACACCTTAGACAGAGATCCAGCT 118459
Qy 19141 GTGTGCGCTGACGGTGTGTTTCCACCTACCGCTTATGCGGATATATGCTTTTATTTT 19200
Dh 118460 GTGTGCGCTGACGGTGTGTTTCCACCTACCGCTTATGCGGATATATGCTTTTATTTT 118519
Qy 19201 TTGCATTAACGCTGTTTGGGAACGCGTGTGCTATATATTTTAAATTTAAAGCGCT 19260
Dh 118520 TTGCATTAACGCTGTTTGGGAACGCGTGTGCTATATATTTTAAATTTAAAGCGCT 118579

QY	19261	CCGCCAACCTCTGAGATGTACTATAGTGGCTGGGTGTGTGTGTAACCTCCCTGTTTCTGTCTCC	19320
Db	118580	CGCCAACTCTGTGGATGTACTATAGTGGCTGGGTGTGTGTGTAACCTCCCTGTTTCTGTCTCC	118633
QY	19321	GTGCTTTTGTTCAGCTGGCTGCTGTACGCGCGGCCACACATGATCTACGTCGCCGGAGCTG	19380
Db	118640	GTGCTTTTGTTCAGCTGGCTGCTGTACGCGCGGCCACACATGATCTACGTCGCCGGAGCTG	118691
QY	19381	CAAGGTGAAATCTTTTCTTTTACCTGTACACGTACTTTGGCGTGTACATTGTGTGTG	19440
Db	118700	CAAGGTGAAATCTTTTCTTTTACCTGTACACGTACTTTGGCGTGTACATTGTGTGTG	118755
QY	19441	TATCAGCCTTATCAGTGGCTGTAACTGTGTTTCCCGCCGCCGTGGGTCAAGCACGG	19500
Db	118760	TATCAGCCTTATCAGTGGCTGTAACTGTGTTTCCCGCCGCCGTGGGTCAAGCACGG	118811
QY	19501	GGCTCCCGGCTTCTCTGCGTGTGTGTCTTAACTGTGGCGCTGGCGCTGTGCA	19560
Db	118820	GGCTCCCGGCTTCTCTGCGTGTGTGTCTTAACTGTGGCGCTGGCGCTGTGCA	118877
QY	19561	CGCGAGCCTCTATAGACGCGCCCTGGGTACCCAGAGACCGAGAGTGTATGCTACGA	19620
Db	118880	CGCGAGCCTCTATAGAGCGCCCTGGGTACCCAGAGACCGAGAGTGTATGCTACGA	118933
QY	19621	AGATCGCGGGGAAGATACCGTCACTGTGAAGCTGAGATCAGAACCAACCGCGCATCTG	19680
Db	118940	AGATCGCGGGGAAGATACCGTCAACCTGTGAAGCTGAGATCAGAACCAACCGCGCATCTG	118999
QY	19681	CGGTTTGTGTTGGTTCGGCTGTGGGTGTATGGCTCTTTACGGACTTACGTGTATGGT	19740
Db	119000	CGGTTTGTGTTGGTTCGGCTGTGGGTGTATGGCTCTTTACGGACTTACGTGTGTATGGT	119055
QY	19741	TAAAGCACGAAGCTGGCCAGAAAGGAGCGCTGTAGGGGTGTAAATTGTGACGGTGTGCT	19800
Db	119060	TAAAGCACGAAGCTGGCCAGAAAGGAGCGCTGTAGGGGTGTAAATTGTGACGGTGTGCT	119111
QY	19801	GCTGTTTAAATTTTTTGGCTGCCCTCATACCTGTGTCAACTTTTGTGACACCTGTGGAG	19860
Db	119120	GCTGTTTAAATTTTTTGGCTGCCCTCATACCTGTGTCAACTTTTGTGACACCTGTGGAG	119179
QY	19861	GACCGGTTTCTGGCCGGAACGTCACCTCAGGGAGCTGATCAGGTGGCCATGTCAT	19920
Db	119180	GACCGGTTTCTGGCCGGAACGTCACCTCAGGGAGCTGATCAGGTGGCCATGTCAT	119233
QY	19921	ATGCTCCCTGTACAGAGCATGTATAGCGCGTGTGCGCACAGTCGTATTTCTGTGTGG	19980
Db	119240	ATGCTCCCTGTACAGAGCATGTATAGCGCGTGTGCGCACAGTCGTATTTCTGTGTGG	119299
QY	19981	GTCCTCTGTTAGGACAGGGGTTAAGGATACCTGTGCTCCGTGTTAGTGTTTTCACCTTC	20040
Db	119300	GTCCTCTGTTAGGACAGGGGTTAAGGATACCTGTGCTCCGTGTTAGTGTTTTCACCTTC	119355
QY	20041	AGGTGTTTATAGACACATCAGCGCGACCTGTGGTTGGATTGTTGTGATATATTTTC	20100
Db	119360	AGGTGTTTATAGACACATCAGCGCGACCTGTGGTTGGATTGTTGTGATATATTTTC	119415
QY	20101	ATTTGTGTACATTTATTTTCAATTAAGGCATCTGACCTGTACAGCCTTACCTAGCTTTA	20160
Db	119420	ATTTGTGTACATTTATTTTCAATTAAGGCATCTGACCTGTACAGCCTTACCTAGCTTTA	119477
QY	20161	CTGTCTGTTTCTTATGACACAGAGAAACAGGGACTGGAAGCCAGCGCCACGGGAAAC	20220
Db	119480	CTGTCTGTTTCTTATGACACAGAGAAACAGGGACTGGAAGCCAGCGCCACGGGAAAC	119539
QY	20221	TGTCAATGTCCGAACCTGGGGGGGACAGTACGCCCACTGCCAGGGGTGCAACGTACAGGC	20280
Db	119540	TGTCAATGTCCGAACCTGGGGGGGACAGTACGCCCACTGCCAGGGGTGCAACGTACAGGC	119599
QY	20281	GGGGTCAGACAGGAGGGCGAGTGGGGCCGTCGCCGTGTAGACGTATGGCGCCACGGCGGA	20340
Db	119600	GGGGTCAGACAGGAGGGCGAGTGGGGCCGTCGCCGTGTAGACGTATGGCGCCACGGCGGA	119655
QY	20341	GTGGCAGACGGGTGCGTGGGTAGTGTGCGCGAAATCTCTGGGTGCGCGTGTGGCCGT	20400

Db	119660	GTGGGACAGCGGGTGGCGGGGAGTGGCTGGCGGAACATCTCGGGGTGGCGTTCGCCGT	119719
Qy	20401	GTGGTAGTTCACAGGGCATGCGCTGCGTGGTGTGAGATGGTACTCCATGGCGTGGCGG	20460
Db	119720	GTGGTAGTTCACAGGGCATGCGCTGCGTGGTGTGAGATGGTACTCCATGGCGTGGCGG	119779
Qy	20461	GTATCTCACGCCAGGTACCGGCCGTTGGCCACCCCTGGAGAGACAGAGGCCCGGAAGAAC	20520
Db	119780	GTATCTCACGCCAGGTACCGGCCGTTGGCCACCCCTGGAGAGACAGAGGCCCGGAAGAAC	119839
Qy	20521	CCTAAACATGATGCTGATGGTGGTCTGGGGGATGTGGAGTTTAGCCAGAGCACTTCGTG	20580
Db	119840	CCTAAACATGATGCTGATGGTGGTCTGGGGGATGTGGAGTTTAGCCAGAGCACTTCGTG	119899
Qy	20581	GTTCCTGTATGGGTTCTCTCCAGGTGGAATGTCCTACTGATCGGGGTTTGGGTCCGGG	20640
Db	119900	GTTCCTGTATGGGTTCTCTCCAGGTGGAATGTCCTACTGATCGGGGTTTGGGTCCGGG	119955
Qy	20641	CGTGTGTGAGGGGTCCTCTTAAGAAAGACCGAGGCCGCCAGAGAGCTGGAACCCAAATC	20700
Db	119960	CGTGTGTGAGGGGTCCTCTTAAGAAAGACCGAGGCCGCCAGAGAGCTGGAACCCAAATC	120019
Qy	20701	CCCCGACGTAAGTGAATAATGATCCGCTGGCGGGAAGAAAGGCATTAAGGCCCATAGCA	20760
Db	120020	CCCCGACGTAAGTGAATAATGATCCGCTGGCGGGAAGAAAGGCATTAAGGCCCATAGCA	120079
Qy	20761	CCGAGGTCGTTGAGAAAGACCCATGATTCGCGATCGGGGCCCCACGTAGCTGTCTTCGAT	20820
Db	120080	CCGAGGTCGTTGAGAAAGACCCATGATTCGCGATCGGGGCCCCACGTAGCTGTCTTCGAT	120139
Qy	20821	GCCACAGGTTCCACCGAGTGGTCAGACCGGAGAAATCCCGAGAGATGTTCCCTCTTAAG	20880
Db	120140	GCCACAGGTTCCACCGAGTGGTCAGACCGGAGAAATCCCGAGAGATGTTCCCTCTTAAG	120199
Qy	20881	GTCTGTGGTGGAGAGAGCGCCGCGACGTCGAACCCGAGCTGTGTAAAGCGGCATCAGCGC	20940
Db	120200	GTCTGTGGTGGAGAGAGCGCCGCGACGTCGAACCCGAGCTGTGTAAAGCGGCATCAGCGC	120259
Qy	20941	CCTGGGAAGCGGGGACCGCGGGGGTGAACAAAGCGGCGACTGCTGGGGGCTCGACAGCGT	21000
Db	120260	CCTGGGAAGCGGGGACCGCGGGGGTGAACAAAGCGGCGACTGCTGGGGGCTCGACAGCGT	120319
Qy	21001	TGCAAAACAGAGTCAGTTGCTGCTTCTGCAAAACCTCGCGGAGGTGGCCAGGTTGTGTTG	21060
Db	120320	TGCAAAACAGAGTCAGTTGCTGCTTCTGCAAAACCTCGCGGAGGTGGCCAGGTTGTGTTG	120379
Qy	21061	GTTGCAACCCGTAGTCTTCTGTAGAGTTCCTGCGGGGCGTGAAGCTGGCCCCCATGA	21120
Db	120380	GTTGCAACCCGTAGTCTTCTGTAGAGTTCCTGCGGGGCGTGAAGCTGGCCCCCATGA	120439
Qy	21121	GTACCACTGTGTGTCGCGAAGAGAGGTCCAGTTTGGCGGACCGAGAGTAGAGGTCGTGA	21180
Db	120440	GTACCACTGTGTGTCGCGAAGAGAGGTCCAGTTTGGCGGACCGAGAGTAGAGGTCGTGA	120499
Qy	21181	ATGAGACTTCATGCTTGTGTGTGTGAGATGACGATTTCTTCTGACAGACCCCTCTGACCCAC	21240
Db	120500	ATGAGACTTCATGCTTGTGTGTGTGAGATGACGATTTCTTCTGACAGACCCCTCTGACCCAC	120559
Qy	21241	GGTGCGGCACACAGGTGGGCCCGGCAGTCAAAAGTTTGGCACGCGCTGGCGCACTCGTCGAC	21300
Db	120560	GGTGCGGCACACAGGTGGGCCCGGCAGTCAAAAGTTTGGCACGCGCGCTGGCGCACTCGTCGAC	120619
Qy	21301	GTGCTGGGGCTGGATTTTGGAAATATACGCCCGGGGGTTTGGACACACAGCACTGCAGGGG	21360
Db	120620	GTGCTGGGGCTGGATTTTGGAAATATACGCCCGGGGGTTTGGACACACAGCACTGCAGGGG	120679
Qy	21361	CGTTTCCTCTGACGGGATGCGAATCTGTATGCGGCTCGGTATACGGCGACGGGCATCTCGAT	21420
Db	120680	CGTTTCCTCTGACGGGATGCGAATCTGTATGCGGCTCGGTATACGGCGACGGGCATCTCGAT	120739
Qy	21421	AGCGGTAACCAACATGCTCGTGCCTGAAGCTGTGGCCGACACCAACGAGACCCGGGA	21480

Db 120740 AGCGTAACCAACCATCCTCCCTGCTGCTGACGTGTGGCCGGACCAACCAACGACCCCGGGA 120799
QY 21481 GACGAGGGCCCTGTTAGATGATGAAGAGTTGGCCAGGTGTCGCCGTAACGTCGGGTAG 21540
Db 120800 GACGAGGGCCCTGTTAGATGATGAAGAGTTGGCCAGGTGTCGCCGTAACGTCGGGTAG 120859
QY 21541 GGTGGGACTTCGGCAGAGACACAGTGTCTCAAGAGTTCGATCCTGTGGTCAAGTGTGGCAC 21600
Db 120860 GGTGGGACTTCGGCAGAGACACAGTGTCTCAAGAGTTCGATCCTGTGGTCAAGTGTGGCAC 120919
QY 21601 GGGGAAGGACACGACGACGATGAGTTACCGGTGGCTTACAGTCAAGTGTGACGGTTG 21660
Db 120920 GGGGAAGGACACGACGATGAGTTACCGGTGGCTTACAGTCAAGTGTGACGGTTG 120979
QY 21661 CTTGAGGACTTACCTCGCGGGTGGCGGCTGATGACGACTGCGTTAAACGGGACGGGGGC 21720
Db 120980 CTTGAGGACTTACCTCGCGGGTGGCGGCTGATGACGACTGCGTTAAACGGGACGGGGGC 121039
QY 21721 TACGCTGTGATGCTGTTGGGTGGCGCTGATCAGTTCTCCGACAGGACGGGTGCTGCC 21780
Db 121040 TACGCTGTGATGCTGTTGGGTGGCGCTGATCAGTTCTCCGACAGGACGGGTGCTGCC 121099
QY 21781 GGGCGACGTCATGCGGACGATGATGCTCAAGTTCCTTCGATAGTTCCTTCGACGCAAAACAG 21840
Db 121100 GGGCGACGTCATGCGGACGATGATGCTCAAGTTCCTTCGATAGTTCCTTCGACGCAAAACAG 121159
QY 21841 TGTGTCTGACGAGGACGAGGCTGTGTCTCTCCGGGTTCCAAACGCAACGCGGCTCAG 21900
Db 121160 TGTGTCTGACGAGGACGAGGCTGTGTCTCTCCGGGTTCCAAACGCAACGCGGCTCAG 121219
QY 21901 CGTGTATGTGCTTAAAGACGCGCACGTGCGCTAGCATGATGTTGGTGAACCGGCTCGCAGAT 21960
Db 121220 CGTGTATGTGCTTAAAGACGCGCACGTGCGCTAGCATGATGTTGGTGAACCGGCTCGCAGAT 121279
QY 21961 GGGGTATGTCGGCCCGCACGTCGGCTGATGATGCCATCTTGTATGCCCTGTCTCATPAAGC 22020
Db 121280 GGGGTATGTCGGCCCGCACGTCGGCTGATGATGCCATCTTGTATGCCCTGTCTCATPAAGC 121339
QY 22021 CACGCACTGTCCGACCCACGAGGTCCTGCTCCGCTGCGGTGACCCAGGTTTCTGAGCT 22080
Db 121340 CACGCACTGTCCGACCCACGAGGTCCTGCTCCGCTGCGGTGACCCAGGTTTCTGAGCT 121399
QY 22081 AACGAGCGTTCCGTGCGCTGCTGCTGCTGATGCGCTGGGGCGATATATGGGACCCG 22140
Db 121400 AACGAGCGTTCCGTGCGCTGCTGCTGCTGATGCGCTGGGGCGATATATGGGACCCG 121459
QY 22141 CGGCATTCGTGCTGTAACACGACGAGTGTGTGACAAATGTGTAATCTGACAGCGGCCG 22200
Db 121460 CGGCATTCGTGCTGTAACACGACGAGTGTGTGACAAATGTGTAATCTGACAGCGGCCG 121519
QY 22201 GCCCAGGGGTCCTCACTTGCAGTGTGAGCCAGAGTCCTTGGAGCATGTGTCACAGT 22260
Db 121520 GCCCAGGGGTCCTCACTTGCAGTGTGAGCCAGAGTCCTTGGAGCATGTGTCACAGT 121579
QY 22261 TCGCGTGACAAACTCTTTGCTGCAACCGTGGACATCGGAGAACTGATCGAACGACGA 22320
Db 121580 TCGCGTGACAAACTCTTTGCTGCAACCGTGGACATCGGAGAACTGATCGAACGACGA 121639
QY 22321 GGGCAGGGCGAATATAGGCCCCAGTGTGTCGGCAGAGGGTGTCTTCCGACCATCTAGG 22380
Db 121640 GGGCAGGGCGAATATAGGCCCCAGTGTGTCGGCAGAGGGTGTCTTCCGACCATCTAGG 121699
QY 22381 TTTCTTGGGGCGCACGACGATTTGGAGAAAGGGGTGCTCGTCGAACCCAAAGTTGC 22440
Db 121700 TTTCTTGGGGCGCACGACGATTTGGAGAAAGGGGTGCTCGTCGAACCCAAAGTTGC 121759
QY 22441 GATGACTTGGCGCGATGTTGGCTGTGTGATCGGCAACGCTCCGAGTTCCACAGCTCCAG 22500
Db 121760 GATGACTTGGCGCGATGTTGGCTGTGTGATCGGCAACGCTCCGAGTTCCACAGCTCCAG 121819
QY 22501 GTGCTTACGAGACTGAATTCGAAGCTTCTTGGCAGGTTTCCCAACGACGGCGAAAGGGCA 22560
Db 121820 GTGCTTACGAGACTGAATTCGAAGCTTCTTGGCAGGTTTCCCAACGACGGCGAAAGGGCA 121879

QY 22561 TCCGAGATGCTGCGGCCCTTCCGTGATGGCATCCAAGGGGCCGGTTCCGGCTCCGGTTC 22620
Db 121880 TCCGAGATGCTGCGGCCCTTCCGTGATGGCATCCAAGGGGCCGGTTCCGGCTCCGGTTC 121939
QY 22621 GCGCGGAGGACGCGCAAAAGACACGACGAGGACGACGTTGTGAACCTTGTATAGAT 22680
Db 121940 GCGCGGAGGACGCGCAAAAGACACGACGAGGACGACGTTGTGAACCTTGTATAGAT 121999
QY 22681 GTGCTTACGCGTTTCCCGTGTGATGTCGTGGCGTGGCGGTGATGTTGGCTTCAGATGTTGG 22740
Db 122000 GTGCTTACGCGTTTCCCGTGTGATGTCGTGGCGTGGCGGTGATGTTGGCTTCAGATGTTGG 122059
QY 22741 TCGAAGCTGAGACAAAGAGGCGGACGAGCCGCCCGGACGACGAGGCTCCAGTGTGCC 22800
Db 122060 TCGAAGCTGAGACAAAGAGGCGGACGAGCCGCCCGGACGACGAGGCTCCAGTGTGCC 122119
QY 22801 GATGACAGAGGCGGTTTCATGAGCGCGATTAATGCTGTGTAATAGGGGCCCTTCCAAAT 22860
Db 122120 GATGACAGAGGCGGTTTCATGAGCGCGATTAATGCTGTGTAATAGGGGCCCTTCCAAAT 122179
QY 22861 CTGCTAAGCCAGGACAAAGTTGGGTGATGCGGGTAAATCTGCGGCGCTTCCCGAGTA 22920
Db 122180 CTGCTAAGCCAGGACAAAGTTGGGTGATGCGGGTAAATCTGCGGCGCTTCCCGAGTA 122239
QY 22921 AAGCAGCGCTGTTGCTATCGCCGCTCAACGGGTTCAAAAGACCAAGACAGATGATAGG 22980
Db 122240 AAGCAGCGCTGTTGCTATCGCCGCTCAACGGGTTCAAAAGACCAAGACAGATGATAGG 122299
QY 22981 CTGACTGAATTAAGACCTCTCTGAGGAATGTGTATGCTTGAAGCAGCAGATTAACGCA 23040
Db 122300 CTGACTGAATTAAGACCTCTCTGAGGAATGTGTATGCTTGAAGCAGCAGATTAACGCA 122359
QY 23041 TGTGTGTGTATTAAGTGTGCTGCGCTGCGGTGGGTGGCGCTGTGAGCGGTTTAAAGAAAGCC 23100
Db 122360 TGTGTGTGTATTAAGTGTGCTGCGCTGCGGTGGGTGGCGCTGTGAGCGGTTTAAAGAAAGCC 122419
QY 23101 ACCGAGGACAGGGGTGCGGCTGCGCGCACGCTGTGCAATGAGTGTGCTGTGTGTT 23160
Db 122420 ACCGAGGACAGGGGTGCGGCTGCGCGCACGCTGTGCAATGAGTGTGCTGTGTGTT 122479
QY 23161 AATAGCTGTGTGCGGTGCGGAGAAATGCGCCACTGACGCGCTAGTGGCGTAATATCC 23220
Db 122480 AATAGCTGTGTGCGGTGCGGAGAAATGCGCCACTGACGCGCTAGTGGCGTAATATCC 122539
QY 23221 ACAAGGGCGCATCTGTTGCGCCCGGGGACAGGCTGTGCAATGGAACGAATGTTTG 23280
Db 122540 ACAAGGGCGCATCTGTTGCGCCCGGGGACAGGCTGTGCAATGGAACGAATGTTTG 122599
QY 23281 CAGCGCACTGCACTGTGTAATGAGCTGTGAGTGTGTAATGAGTCAAGTATGTG 23340
Db 122600 CAGCGCACTGCACTGTGTAATGAGCTGTGAGTGTGTAATGAGTCAAGTATGTG 122659
QY 23341 GGTTCAGTTTTCGACGGGAGGCGCTGGAAGACGACGCTGATGCTCTGCGGGCATATG 23400
Db 122660 GGTTCAGTTTTCGACGGGAGGCGCTGGAAGACGACGCTGATGCTCTGCGGGCATATG 122719
QY 23401 GGGGTATCTGACACCTATAGCTGTGCGGTTGGAGGCTGTGACGGCCAGCGGTATAT 23460
Db 122720 GGGGTATCTGACACCTATAGCTGTGCGGTTGGAGGCTGTGACGGCCAGCGGTATAT 122779
QY 23461 GTTCCGTTGTAAAGGAGATCAACCGCGGCGCATATATGAGTCTCTCGGCAACGGTCT 23520
Db 122780 GTTCCGTTGTAAAGGAGATCAACCGCGGCGCATATATGAGTCTCTCGGCAACGGTCT 122839
QY 23521 CCAAGCGGTGATGTCAATGTACCGGAGCTGGCGTGCACGCGCATCATATTTCTAC 23580
Db 122840 CCAAGCGGTGATGTCAATGTACCGGAGCTGGCGTGCACGCGCATCATATTTCTAC 122899
QY 23581 TATGTGTCCAAGTGTCAAGGCGGCGCAAGGTGTCCCGGGGGTACCCGATCGCGGCAACCG 23640
Db 122900 TATGTGTCCAAGTGTCAAGGCGGCGCAAGGTGTCCCGGGGGTACCCGATCGCGGCAACCG 122959

QY	23641	TCCTGCTGGCAGCTCAGATGCTGCCACCTCTAACCCGACGTTCTATCGAGGCCGT	23700
Db	122960	TCCTGCTGGCAGCTCAGATGCTGCCACCTCTAACCCGACGTTCTATCGAGGCCGT	123019
QY	23701	GTCCTTAAGGCACTCAGATTTCCGTAGATCTTGAGAGTGGCGATCAGGTCTGG	23760
Db	123020	GTCCTTAAGGCACTCAGATTTCCGTAGATCTTGAGAGTGGCGATCAGGTCTGG	123079
QY	23761	GCCATAGGCGAGGATATAGTATGATGGCCCTGAGGTGGCCGACCGAGTTTCCAGAG	23820
Db	123080	GCCATAGGCGAGGATATAGTATGATGGCCCTGAGGTGGCCGACCGAGTTTCCAGAG	123139
QY	23821	TGCATATTTAACCAAGGCGCAGAGATGCGAGATTAACGCCACGCTGGCTCTCATC	23880
Db	123140	TGCATATTTAACCAAGGCGCAGAGATGCGAGATTAACGCCACGCTGGCTCTCATC	123199
QY	23881	GTCCTTGTCAAGTTATCAGAGGGGCGTTTCAAGCCAAAGTAAATAATTCCTAAAGCA	23940
Db	123200	GTCCTTGTCAAGTTATCAGAGGGGCGTTTCAAGCCAAAGTAAATAATTCCTAAAGCA	123259
QY	23941	CTGTTCTGGCACAGCGCCAAACACTTCTGCGCCGAAATTCATGATTAAGCCCTC	24000
Db	123260	CTGTTCTGGCACAGCGCCAAACACTTCTGCGCCGAAATTCATGATTAAGCCCTC	123319
QY	24001	CTCTCTGGACTAAGGGGTGAGGGCCGAGAGGGTTGCGTGGGCGCATTTTTC	24060
Db	123320	CTCTCTGGACTAAGGGGTGAGGGCCGAGAGGGTTGCGTGGGCGCATTTTTC	123379
QY	24061	TAACTCTAGCCGCGCAAAAGCAAGCGGGTGGGACTTTAATAGGGCGTATAGGGTGT	24120
Db	123380	TAACTCTAGCCGCGCAAAAGCAAGCGGGTGGGACTTTAATAGGGCGTATAGGGTGT	123439
QY	24121	AGGATGCGGTGGGAGCGGCTCCATGTCATGCACTTCAATATTAATTTATGTTT	24180
Db	123440	AGGATGCGGTGGGAGCGGCTCCATGTCATGCACTTCAATATTAATTTATGTTT	123499
QY	24181	TGGGCACTTGGGATGTTACACTTATTAATCTCCCATAGTCAACATTAATCACTTACAGA	24240
Db	123500	TGGGCACTTGGGATGTTACACTTATTAATCTCCCATAGTCAACATTAATCACTTACAGA	123559
QY	24241	TCCTCTTCTAATCAATAACAATGTTTCGGGGTGTAGGTTACAGGTAAAGGTGGAGG	24300
Db	123560	TCCTCTTCTAATCAATAACAATGTTTCGGGGTGTAGGTTACAGGTAAAGGTGGAGG	123619
QY	24301	GGAATGTAAGTGGGGAACCAAGCATTAAGTCCGGGGCGGAGTGGGAGCCCTTAAC	24360
Db	123620	GGAATGTAAGTGGGGAACCAAGCATTAAGTCCGGGGCGGAGTGGGAGCCCTTAAC	123679
QY	24361	CCAGAGATGTCACCTTACCTTGTAGGCGATCGAACACTACCTCCGAAGTGTCTCTGT	24420
Db	123680	CCAGAGATGTCACCTTACCTTGTAGGCGATCGAACACTACCTCCGAAGTGTCTCTGT	123739
QY	24421	TGGAATGTTTGTGATTAAGTAAACAGAAAGTGTGGAGAAAGTAACTTATAGATGAC	24480
Db	123740	TGGAATGTTTGTGATTAAGTAAACAGAAAGTGTGGAGAAAGTAACTTATAGATGAC	123799
QY	24481	CTCCGCTGGGCGGCGTGGGTGACAGCTGTTGATGAATGAACACTTCCCTGGGC	24540
Db	123800	CTCCGCTGGGCGGCGTGGGTGACAGCTGTTGATGAATGAACACTTCCCTGGGC	123859
QY	24541	GTTCTGGGCGTGGGTGATGCTCACTAAGGAGCGCAACTCAACTAATCTCTCC	24600
Db	123860	GTTCTGGGCGTGGGTGATGCTCACTAAGGAGCGCAACTCAACTAATCTCTCC	123919
QY	24601	CGTTTACAGCCGTGAGCGGTTTCTGCTGTAGCGCTTGTGAGGGGGTTCCTGAACCTT	24660
Db	123920	CGTTTACAGCCGTGAGCGGTTTCTGCTGTAGCGCTTGTGAGGGGGTTCCTGAACCTT	123979
QY	24661	GTTGTTGAACATTCAGGTAACCGGTAATGACCGGCTCAGGGCGATTTGTAACAA	24720
Db	123980	GTTGTTGAACATTCAGGTAACCGGTAATGACCGGCTCAGGGCGATTTGTAACAA	124039
QY	24721	CCTAAAAACGATATAAGCTTACAAACGATTTTGTGTAACAGTTTGTATATTTAGCC	24780

Db	124040	CCTAAAAACGATATAAGCTTACAAACGATTTTGTGTAACAGTTTGTATATTTAGCC	124099
QY	24781	CCAAAGTTTATCAAAAGCGAAACCTACTTACCGATTAAGTAAATGCAAAACCGCAAGAGA	24840
Db	124100	CCAAAGTTTATCAAAAGCGAAACCTACTTACCGATTAAGTAAATGCAAAACCGCAAGAGA	124159
QY	24841	TAAACATCAGTATCTGTCCCAATGTTGTTGCAATTAAGAAATGAGATTAATTTGCC	24900
Db	124160	TAAACATCAGTATCTGTCCCAATGTTGTTGCAATTAAGAAATGAGATTAATTTGCC	124219
QY	24901	CGCTGAGATGCTGGGAAATTAAGGGCGGTAATTTTACATGCTGACGAGGTAAGAAC	24960
Db	124220	CGCTGAGATGCTGGGAAATTAAGGGCGGTAATTTTACATGCTGACGAGGTAAGAAC	124279
QY	24961	TTGTGAGTTTCAAGTTAGTCAACCCGCGCAACGTAAGCCGCTAGAGTCTGACGCGGTG	25020
Db	124280	TTGTGAGTTTCAAGTTAGTCAACCCGCGCAACGTAAGCCGCTAGAGTCTGACGCGGTG	124339
QY	25021	TTGTGAGGAGAGTACATCTTAATTTTAACTTAAAGGGGTCTCTGTAATTAATTT	25080
Db	124340	TTGTGAGGAGAGTACATCTTAATTTTAACTTAAAGGGGTCTCTGTAATTAATTT	124399
QY	25081	AAGTTATGCTTACTTACATATATCAATGATGATGTTTACCTCCAAAGATATCGAT	25140
Db	124400	AAGTTATGCTTACTTACATATATCAATGATGATGTTTACCTCCAAAGATATCGAT	124459
QY	25141	AAAATGCGTGAATGTAAGTTTGCACAAATGACGCGGTAGTAGGCCCAAGAAATGA	25200
Db	124460	AAAATGCGTGAATGTAAGTTTGCACAAATGACGCGGTAGTAGGCCCAAGAAATGA	124519
QY	25201	TAAACCTATATGAGAAATTTTATTAAGTGTGTGTACTGTAACGCAAAATTAATTTAA	25260
Db	124520	TAAACCTATATGAGAAATTTTATTAAGTGTGTGTACTGTAACGCAAAATTAATTTAA	124579
QY	25261	ATAAATCTTATATTCATGTTTACCAAGTTTAATTTGAGGGTGTCTGTAATTAAT	25320
Db	124580	ATAAATCTTATATTCATGTTTACCAAGTTTAATTTGAGGGTGTCTGTAATTAAT	124639
QY	25321	GTACTCTGATTTCTGAGGCAACTGTATGATGCAAGGAGCGTGCCTTGAACATTAACA	25380
Db	124640	GTACTCTGATTTCTGAGGCAACTGTATGATGCAAGGAGCGTGCCTTGAACATTAACA	124699
QY	25381	ATAGGCAATGTCATGATGTCATATGCGCATGTCATTTAAGGCCAGGAGATTTGAG	25440
Db	124700	ATAGGCAATGTCATGATGTCATATGCGCATGTCATTTAAGGCCAGGAGATTTGAG	124759
QY	25441	CAATAGCTATTAATAAACAAGATGTTAATAGTCTAATAAGTATAAATTAATTAACA	25500
Db	124760	CAATAGCTATTAATAAACAAGATGTTAATAGTCTAATAAGTATAAATTAATTAACA	124819
QY	25501	AAATTAATAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA	25560
Db	124820	AAATTAATAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA	124879
QY	25561	TAAAGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG	25620
Db	124880	TAAAGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG	124939
QY	25621	AAATTAATGTTAGTTATTTAATTTTAAAGTTTAACTATTAATTAATTAATTAATTAAT	25680
Db	124940	AAATTAATGTTAGTTATTTAATTTTAAAGTTTAACTATTAATTAATTAATTAATTAAT	124999
QY	25681	GTCATACCTGCGTAATTTGCAACCAAGATCAATTAATTAATTAATTAATTAATTAAT	25740
Db	125000	GTCATACCTGCGTAATTTGCAACCAAGATCAATTAATTAATTAATTAATTAATTAAT	125059
QY	25741	CATAGCCACATATACATTAACACAAATGAGGCAATTAATTAATTAATTAATTAATTAAT	25800
Db	125060	CATAGCCACATATACATTAACACAAATGAGGCAATTAATTAATTAATTAATTAATTAAT	125119
QY	25801	ACTTTGATTTGAGATGTCACATTAAGAAATGCGTAAAGATTAAGATGCTCATGTT	25860

Dd 125120 ACTTTGATGTTGGAGTCCACATAGAAATGCCGTAGAAATACAGTCCATTCACGT 125179
Qy 25861 GGTCACACAGAAGACATGATGTTGTTTACTAGAAACAATTTTCGCGTGTATTAACA 25920
Dd 125180 GGTCACACAGAAGACATGATGTTGTTTACTAGAAACAATTTTCGCGTGTATTAACA 125239
Qy 25921 AATTTAATATGCTGGAATAATTAACAAACGATTAATTTAAGGCCAATATCATAGTAA 25980
Dd 125240 AATTTAATATGCTGGAATAATTAACAAACGATTAATTTAAGGCCAATATCATAGTAA 125299
Qy 25981 AACAACTTTAACAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA 26040
Dd 125300 AACAACTTTAACAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA 125359
Qy 26041 AATGACACTACAGCTCTGTACCAAAATCTGCGTGTGCAAGGCCAATGCGCATGTAA 26100
Dd 125360 AATGACACTACAGCTCTGTACCAAAATCTGCGTGTGCAAGGCCAATGCGCATGTAA 125419
Qy 26101 AACACACATGCTGCAAAACAGTACACAAAATATTAAGTTTAATTTGCTAATTAATAA 26160
Dd 125420 AACACACATGCTGCAAAACAGTACACAAAATATTAAGTTTAATTTGCTAATTAATAA 125479
Qy 26161 TATTTCAAATGATTTAATAATCAATACCTGTAATCCATGGGAAAAAATTAAGSCAACG 26220
Dd 125480 TATTTCAAATGATTTAATAATCAATACCTGTAATCCATGGGAAAAAATTAAGSCAACG 125539
Qy 26221 GAGTTAATTTGACCTGCTGCTGCTGATACAAATACAACTAATAGTTTCCATAAAGAG 26280
Dd 125540 GAGTTAATTTGACCTGCTGCTGCTGATACAAATACAACTAATAGTTTCCATAAAGAG 125599
Qy 26281 AACACACGTAAACAATGACAAATTAATTTGACTGCTTGTATTAAGTGTCCCTGCAT 26340
Dd 125600 AACACACGTAAACAATGACAAATTAATTTGACTGCTTGTATTAAGTGTCCCTGCAT 125659
Qy 26341 GTTGTACCAAGGCTATTATCCAAAACGTTAATGTAAGAAGTGTGTAGTAAACCACTAC 26400
Dd 125660 GTTGTACCAAGGCTATTATCCAAAACGTTAATGTAAGAAGTGTGTAGTAAACCACTAC 125719
Qy 26401 TCCAAAATAAAAAGTATAGTACAGCCATTTTAAATCAAAACCTGATTTATCAAG 26460
Dd 125720 TCCAAAATAAAAAGTATAGTACAGCCATTTTAAATCAAAACCTGATTTATCAAG 125779
Qy 26461 TTAAGGGGAGTTTGAGCTTTAAAAAGTGTGTACATCGTTTCCAGGCAAACTTCACACT 26520
Dd 125780 TTAAGGGGAGTTTGAGCTTTAAAAAGTGTGTACATCGTTTCCAGGCAAACTTCACACT 125839
Qy 26521 GAGTCACACAAAGGTTCTGTGTGCTGCTGTAACGGGAATCTGCCATTTGCTGATTTGT 26580
Dd 125840 GAGTCACACAAAGGTTCTGTGTGCTGCTGTAACGGGAATCTGCCATTTGCTGATTTGT 125899
Qy 26581 TGCGAACCCACAAAGAAATCATGGAAGAACAGAGTGGGAATTTGTTTTGTTGTCGTG 26640
Dd 125900 TGCGAACCCACAAAGAAATCATGGAAGAACAGAGTGGGAATTTGTTTTGTTGTCGTG 125959
Qy 26641 GCCTGAGATGTTGGAACATTCCTGTTATTTTGTATGTTAGGCCAAACTGTGGAACAAT 26700
Dd 125960 GCCTGAGATGTTGGAACATTCCTGTTATTTTGTATGTTAGGCCAAACTGTGGAACAAT 126019
Qy 26701 AAGAGTGTATTTGAAATATTTTGTGTAAACAAACCATGTTTAAAGTCCCAAAAGAA 26760
Dd 126020 AAGAGTGTATTTGAAATATTTTGTGTAAACAAACCATGTTTAAAGTCCCAAAAGAA 126079
Qy 26761 CATAAAAATGTTTAAATAGAACATGCTAGTACAGAACATTTTGTGTACGTAAACTA 26820
Dd 126080 CATAAAAATGTTTAAATAGAACATGCTAGTACAGAACATTTTGTGTACGTAAACTA 126139
Qy 26821 AAAATATGTATGTAAGGCTAAGGGTAAAGGCCAAGGGCTAAGGGCTAAGGGCTAAGGCA 26880
Dd 126140 AAAATATGTATGTAAGGCTAAGGGTAAAGGGCTAAGGGCTAAGGGCTAAGGGCTAAGGCA 126199
Qy 26881 AGGGGTAAGGGCAAGGGCTAAGGGCTAAGGGCTAAGGGCTAAGGGCTAAGGGCTAAGGGCTA 26940
Dd 126200 AGGGGTAAGGGCAAGGGCTAAGGGCTAAGGGCTAAGGGCTAAGGGCTAAGGGCTAAGGGCTA 126259

Qy 26941 GGGCAAGGGCTAAGGGCTAAGGGCTAAGGGCTAAGGGCTAAGGGCTAAGGGCTAAGGGCTAAGG 27000
Dd 126260 GGGCAAGGGCTAAGGGCTAAGGGCTAAGGGCTAAGGGCTAAGGGCTAAGGGCTAAGGGCTAAGG 126319
Qy 27001 GGTAAAGGCTAAGGGCTAAGGGCTAAGGGCTAAGGGCTAAGGGCTAAGGGCTAAGGGCTAAGG 27060
Dd 126320 GGTAAAGGCTAAGGGCTAAGGGCTAAGGGCTAAGGGCTAAGGGCTAAGGGCTAAGGGCTAAGG 126379
Qy 27061 GTAAATATATAGGCTACGATTAATAATGCAATATATTTTAAATTTGTTTCATTTAA 27120
Dd 126380 GTAAATATATAGGCTACGATTAATAATGCAATATATTTTAAATTTGTTTCATTTAA 126439
Qy 27121 CAGCCATGCTATTTAGAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 27180
Dd 126440 CAGCCATGCTATTTAGAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 126499
Qy 27181 CCACACGAATTTATATATATTTTACAAAAGCAACCAAGCTGACATGTAACTTACACG 27240
Dd 126500 CCACACGAATTTATATATATTTTACAAAAGCAACCAAGCTGACATGTAACTTACACG 126559
Qy 27241 TACCTTAAGCTACATCTGGGACTAGAACCCAGAGTATAGTAAATATACGTAAGTTA 27300
Dd 126580 TACCTTAAGCTACATCTGGGACTAGAACCCAGAGTATAGTAAATATACGTAAGTTA 126619
Qy 27301 CAGAACTTTGACGTTCCCTTAGGCGCAGAGGCTCTGCGTTAATTAACAAGTTTAA 27360
Dd 126620 CAGAACTTTGACGTTCCCTTAGGCGCAGAGGCTCTGCGTTAATTAACAAGTTTAA 126679
Qy 27361 GATTAATGAAACTTTAGGAAAGTATGCTATGCTGTAATGTTTCCAAATAGGCAAGGTT 27420
Dd 126680 GATTAATGAAACTTTAGGAAAGTATGCTATGCTGTAATGTTTCCAAATAGGCAAGGTT 126739
Qy 27421 ACATTAATGTTGCTACG 27480
Dd 126740 ACATTAATGTTGCTACG 126799
Qy 27481 GCGCGCGCATCTTGCG 27540
Dd 126800 GCGCGCGCATCTTGCG 126859
Qy 27541 GGGGCGCGCGCGCTCCCGCGCGCTCCCGCGCGCTCCCGCGCGCGCGCGCGCGCGCGCGCGCG 27600
Dd 126860 GGGGCGCGCGCGCTCCCGCGCGCTCCCGCGCGCTCCCGCGCGCGCGCGCGCGCGCGCGCGCG 126919
Qy 27601 GCG 27660
Dd 126920 GCG 126979
Qy 27661 CCCGCGGGGCGCGGGCG 27720
Dd 126980 CCCGCGGGGCGCGGGCG 127039
Qy 27721 AGCGCCCGGCTCGGGCGAGCG 27780
Dd 127040 AGCGCCCGGCTCGGGCGAGCG 127099
Qy 27781 CCCACAAACCG 27840
Dd 127100 CCCACAAACCG 127159
Qy 27841 TCCGCGGCGCTCCCTCCCGACG 27900
Dd 127160 TCCGCGGCGCTCCCTCCCGACG 127219
Qy 27901 GGGCGGGGCGCGGGGCGCTCGGGCGGGGCGCGGGGCGCGGGGCGCGGGGCGCGGGGCGCGGGG 27960
Dd 127220 GGGCGGGGCGCGGGGCGCTCGGGCGGGGCGCGGGGCGCGGGGCGCGGGGCGCGGGGCGCGGGG 127279
Qy 27961 AGAACGGGGGATCGGGGAAAAAGCGAGGGGAGCGGGGAGCGGGGAGCGGGGAGCGGGGAGCGGGG 28020
Dd 127280 AGAACGGGGGATCGGGGAAAAAGCGAGGGGAGCGGGGAGCGGGGAGCGGGGAGCGGGGAGCGGGG 127339

QY	301	ATCATCAGGGGCGCTACGAGAGCCCTGACGCTCCCGAAGTTACCGAGACCGCGCGTCGAT	360
Db	105200	ATCATCAGGGGGGCTACGAGAGCCCTGACGCTCCCGAAGTTACCGAGACCGCGCGTCGAT	105259
QY	361	TTTCCAGGAAGATGCTGTTCAACACCCGAGGGAATGCACACACTGGTCCGCGCAATGTG	420
Db	105260	TTTCCAGGAAGATGCTGTTCAACACCCGAGGGAATGCACACACTGGTCCGCGCAATGTG	105319
QY	421	CCCAACCTTGGGGCGCGCAATCTTACGATTTAAATCTTACTCTCGAAGCCCTTAGACTAATG	480
Db	105320	CCCAACCTTGGGGCGCGCAATCTTACGATTTAAATCTTACTCTCGAAGCCCTTAGACTAATG	105379
QY	481	AGTCGTTTCTCCGCTAATGTTCCAGGCGCTGCGCACCTAACGCTAGAGGCCGACGTC	540
Db	105380	AGTCGTTTCTCCGCTAATGTTCCAGGCGCTGCGCACCTAACGCTAGAGGCCGACGTC	105439
QY	541	AAAAACGGCCCAATACACCCCGCTCAGTTGAGATGCTTTGGCCAAACACAGCAAT	600
Db	105440	AAAAACGGCCCAATACACCCCGCTCAGTTGAGATGCTTTGGCCAAACACAGCAAT	105499
QY	601	CCGATTTTCCCGCCCAATGAGAGTCAGGAGCACTAGACAGAGCCTGTGGGAGCAGAG	660
Db	105500	CCGATTTTCCCGCCCAATGAGAGTCAGGAGCACTAGACAGAGCCTGTGGGAGCAGAG	105559
QY	661	GACTTTTTCGAAATCTGGGATTAACATCAACGCAAGGCCAGGGTGGCGGCGCTACCTGG	720
Db	105560	GACTTTTTCGAAATCTGGGATTAACATCAACGCAAGGCCAGGGTGGCGGCGCTACCTGG	105619
QY	721	GGCTTCACGACGATAGACGGCGTGGTTTGGACCAACTGTGTCCACTTTAAACCAATG	780
Db	105620	GGCTTCACGACGATAGACGGCGTGGTTTGGACCAACTGTGTCCACTTTAAACCAATG	105679
QY	781	ACAGCGGGCTCAGACGACGCTAGCGTCGACTAAGTCGAAACCTTACACCTGACCACTTT	840
Db	105680	ACAGCGGGCTCAGACGACGCTAGCGTCGACTAAGTCGAAACCTTACACCTGACCACTTT	105739
QY	841	GGCGCGCGGGTCCAAACGCCGAGGCGAGAAACGACCACCGAGACCCGCGCTACGAGTAC	900
Db	105740	GGCGCGCGGGTCCAAACGCCGAGGCGAGAAACGACCACCGAGACCCGCGCTACGAGTAC	105799
QY	901	GGACAGCCCAAGGGCTACTGCATCTCGGGTCAATGAGACAGCGCGGTTCCAGGCTTAAC	960
Db	105800	GGACAGCCCAAGGGCTACTGCATCTCGGGTCAATGAGACAGCGCGGTTCCAGGCTTAAC	105859
QY	961	ACACGGATCCGCTTGGAGGCGGGTCTCGGAGCAATGGTGTTCACGTAACGATCAGA	1020
Db	105860	ACACGGATCCGCTTGGAGGCGGGTCTCGGAGCAATGGTGTTCACGTAACGATCAGA	105919
QY	1021	ATATTTTGGCGGCCACGCGCCAAAGCGCTTTGGCCAGGCGCGGCGGCGCATGGGGCTCTC	1080
Db	105920	ATATTTTGGCGGCCACGCGCCAAAGCGCTTTGGCCAGGCGCGGCGGCGCATGGGGCTCTC	105979
QY	1081	ACACCCATCTTGGAAATGCGTCCCGACGTCGAGCCCTTAANAAGCTGTATTAACGACCC	1140
Db	105980	ACACCCATCTTGGAAATGCGTCCCGACGTCGAGCCCTTAANAAGCTGTATTAACGACCC	106039
QY	1141	CGCAAAACCGTCCCATTTGAACGGTACCCGCAATCCCTCACCCCGACGACGAGCACA	1200
Db	106040	CGCAAAACCGTCCCATTTGAACGGTACCCGCAATCCCTCACCCCGACGACGAGCACA	106099
QY	1201	GTCCTTTCAGACAGGACAGTGGGTATCTACCGATTCACACACACAGCAAGCGCGCG	1260
Db	106100	GTCCTTTCAGACAGGACAGTGGGTATCTACCGATTCACACACACAGCAAGCGCGCG	106159
QY	1261	TCGTCGACTCCGCGCGCTTCTGCTGTCATAGACCTGAAAACTCGTAAACGCACTAC	1320
Db	106160	TCGTCGACTCCGCGCGCTTCTGCTGTCATAGACCTGAAAACTCGTAAACGCACTAC	106219
QY	1321	TCCAATGGGGGCGCGCAATTTCCAGACAGACCGCTTTTACGTGATGGCCGACATAC	1380
Db	106220	TCCAATGGGGGCGCGCAATTTCCAGACAGACCGCTTTTACGTGATGGCCGACATAC	106279

QY	1381	CCCCCAGACTGGCCAAAAACGCTGTCGGTAACATCAAAACAGCTCCGTACACACCTCCAC	1440
Db	106280	CCCCCAGACTGGCCAAAAACGCTGTCGGTAACATCAAAACAGCTCCGTACACACCTCCAC	106339
QY	1441	CACGACGAGATATGTAACTCTTTTACTACGTAATCCCGAAGAACAGCGGACCGTCGAAGC	1500
Db	106340	CACGACGAGATATGTAACTCTTTTACTACGTAATCCCGAAGAACAGCGGACCGTCGAAGC	106399
QY	1501	AGGGATATCTTTCGCAAGCGGCTCCGCAAAACGTCACACCGCAAAACCGCCAAATCCTCG	1560
Db	106400	AGGGATATCTTTCGCAAGCGGCTCCGCAAAACGTCACACCGCAAAACCGCCAAATCCTCG	106459
QY	1561	GCATGGGAAACGGATTAACCGATTAAACGCAAAACGAAACCGCCAAAAAACCCTCATTA	1620
Db	106460	GCATGGGAAACGGATTAACCGATTAAACGCAAAACGAAACCGCCAAAAAACCCTCATTA	106519
QY	1621	ATTCTGGGTCTCTTAAAGCGGGGACAGTATCAACGGGTGGAAACGACGACCCACCATTA	1680
Db	106520	ATTCTGGGTCTCTTAAAGCGGGGACAGTATCAACGGGTGGAAACGACGACCCACCATTA	106579
QY	1681	CAGGGGCAAGCCTCGCAACACGCAAAACACAAACGTAACACAGCCCGGTCAAATTAATTGA	1740
Db	106580	CAGGGGCAAGCCTCGCAACACGCAAAACACAAACGTAACACAGCCCGGTCAAATTAATTGA	106639
QY	1741	CACGGCTCAGTAACACACCGCTAACCGCAGCTCAGGCTCATCTTCACCGGAAAAATTC	1800
Db	106640	CACGGCTCAGTAACACACCGCTAACCGCAGCTCAGGCTCATCTTCACCGGAAAAATTC	106699
QY	1801	AACACGGCAAGGGTGCCTGACATAATATCTCAACGTGGGAAAGGGCCCATATAAACCGAG	1860
Db	106700	AACACGGCAAGGGTGCCTGACATAATATCTCAACGTGGGAAAGGGCCCATATAAACCGAG	106759
QY	1861	CCAGGCTCCGGCCAGGTACACGAAACCAAGGGGAAATTTTGGAGCTATAAACCCGCAAGTG	1920
Db	106760	CCAGGCTCCGGCCAGGTACACGAAACCAAGGGGAAATTTTGGAGCTATAAACCCGCAAGTG	106819
QY	1921	CTCACCGAACCAGCCCAAAACCGCGCAAAACGCGCGCTGCTTCGCCAACAGAGCAACC	1980
Db	106820	CTCACCGAACCAGCCCAAAACCGCGCAAAACGCGCGCTGCTTCGCCAACAGAGCAACC	106879
QY	1981	ACCACGGTCCCAAGTTACGATTAATCCACCCAGCGGTAGGGTCTTTATAGGAGCCGCG	2040
Db	106880	ACCACGGTCCCAAGTTACGATTAATCCACCCAGCGGTAGGGTCTTTATAGGAGCCGCG	106939
QY	2041	TCCAAACTCTCGCCAGCCCTGCAAGAGAGCCACAGCGGCCACACCCGACGACATCACTG	2100
Db	106940	TCCAAACTCTCGCCAGCCCTGCAAGAGAGCCACAGCGGCCACACCCGACGACATCACTG	106999
QY	2101	AAGATAGATCGGAAAAAATATAGCGCCGAGAGTCCGGCTTCGCCGACCCCACTTCGAAGAG	2160
Db	107000	AAGATAGATCGGAAAAAATATAGCGCCGAGAGTCCGGCTTCGCCGACCCCACTTCGAAGAG	107059
QY	2161	GGGCCACGGGACCTCAGTCAAACTCTCAACAGGCGACACTATAAGCTCCCTTAGC	2220
Db	107060	GGGCCACGGGACCTCAGTCAAACTCTCAACAGGCGACACTATAAGCTCCCTTAGC	107119
QY	2221	CAGGTCAAAAAAGATACACGCGCCGAAAAATCCCGGCTTCAAAACAGCAACTCCAGC	2280
Db	107120	CAGGTCAAAAAAGATACACGCGCCGAAAAATCCCGGCTTCAAAACAGCAACTCCAGC	107179
QY	2281	GGCCCCCAACCAACCGCATCAAAACCCGCGCATTTCAATACAGCTCCCCAGAACGAGCGC	2340
Db	107180	GGCCCCCAACCAACCGCATCAAAACCCGCGCATTTCAATACAGCTCCCCAGAACGAGCGC	107239
QY	2341	CGGTTGCTTCAGACAGAAATCGGAGGTGGAAATGACCCCAACGAGGAGGTAAAAAGATCG	2400
Db	107240	CGGTTGCTTCAGACAGAAATCGGAGGTGGAAATGACCCCAACGAGGAGGTAAAAAGATCG	107299
QY	2401	CCAAAAAACCAAGATGTGTCTACAGGGCCCGAAACCGAGACTCCAGGTGACACGGCCCG	2460
Db	107300	CCAAAAAACCAAGATGTGTCTACAGGGCCCGAAACCGAGACTCCAGGTGACACGGCCCG	107359
QY	2461	CTCGGTCCAACCATAGATATCATGACGTGGAACACCCCAAAATTTCTCAAAAAATATTAACA	2520

```

Db      107360 CTGGTCACACCATAGATGATGATGAGGAAACACCCCAATTTCTCAAAATATTAACA 107419
QY      2521 TCACTCACCGTCCCACTCCAGAGTACACCCCAATCCCTCCCACTAATCTGATATCCC 2580
Db      107420 TCACTCACCGTCCCACTCCAGAGTACACCCCAATCCCTCCCACTAATCTGATATCCC 107479
QY      2581 CTAATCCACGTCAACATCCACACGAAATATCACAGAGCCCAAGATGTTAATGCA 2640
Db      107480 CTATCCACGTCAACATCCACACGAAATATCACAGAGCCCAAGATGTTAATGCA 107539
QY      2641 TTTATCAAAAGCTAGCAAGAAACTTCAAGGCTGCTGAGCGCTATCCGAGGCTATT 2700
Db      107540 TTTATCAAAAGCTAGCAAGAAACTTCAAGGCTGCTGAGCGCTATCCGAGGCTATT 107599
QY      2701 GCGAGATTAAGTTTTTATATCTGTATACCGGCCATCTCACTGCTTTTATTTATTTAG 2760
Db      107600 GCGAGATTAAGTTTTTATATCTGTATACCGGCCATCTCACTGCTTTTATTTATTTAG 107659
QY      2761 AGAGGCTGTTGTGTCCAGATAGTGGCTCGCTAGGTATTAACGATGAGACCTATGC 2820
Db      107660 AGAGGCTGTTGTGTCCAGATAGTGGCTCGCTAGGTATTAACGATGAGACCTATGC 107719
QY      2821 CAGAAGACGCCAGCTCCCGGGTCCGCGCCACCGGGGCGGGGGCCCATCGAGCTATCA 2880
Db      107720 CAGAAGACGCCAGCTCCCGGGTCCGCGCCACCGGGGCGGGGGCCCATCGAGCTATCA 107779
QY      2881 ATGAATGGGGCCCGCTGGAGATCTGATTAAGCTATTTGACCCGAGGTTGAGAGCCACG 2940
Db      107780 ATGAATGGGGCCCGCTGGAGATCTGATTAAGCTATTTGACCCGAGGTTGAGAGCCACG 107839
QY      2941 GGGCAACGCTCGGGGGGGGGGGCGGAGCCGAGCCGAGCAAAACGCCGAGATCTAGAACTAG 3000
Db      107840 GGGCAACGCTCGGGGGGGGGGGCGGAGCCGAGCCGAGCAAAACGCCGAGATCTAGAACTAG 107899
QY      3001 CGTCTTTTGGCGGCAAGGCCCGGAGGTGGTCTTTGCGAGAAATTCATCTCTTTT 3060
Db      107900 CGTCTTTTGGCGGCAAGGCCCGGAGGTGGTCTTTGCGAGAAATTCATCTCTTTT 107959
QY      3061 GCATATACATGTCGTATGATGTTGGCCGTTAAAAACACAGATTAATTACGTTTCGCA 3120
Db      107960 GCATATACATGTCGTATGATGTTGGCCGTTAAAAACACAGATTAATTACGTTTCGCA 108019
QY      3121 TGGCAATCTGGGGGGGAGACATGTCAACCTGGGGAAAGTTGTCATCTGGCAACGACG 3180
Db      108020 TGGCAATCTGGGGGGGAGACATGTCAACCTGGGGAAAGTTGTCATCTGGCAACGACG 108079
QY      3181 GGTGATTTGGTAATCTGCTCAAGGCGTCCCTGAAGCATGTTGCTCTTAACCCGCAAG 3240
Db      108080 GGTGATTTGGTAATCTGCTCAAGGCGTCCCTGAAGCATGTTGCTCTTAACCCGCAAG 108139
QY      3241 ACGACATCTTTTAACTTCTATTAACACTTTCACAGACAGGAGCATATAGACGAGT 3300
Db      108140 ACGACATCTTTTAACTTCTATTAACACTTTCACAGACAGGAGCATATAGACGAGT 108199
QY      3301 CAAATATTAACACACTGGGCGCACACGCAATGCTTATAGCGCGGTCCGCACTCCGCA 3360
Db      108200 CAAATATTAACACACTGGGCGCACACGCAATGCTTATAGCGCGGTCCGCACTCCGCA 108259
QY      3361 CGCCAAACAGGGGACGACGAGCTTAACAGGAGTTCCGCTCGATGAGCATGTGCCG 3420
Db      108260 CGCCAAACAGGGGACGACGAGCTTAACAGGAGTTCCGCTCGATGAGCATGTGCCG 108319
QY      3421 GTTGTGGGAGACGACGACCGTAATAGGATCTCCACACACGATGATCCGAATAGAGA 3480
Db      108320 GTTGTGGGAGACGACGACCGTAATAGGATCTCCACACACGATGATCCGAATAGAGA 108379
QY      3481 TATTAACCGGCAATGTGCGATCCGCCAACAATAGAGCAATATACGCGCCGCGGTGATGAC 3540
Db      108380 TATTAACCGGCAATGTGCGATCCGCCAACAATAGAGCAATATACGCGCCGCGGTGATGAC 108439
QY      3541 GATCGAAGCTGCTTCTTTTGGTCCGAGTGAAGAAACAGTGTGGTGGGCAATT 3600
Db      108440 GATCGAAGCTGCTTCTTTTGGTCCGAGTGAAGAAACAGTGTGGTGGGCAATT 108499
QY      3601 TAGGTTTCAAAATTAACCCCGTCCGAAATTAACAAAGTAACGCACTCGAGGACACG 3660
Db      108500 TAGGTTTCAAAATTAACCCCGTCCGAAATTAACAAAGTAACGCACTCGAGGACACG 108559
QY      3661 CACCTTGGAGGCTGGGACGCTCTTCTCCAGTACGCTCTCTGGCCACCACTGGGACCAAC 3720
Db      108560 CACCTTGGAGGCTGGGACGCTCTTCTCCAGTACGCTCTCTGGCCACCACTGGGACCAAC 108619
QY      3721 AGGTAGAGATTAACAGGAAACGATACGTTATACGCCAATCTTTTGAACCAAGGCGG 3780
Db      108620 AGGTAGAGATTAACAGGAAACGATACGTTATACGCCAATCTTTTGAACCAAGGCGG 108679
QY      3781 GGATATCTCGTCTCGTGGTGAATCCCTATGGGCAACACAGACGGGACATCTCAGCAG 3840
Db      108680 GGATATCTCGTCTCGTGGTGAATCCCTATGGGCAACACAGGACATCTCAGCAG 108739
QY      3841 GGCCTTAACGTCAGGCTCTCTCAGAAAGGCGTTAAAGGGTTGCCGACAGGACGTCGG 3900
Db      108740 GGCCTTAACGTCAGGCTCTCTCAGAAAGGCGTTAAAGGGTTGCCGACAGGACGTCGG 108799
QY      3901 CGCAGATTCTCGAGAGGAGCCAGAAATCCCGGCTCCGAAGGGCCGGGACACTCTCAT 3960
Db      108800 CGCAGATTCTCGAGAGGAGCCAGAAATCCCGGCTCCGAAGGGCCGGGACACTCTCAT 108859
QY      3961 CAGGTTAGCTCCAGAGCTGTGGAATAGACGGAACGTTCAACTGCATCGAGACACAC 4020
Db      108860 CAGGTTAGCTCCAGAGCTGTGGAATAGACGGAACGTTCAACTGCATCGAGACACAC 108919
QY      4021 GCGCCGCTTCATTTCTTCGGAACCGGGGAGATCAACGGGTGTGTGGCAACAGT 4080
Db      108920 GCGCCGCTTCATTTCTTCGGAACCGGGGAGATCAACGGGTGTGTGGCAACAGT 108979
QY      4081 AACCAAGGGGAAACCGGTGCGACAGTTAAGGGTTTGGACACAGACAAACAGCCCTCG 4140
Db      108980 AACCAAGGGGAAACCGGTGCGACAGTTAAGGGTTTGGACACAGACAAACAGCCCTCG 109039
QY      4141 AAACGACACACAGATACCTTGACACGCGCTCTGGAAGCGGCCGTTAACTTAAC 4200
Db      109040 AAACGACACACAGATACCTTGACACGCGCTCTGGAAGCGGCCGTTAACTTAAC 109099
QY      4201 TTGCTGCTGGGAGACCCCGGCTGGAGATTAACCTTCACACCCAGCGTACGCCG 4260
Db      109100 TTGCTGCTGGGAGACCCCGGCTGGAGATTAACCTTCACACCCAGCGTACGCCG 109159
QY      4261 TAAACAAGACCGGCGCATATCTGACGCGCATCAAGTGGCCGTTTATAGTGGT 4320
Db      109160 TAAACAAGACCGGCGCATATCTGACGCGCATCAAGTGGCCGTTTATAGTGGT 109219
QY      4321 ATCCGGCTCCAGCGCGTGAATCTGTTCAAGGGCGTCTGAAGATGGGCGCAAA 4380
Db      109220 ATCCGGCTCCAGCGCGTGAATCTGTTCAAGGGCGTCTGAAGATGGGCGCAAA 109279
QY      4381 TAAAGTGAAGGCCATTTTGGGGGTGCTGCTCCAGAGGACGAGGCCCTAGTCAACA 4440
Db      109280 TAAAGTGAAGGCCATTTTGGGGGTGCTGCTCCAGAGGACGAGGCCCTAGTCAACA 109339
QY      4441 ACACAGTGAATTTGGGGGATATGTCGATTAAGGCTATAGAGGCGCAGATCTAAGC 4500
Db      109340 ACACAGTGAATTTGGGGGATATGTCGATTAAGGCTATAGAGGCGCAGATCTAAGC 109399
QY      4501 CAGCGAGAACCATCCAGCCAAAGATGGGACAGATTAAGAACCGGCCCATGAAGGAC 4560
Db      109400 CAGCGAGAACCATCCAGCCAAAGATGGGACAGATTAAGAACCGGCCCATGAAGGAC 109459
QY      4561 TTGCTTTCAGCCAGGTTAGGCAAGGCGCCGACATCCCAATTTTACCAGTTGA 4620
Db      109460 TTGCTTTCAGCCAGGTTAGGCAAGGCGCCGACATCCCAATTTTACCAGTTGA 109519
QY      4621 TTGCTTAATTTGGTCAATCCGCGACGCTCCGCGCCCAATATCTTCAACTCGACCCG 4680
Db      109520 TTGCTTAATTTGGTCAATCCGCGACGCTCCGCGCCCAATATCTTCAACTCGACCCG 109579
```

4681 AAGGCGGCGCCAGGAGCCGCTTGCCTCAACGACACCGAGGCGCTCGAGTACCCGCTCA 4740
109580 AAGGGCGGCGCCAGGAGCCGCTTGCCTCAACGACACCGAGGCGCTCGAGTACCCGCTCA 109639
4741 GGGCAAAACCCTTCAAGAGGCTTTTAAACCTTTAGCGCTCTTGGAGTCAACGACCA 4800
109640 GGGGAAAAACCTTCAAGAGGCTTTTAAACCTTTAGCGCTCTTGGAGTCAACGACCA 109699
4801 AAAACTGTAAACCTGTGCGGTCCGTAAGTAGTGGGCGCATATGACCATGAGAGCTGT 4860
109700 AAAACTGTAAACCTGTGCGGTCCGTAAGTAGTGGGCGCATATGACCATGAGAGCTGT 109759
4861 AAACGTTAGTCTCCGAGAGAAAAACAGACGCTGCCTTAAATTCATAAAATCGTCTGGC 4920
109760 AAACGTTAGTCTCCGAGAGAAAAACAGACGCTGCCTTAAATTCATAAAATCGTCTGGC 109819
4921 CCAGGACACGAGAGAGTCTCTCTCAGATACAGTCCGAATTTATAGCAGAGTTTTC 4980
109820 CCAGGACACGAGAGAGTCTCTCTCAGATACAGTCCGAATTTATAGGCGAGTTTTC 109879
4981 CAAAGTGGGCAATGGCGTCACAGTGGCTTACAAAAAATTTGAGGCTGGGCGCAAC 5040
109880 CAAAGTGGGCAATGGCGTCACAGTGGCTTACAAAAAATTTGAGGCTGGGCGCAAC 109939
5041 CGTTGTGATTAATTAACAAACACGAGGCAACGGGTAGGCGAGTCTCTAGTTTGTGA 5100
109940 CGTTGTGATTAATTAACAAACACGAGGCAACGGGTAGGCGAGTCTCTAGTTTGTGA 109999
5101 GCCAAACTTATACAAACTCGAGATGATAGACGACGCGTCTGACAGGCGCAACGCTGC 5160
110000 GCCAAACTTATACAAACTCGAGATGATAGACGACGCGTCTGACAGGCGCAACGCTGC 110059
5161 ACAGGGGACCGCCCGCTTACGATATACGGAGGCGGCTCCGACACCTCTCCCAAGT 5220
110060 ACAGGGGACCGCCCGCTTACGATATACGGAGGCGGCTCCGACACCTCTCCCAAGT 110119
5221 CCAGGAGATTCAGAGAGGCTCCAGATAGAGACAACTAAATTCGACAGCTCTCAACTA 5280
110120 CCAGGAGATTCAGAGAGGCTCCAGATAGAGACAACTAAATTCGACAGCTCTCAACTA 110179
5281 AACCTTTCCGGAATCATCTGTATATAAGATTCCTTTAGTGTCTGTGGCTCCGCTAA 5340
110180 AACCTTTCCGGAATCATCTGTATATAAGATTCCTTTAGTGTCTGTGGCTCCGCTAA 110239
5341 AACCGGCTCCGCTCAACGATTTTGTGAATGACCTGTTTACGGCGTTTACTTGGCGT 5400
110240 AACCGGCTCCGCTCAACGATTTTGTGAATGACCTGTTTACGGCGTTTACTTGGCGT 110299
5401 CCAGGACCATGCTGCTCACAGTGAAGTGAACGCGCTGTGAGCAGATGACAGAGAAAG 5460
110300 CCAGGACCATGCTGCTCACAGTGAAGTGAACGCGCTGTGAGCAGATGACAGAGAAAG 110359
5461 TTTTAAATACTGACAGTGAATGAGGTGGGTGAGCTGTGAGTATATGTTGGGAAACATTA 5520
110360 TTTTAAATACTGACAGTGAATGAGGTGGGTGAGCTGTGAGTATATGTTGGGAAACATTA 110419
5521 TTTTCATGTCACTCGGAGCAGAGGACTCGAACGCCAATTAATTCGACCAACATTCAGT 5580
110420 TTTTCATGTCACTCGGAGCAGAGGACTCGAACGCCAATTAATTCGACCAACATTCAGT 110479
5581 GAGACAGAGTAAAGATGCTCACGCGCGGTACCGGCTAACACGCGACGACGACCCCTT 5640
110480 GAGACAGAGTAAAGATGCTCACGCGCGGTACCGGCTAACACGCGACGACGACCCCTT 110539
5641 CAAATATTTAGCTTTAAAAAGCGGCGCCCTTAAAGTGTGCAACTAGCTTTAAAAATC 5700
110540 CAAATATTTAGCTTTAAAAAGCGGCGCCCTTAAAGTGTGCAACTAGCTTTAAAAATC 110599
5701 CTACCCATATATGCTGCTCCGCTGAGCACTGAGACCTCATGAGACACTGCGCTCTG 5760
110600 CTACCCATATATGCTGCTCCGCTGAGCACTGAGACCTCATGAGACACTGCGCTCTCTG 110659

5761 CGGGAGCTGTAGAACATCTCTCCCGGTACCCCGAGCGAGGCTTTTACAGCCG 5820
110660 CGGGAGCTGTAGAACATCTCTCCCGGTACCCCGAGCGAGGCTTTTACAGCCG 110719
5821 GTATTAATCCACTCAGAGCTCTCTACAAACCCGCTCATGTGTGAGGCTGTGACCTC 5880
110720 GTATTAATCCACTCAGAGCTCTCTACAAACCCGCTCATGTGTGAGGCTGTGACCTC 110779
5881 CTGTTCACCTGTGTCGCGAGCTTCCGACCCCGGACCTTCTTGTGAAGACTACGGCTG 5940
110780 CTGTTCACCTGTGTCGCGAGCTTCCGACCCCGGACCTTCTTGTGAAGACTACGGCTG 110839
5941 TTGTGCTCCTACCTGCTATACGCCCCCGGATCATGAGAGGCTACCTCATAGTGGCTGCC 6000
110840 TTGTGCTCCTACCTGCTATACGCCCCCGGATCATGAGAGGCTACCTCATAGTGGCTGCC 110899
6001 GACCTTTTGGAACTAACGACAGTGTACTTCCCGCAATGCTGAAAGATGGGCGCATATAC 6060
110900 GACCTTTTGGAACTAACGACAGTGTACTTCCCGCAATGCTGAAAGATGGGCGCATATAC 110959
6061 ACCGCGCAAGCATCTCGGAAATGAGAGTCCAGCTTCCGCAACCGCTGCTTC 6120
110960 ACCGCGCAAGCATCTCGGAAATGAGAGTCCAGCTTCCGCAACCGCTGCTTC 111019
6121 CGACCATTCGACAGAGAAACAATACTCCACATCTCATTTAAATTTTACAACCGAG 6180
111020 CGACCATTCGACAGAGAAACAATACTCCACATCTCATTTAAATTTTACAACCGAG 111079
6181 TTTATTAAGGGCATGTTAAGAACGATTCGCGGATGCTGTGTTTAAACGCTCTG 6240
111080 TTTATTAAGGGCATGTTAAGAACGATTCGCGGATGCTGTGTTTAAACGCTCTG 111139
6241 CCGGCGACAGAAAGAGAGCAACAACCTACGCTGTGCTGCTGCTGGCGGCGGA 6300
111140 CCGGCGACAGAAAGAGAGCAACAACCTACGCTGTGCTGCTGCTGGCGGCGGA 111199
6301 AGTCACACCAACCGGAGTAAACCGCTACCCGAGAGCTGGAAGAGGCTTCACTCCAG 6360
111200 AGTCACACCAACCGGAGTAAACCGCTACCCGAGAGCTGGAAGAGGCTTCACTCCAG 111259
6361 AACCGCGAGAAAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 6420
111260 AACCGCGAGAAAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 111319
6421 CTTCCTTGGCTCCGACACAAACAGGAGATACCATTTACAAACCTCCGCTTCCCAAC 6480
111320 CTTCCTTGGCTCCGACACAAACAGGAGATACCATTTACAAACCTCCGCTTCCCAAC 111379
6481 CCAGAGATGCTGACCAATACAGAGGCGCTGCTGATGACCCACGCTCAACCTAAAA 6540
111380 CCAGAGATGCTGACCAATACAGAGGCGCTGCTGATGACCCACGCTCAACCTAAAA 111439
6541 ACAAAAAACACACCGGATCATATGCGTGTATGCGAGTGTGCGGCGCACACCGGAC 6600
111440 ACAAAAAACACACCGGATCATATGCGTGTATGCGAGTGTGCGGCGCACACCGGAC 111499
6601 GCCGCTCCGCTTGAAGAGATCTGCTGCGACATTCGGAACCAATGGAACCAACGTT 6660
111500 GCCGCTCCGCTTGAAGAGATCTGCTGCGACATTCGGAACCAATGGAACCAACGTT 111559
6661 AAGCTGCTCAATGCTATATGCTATCATCTTAAACGATCCGAGCTCATGTGCACAGTGGC 6720
111560 AAGCTGCTCAATGCTATATGCTATCATCTTAAACGATCCGAGCTCATGTGCACAGTGGC 111619
6721 GAGCAATCTGCGCGGCTTAATTAACGAGTGTGCGGACAGAAATTCACACATTTT 6780
111620 GAGCAATCTGCGCGGCTTAATTAACGAGTGTGCGGACAGAAATTCACACATTTT 111679
6781 TTTTGGACCGGCTGCTGCTGCTGACACGATCTGAGTGTGCGGCTGCTTATTTAAA 6840
111680 TTTTGGACCGGCTGCTGCTGCTGACACGATCTGAGTGTGCGGCTGCTTATTTAAA 111739
6841 TGCCCACTCCGAAAGATTAAGAGCTCAAAAGCTGCTGTGCGAACCGGAGAGTTCCTA 6900


```
Db 111740 TCCACACCTCCGAAAAAGTATAGAGCTCAAGCTCGCTGCAACCGGAGAGTTCCTA 111799
Qy 6901 GACTGCACAGAGATATTTGACTGCGAGACCTTACAGACCTTGCGCGTCTCTTTAAGGGG 6960
Db 111800 GACTGCACAGAGATATTTGACTGCGAGACCTTACAGACCTTGCGCGTCTCTTTAAGGGG 111859
Qy 6961 TCTCACTGCGCAAAATGCGCAAAACACGCTGCTCGAGATATCCGTGACCTCGGATTT 7020
Db 111860 TCTCAACTGCGCAAAATGCGCAAAACACGCTGCTCGAGATATCCGTGACCTCGGATTT 111919
Qy 7021 CAGCTGCGTGCACACATTCGAATACCCGCTTCAACCTGCAACCTCATATACAT 7080
Db 111920 CAGCTGCGTGCACACATTCGAATACCCGCTTCAACCTGCAACCTCATATACAT 111979
Qy 7081 TATCTTTCAGAGCGCAGACAGAAATGCGCAAAACAGCCGAGAGTGCATTTGGCGTCCGA 7140
Db 111980 TATCTTTCAGAGCGCAGACAGAAATGCGCAAAACAGCCGAGAGTGCATTTGGCGTCCGA 112039
Qy 7141 GCGCGGTACGACCTAGCGTCAAGCGGACCGGAGCGGCGCCAGTCCAGCGGACCGGATCC 7200
Db 112040 GCGCGGTACGACCTAGCGTCAAGCGGACCGGAGCGGCGCCAGTCCAGCGGACCGGATCC 112099
Qy 7201 AGGACGGGACGCTGCAAAAGCAAAATCATGAGTGGAAAAAGTTAGTTTCAGACACGCGAG 7260
Db 112100 AGGACGGGACGCTGCAAAAGCAAAATCATGAGTGGAAAAAGTTAGTTTCAGACACGCGAG 112159
Qy 7261 TTTTTCCTGCGCTTAACGCGCGCCCAAGAGCTGCGGGGTGAGCTTTTAAAGAAATGGGG 7320
Db 112160 TTTTTCCTGCGCTTAACGCGCGCCCAAGAGCTGCGGGGTGAGCTTTTAAAGAAATGGGG 112219
Qy 7321 ACCCGGATATGACCTCAAAAGTCCGTTATGTTCCGCTTAAACCTTAAACCATCGCCCG 7380
Db 112220 ACCCGGATATGACCTCAAAAGTCCGTTATGTTCCGCTTAAACCTTAAACCATCGCCCG 112279
Qy 7381 GGTGCGTGGCTCTCTCTCATCATTTGCGAGACTGCTCAACATGGGGTTTCAACTGTGCG 7440
Db 112280 GGTGCGTGGCTCTCTCTCATCATTTGCGAGACTGCTCAACATGGGGTTTCAACTGTGCG 112339
Qy 7441 TCGTGACGCGCAACTGACAGGTGACGCGGTCTCTGAGCGCAACGCGCTGCGCGAAGAT 7500
Db 112340 TCGTGACGCGCAACTGACAGGTGACGCGGTCTCTGAGCGCAACGCGCTGCGCGAAGAT 112399
Qy 7501 TCGCGCAGGAAAAACGAGAGCTGTGTGTAGTGGGTTAACTTTTACACACACGCGGAA 7560
Db 112400 TCGCGCAGGAAAAACGAGAGCTGTGTGTAGTGGGTTAACTTTTACACACACGCGGAA 112459
Qy 7561 AAGTGTGTCAGACACAAGGGCTTTTACGCTGCTGCTCAGCCACTCATGGAAGTCTT 7620
Db 112460 AAGTGTGTCAGACACAAGGGCTTTTACGCTGCTGCTCAGCCACTCATGGAAGTCTT 112519
Qy 7621 AGGAAAAAGCTTACGCAACCGGGGTGCTCTACGCCACCTTAGTCTTAAAAAACCCTTTGGC 7680
Db 112520 AGGAAAAAGCTTACGCAACCGGGGTGCTCTACGCCACCTTAGTCTTAAAAAACCCTTTGGC 112579
Qy 7681 CAGGATTCCTTACATTTTTCACAGTGCATGCGGATGAGAGACTGCGACTGTGGGGGGTG 7740
Db 112580 CAGGATTCCTTACATTTTTCACAGTGCATGCGGATGAGAGACTGCGACTGTGGGGGGTG 112639
Qy 7741 TTTCCACACTAGACCTACACTGGGGGAAACACAGTCTGCACTATTATGCAACAACCTT 7800
Db 112640 TTTCCACACTAGACCTACACTGGGGGAAACACAGTCTGCACTATTATGCAACAACCTT 112699
Qy 7801 CCAAAATATGACATTAACGGTGTGACTGATCAAGCAAAACGTACATATGAAGTTTACACCC 7860
Db 112700 CCAAAATATGACATTAACGGTGTGACTGATCAAGCAAAACGTACATATGAAGTTTACACCC 112759
Qy 7861 TCGCGACCGGAAACGCAACCTGAGCGTCTGTGCACAGATTTGCAAGCGCGTGGCC 7920
Db 112760 TCGCGACCGGAAACGCAACCTGAGCGTCTGTGCACAGATTTGCAAGCGCGTGGCC 112819
Qy 7921 ACCCTAGACTGCAGGAGTTTGCAGAGAAATTCAAAGGGGACGCGCATTCATTAAC 7980
Db 112820 ACCCTAGACTGCAGGAGTTTGCAGAGAAATTCAAAGGGGACGCGCATTCATTAAC 112879
Qy 7981 TCCAGAGGGCTATGTAACTTCCCTAGACGGAACAGATGTAAATTCATTTCAAT 8040
Db 112880 TCCAGAGGGCTATGTAACTTCCCTAGACGGAACAGATGTAAATTCATTTCAAT 112939
Qy 8041 GTTAAGTTTGTGTTGAACATATCACCATAATAAAAAACAATTATGTTTCAAAATGGA 8100
Db 112940 GTTAAGTTTGTGTTGAACATATCACCATAATAAAAAACAATTATGTTTCAAAATGGA 112999
Qy 8101 GAGCGTTCAATTTTACATTAACATAGCAAAACACAGGTAATTAATCAATAGCA 8160
Db 113000 GAGCGTTCAATTTTACATTAACATAGCAAAACACAGGTAATTAATCAATAGCA 113059
Qy 8161 TATTCGGATGGATCCCTAGAGAGCAATGACGTGCGCGGTATTAATGACGGAGCG 8220
Db 113060 TATTCGGATGGATCCCTAGAGAGCAATGACGTGCGCGGTATTAATGACGGAGCG 113119
Qy 8221 AGCTTACCTGCTCTCAGCAATCGCAAACTCCGCGTTTATGACCATTCGACGCGCTTA 8280
Db 113120 AGCTTACCTGCTCTCAGCAATCGCAAACTCCGCGTTTATGACCATTCGACGCGCTTA 113179
Qy 8281 ATAAATTCGAGTAATCTGCGAAAGGCGTACATCGCAGTATGATTTTACGATGTGCACA 8340
Db 113180 ATAAATTCGAGTAATCTGCGAAAGGCGTACATCGCAGTATGATTTTACGATGTGCACA 113239
Qy 8341 CCTTTCGCGGTTTACCGCAACACAAAGCGGGTACACGACCTTAATTCGCCCGG 8400
Db 113240 CCTTTCGCGGTTTACCGCAACACAAAGCGGGTACACGACCTTAATTCGCCCGG 113299
Qy 8401 CCTTTATGCGCAAGTACAAAGGGGACGCGGCTTACGTTACGAAACAACCTGTGAT 8460
Db 113300 CCTTTATGCGCAAGTACAAAGGGGACGCGGCTTACGTTACGAAACAACCTGTGAT 113359
Qy 8461 CGCAATATACATAGTGTGTTGTTGTCACCGCAAACTGCCAAATCTTAAATGATGAGAT 8520
Db 113360 CGCAATATACATAGTGTGTTGTTGTCACCGCAAACTGCCAAATCTTAAATGATGAGAT 113419
Qy 8521 AGTCTCAAAATCTAGACAGAACTTCCAAAAACATGCGGCAATTAACAAACCCCTTGCA 8580
Db 113420 AGTCTCAAAATCTAGACAGAACTTCCAAAAACATGCGGCAATTAACAAACCCCTTGCA 113479
Qy 8581 TATGACATTCGTAAACGAGAGGAAATCCAAAGAACGCGCGATCTTAAGACACAGGGA 8640
Db 113480 TATGACATTCGTAAACGAGAGGAAATCCAAAGAACGCGCGATCTTAAGACACAGGGA 113539
Qy 8641 CGTGTCTTGGGTTCCGCGGGGCGTTACGATGGAAGTTCAACCAAGTATCCATCAACC 8700
Db 113540 CGTGTCTTGGGTTCCGCGGGGCGTTACGATGGAAGTTCAACCAAGTATCCATCAACC 113599
Qy 8701 TGTTCAAAAAGCGTAAAGTAAATCGGTTTACAAATAAATAAATAATGTTGAGAGAT 8760
Db 113600 TGTTCAAAAAGCGTAAAGTAAATCGGTTTACAAATAAATAAATAATGTTGAGAGAT 113659
Qy 8761 TACATTCGCAATACAGCGGACCCAAAAAACACCCCAACCAACCACTGAGAGACTG 8820
Db 113660 TACATTCGCAATACAGCGGACCCAAAAAACACCCCAACCAACCACTGAGAGACTG 113719
Qy 8821 TGTCTTGGGTCCTTCCACGTCGCAATGAGATTTCTGTGACCGGTCTCTTAACGC 8880
Db 113720 TGTCTTGGGTCCTTCCACGTCGCAATGAGATTTCTGTGACCGGTCTCTTAACGC 113779
Qy 8881 GTTACAGTGTGTTTATGAGCTACGTTAAACACACCAATCTAATATGCTAACAGCGTGCAC 8940
Db 113780 GTTACAGTGTGTTTATGAGCTACGTTAAACACACCAATCTAATATGCTAACAGCGTGCAC 113839
Qy 8941 GCGCTTAGGCGGCTTGTGCACTAATCTCTGAGAGTACTACTATTTTAAACAAG 9000
Db 113840 GCGCTTAGGCGGCTTGTGCACTAATCTCTGAGAGTACTACTATTTTAAACAAG 113899
Qy 9001 TAGCATATCCAACTGCAATTAATGCACTAAACCAAGTTATGCTTTTATGAGTCCGCG 9060
Db 113900 TAGCATATCCAACTGCAATTAATGCACTAAACCAAGTTATGCTTTTATGAGTCCGCG 113959
```

OY	9061	CCATAGTCTCATGGAGAACCATCATCTCCGTCAACGGCGTGGGTATCCGTTGT	9120
Db	113960	CCATAGTCTCATGGAGAACCATCATCTCCGTCAACGGCGTGGGTATCCGTTGT	114019
OY	9121	TATTGGGGGCAAAACAGGCTGGGGGGCAAAAAAGACAACATATGCTCAGTTTAAACAAC	9180
Db	114020	TATTGGGGGCAAAACAGGCTGGGGGGCAAAAAAGACAACATATGCTCAGTTTAAACAAC	114079
OY	9181	TCAGATTCTAAATCTCAACCCACTCGTAAACAAAAAAGCATGCACTTAAGTGTATGTAC	9240
Db	114080	TCAGATTCTAAATCTCAACCCACTCGTAAACAAAAAAGCATGCACTTAAGTGTATGTAC	114139
OY	9241	CGAACATTAACAACACAAAGTTTTTTTAAACACACAGCTGGGTAGTAAACCCCATTTGCACAG	9300
Db	114140	CGAACATTAACAACACAAAGTTTTTTTAAACACACAGCTGGGTAGTAAACCCCATTTGCACAG	114199
OY	9301	CGTGCAGCTCTAAGTGTATTTTAAATATCTTGCCTTTTACACACGACAGTAGTAT	9360
Db	114200	CGTGCAGCTCTAAGTGTATTTTAAATATCTTGCCTTTTACACACGACAGTAGTAT	114259
OY	9361	CTCAGGAGGGGGGTTTAACGAGCGATATACATATTCCTTAACACGGGGAACGGCGCTGAC	9420
Db	114260	CTCAGGAGGGGGGTTTAACGAGCGATATACATATTCCTTAACACGGGGAACGGCGCTGAC	114319
OY	9421	CGCCCTCCCAATATACAACAGGGAGCTACAAAGCCTAGTGAATATATCAAAATTAA	9480
Db	114320	CGCCCTCCCAATATACAACAGGGAGCTACAAAGCCTAGTGAATATATCAAAATTAA	114379
OY	9481	AAACACAGAAACCTTTAGTCGTGGCAAAACACTAGCAAAAGGTACCTAGAGTTCCCT	9540
Db	114380	AAACACAGAAACCTTTAGTCGTGGCAAAACACTAGCAAAAGGTACCTAGAGTTCCCT	114439
OY	9541	ATACTCTCAAAAAACAGCGGTGGGTATTTGACCACACGTAGTAAACCCGGTAAAGAT	9600
Db	114440	ATACTCTCAAAAAACAGCGGTGGGTATTTGACCACACGTAGTAAACCCGGTAAAGAT	114499
OY	9601	TATTCGCGTTTATCAAAATGAAAAATTAAAGCTTTGCGTTAAATCTGCTAACGCAAG	9660
Db	114500	TATTCGCGTTTATCAAAATGAAAAATTAAAGCTTTGCGTTAAATCTGCTAACGCAAG	114559
OY	9661	GGCACTTAATTTTCCAGTTTGGACTGCGCAACTTTAACGCTTAACGTTAAATTTAAT	9720
Db	114560	GGCACTTAATTTTCCAGTTTGGACTGCGCAACTTTAACGCTTAACGTTAAATTTAAT	114619
OY	9721	GCAAAAGGCACATATTTTGTGTAACTCTAAACCTCTACAGCTAAAGTTAATAAG	9780
Db	114620	GCAAAAGGCACATATTTTGTGTAACTCTAAACCTCTACAGCTAAAGTTAATAAG	114679
OY	9781	GGCACTTTGGGCGAGCAATCAGTGTCTGCGCAAAACCTGTTAAATTTAAACAACAAG	9840
Db	114680	GGCACTTTGGGCGAGCAATCAGTGTCTGCGCAAAACCTGTTAAATTTAAACAACAAG	114739
OY	9841	GAGCGGAGCTAAACACGAGCTAAGCTCATGCGGGCCCTGTTGAAGAAATGGTGTTGCA	9900
Db	114740	GAGCGGAGCTAAGCAACGAGCTAAGCTCATGCGGGCCCTGTTGAAGAAATGGTGTTGCA	114799
OY	9901	ATGCACTTAGGGAATCTAAAAAAAGAAATCCTGCTGGTAAACACAGGAATTTGCTTTAGTTC	9960
Db	114800	ATGCACTTAGGGAATCTAAAAAAAGAAATCCTGCTGGTAAACACAGGAATTTGCTTTAGTTC	114859
OY	9961	CCTACAGCATCAACAACATTTGTAAACCATTAACGTCGCGCGTGGGGTTGGTGTGTG	10020
Db	114860	CCTACAGCATCAACAACATTTGTAAACCATTAACGTCGCGCGTGGGGTTGGTGTGTG	114919
OY	10021	AAATGCTTGGTCAACTGTTTACATGAGGCGGATTTGTAATGTGGTCTGGTGCACAGCTG	10080
Db	114920	AAATGCTTGGTCAACTGTTTACATGAGGCGGATTTGTAATGTGGTCTGGTGCACAGCTG	114979
OY	10081	GTTGGGATGCAGTCCCGCGGTGGGTGCAAGTCCCGGTGGGGTCCAGGTCCCGCGGTG	10140
Db	114980	GTTGGGATGCAGTCCCGCGGTGGGTGCAAGTCCCGGTGGGGTCCAGGTCCCGCGGTG	115039

QY	10141	GGGTGCAAGTCCCCCGGTGGGGGTGCAGATCCCCGGTGGAGTGCAGTCCCCGGTGGGG	10200
Db	115040	GGGTGCAAGTCCCCCGGTGGGGGTGCAGATCCCCGGTGGAGTGCAGTCCCCGGTGGGG	1150995
QY	10201	TGCAGTCCCCCGGTGGGGGTGCAGATCCCCCGGTGGAGTGCAGTCCCCGGTGGGGTGC	10260
Db	115100	TGCAGTCCCCCGGTGGGGGTGCAGATCCCCCGGTGGAGTGCAGTCCCCGGTGGGGTGC	115155
QY	10261	AAGTCCCCCGGTGGGGGTGCAGTCCCCCGGTGGAGTGCAGTCCCCGGTGGGGTGCAG	10320
Db	115160	AAGTCCCCCGGTGGGGGTGCAGTCCCCCGGTGGAGTGCAGTCCCCGGTGGGGTGCAG	115215
QY	10321	TCCCCCGGTGGGGGTGCAGTCCCCCGGTGGAGTGCAGTCCCCGGTGGGGTGCAGTCC	10380
Db	115220	TCCCCCGGTGGGGGTGCAGTCCCCCGGTGGAGTGCAGTCCCCGGTGGGGTGCAGTCC	115275
QY	10381	CCCGGTGGGGGTGCAGTCCCCCGGTGGAGTGCAGTCCCCCGGTGGGGTGCAGTCCCC	10440
Db	115280	CCCGGTGGGGGTGCAGTCCCCCGGTGGAGTGCAGTCCCCCGGTGGGGTGCAGTCCCC	115335
QY	10441	GGTGGGGGTGCAGTCCCCCGGTGGAGTGCAGTCCCCCGGTGGAGTGCAGTCCCCGG	10500
Db	115340	GGTGGGGGTGCAGTCCCCCGGTGGAGTGCAGTCCCCCGGTGGAGTGCAGTCCCCGG	115395
QY	10501	GGTGGCTCCGGGTGGGGGTGCAGTCCGGGTGGAGTGCAGTCCGGGTGGGGGTGCAGT	10560
Db	115400	GGTGGCTCCGGGTGGGGGTGCAGTCCGGGTGGAGTGCAGTCCGGGTGGGGGTGCAGT	115455
QY	10561	CCGGGGGTGCAGTCCGGGTGGGGGTGCAGTCCGGGTGGAGTGCAGTCCGGGTGGGGGTGC	10620
Db	115460	CCGGGGGTGCAGTCCGGGTGGGGGTGCAGTCCGGGTGGAGTGCAGTCCGGGTGGGGGTGC	115515
QY	10621	GGCTCCGGGGGTGCAGTCCGGGTGGGGGTGCAGTCCGGGTGGAGTGCAGTCCGGGTGGGGGTGC	10680
Db	115520	GGCTCCGGGGGTGCAGTCCGGGTGGGGGTGCAGTCCGGGTGGAGTGCAGTCCGGGTGGGGGTGC	115575
QY	10681	GCTCGAGCTCCGGGGGTGCAGTCCGGGTGGGGGTGCAGTCCGGGTGGAGTGCAGTCCGGGTGGG	10740
Db	115580	GCTCGAGCTCCGGGGGTGCAGTCCGGGTGGGGGTGCAGTCCGGGTGGAGTGCAGTCCGGGTGGG	115635
QY	10741	GGCGGCTCCGGGTCCGGGGGTGCAGTCCGGGTGGGGGTGCAGTCCGGGTGGAGTGCAGTCCGGG	10800
Db	115640	GGCGGCTCCGGGTCCGGGGGTGCAGTCCGGGTGGGGGTGCAGTCCGGGTGGAGTGCAGTCCGGG	115695
QY	10801	TGGGGGGGTGCAGTCCGGGTGGGGGTGCAGTCCGGGTGGAGTGCAGTCCGGGTGGAGTGC	10860
Db	115700	TGGGGGGGTGCAGTCCGGGTGGGGGTGCAGTCCGGGTGGAGTGCAGTCCGGGTGGAGTGC	115755
QY	10861	CGGGGTGGGGGTGCAGTCCGGGTGGGGGTGCAGTCCGGGTGGAGTGCAGTCCGGGTGGAGTGC	10920
Db	115760	CGGGGTGGGGGTGCAGTCCGGGTGGGGGTGCAGTCCGGGTGGAGTGCAGTCCGGGTGGAGTGC	115815
QY	10921	GCTCCGGGTGGGGGTGCAGTCCGGGTGGGGGTGCAGTCCGGGTGGAGTGCAGTCCGGGTGGG	10980
Db	115820	GCTCCGGGTGGGGGTGCAGTCCGGGTGGGGGTGCAGTCCGGGTGGAGTGCAGTCCGGGTGGG	115875
QY	10981	GGTGGGTCCGGGGGTGCAGTCCGGGTGGGGGTGCAGTCCGGGTGGAGTGCAGTCCGGGTGGG	11040
Db	115880	GGTGGGTCCGGGGGTGCAGTCCGGGTGGGGGTGCAGTCCGGGTGGAGTGCAGTCCGGGTGGG	115935
QY	11041	CCGGGGGTGCAGTCCGGGTGGGGGTGCAGTCCGGGTGGAGTGCAGTCCGGGTGGAGTGC	11100
Db	115940	CCGGGGGTGCAGTCCGGGTGGGGGTGCAGTCCGGGTGGAGTGCAGTCCGGGTGGAGTGC	115995
QY	11101	GGCTCCGGGGGTGCAGTCCGGGTGGGGGTGCAGTCCGGGTGGAGTGCAGTCCGGGTGGGGGTGC	11160
Db	116000	GGCTCCGGGGGTGCAGTCCGGGTGGGGGTGCAGTCCGGGTGGAGTGCAGTCCGGGTGGGGGTGC	116055
QY	11161	GCTCGGGGTGCAGTCCGGGTGGGGGTGCAGTCCGGGTGGAGTGCAGTCCGGGTGGGGGTGC	11220
Db	116060	GCTCGGGGTGCAGTCCGGGTGGGGGTGCAGTCCGGGTGGAGTGCAGTCCGGGTGGGGGTGC	116115
QY	11221	GGCGGCTCCGGGTCCGGGGGTGCAGTCCGGGTGGGGGTGCAGTCCGGGTGGAGTGCAGTCCGGG	11280

116120 GCGGCTCGGCTCGGGGTGGCTCCGGGTGGGGGGCGCTCGGCTCCGGGGTGGCTCCGG 116179
11281 TGGGGGCGGCTCGGCTCCGGGGTGGCTCCGGGTGGGGGGCGCTCGGCTCCGGGGTGGCTC 11340
116180 TGGGGGCGGCTCGGCTCCGGGGTGGCTCCGGGGTGGGGGGCGCTCGGCTCCGGGGTGGCTC 116239
11341 CGGGTGGGGGGCGCTCGGCTCCGGGGTGGCTCCGGGGTGGGGGGCGCTCGGCTCCGGGGTGG 11400
116240 CGGGTGGGGGGCGCTCGGCTCCGGGGTGGCTCCGGGGTGGGGGGCGCTCGGCTCCGGGGTGG 116299
11401 GCTCCGGGGTGGGGGGCGCTCGGCTCCGGGGTGGCTCCGGGGTGGGGGGCGCTCGGCTCCGG 11460
116300 GCTCCGGGGTGGGGGGCGCTCGGCTCCGGGGTGGCTCCGGGGTGGGGGGCGCTCGGCTCCGG 116359
11461 GGTGGCTCCGGGTGGGGGGCGCTCGGCTCCGGGGTGGCTCCGGGGTGGGGGGCGCTCCGG 11520
116360 GGTGGCTCCGGGTGGGGGGCGCTCGGCTCCGGGGTGGCTCCGGGGTGGGGGGCGCTCCGG 116419
11521 TCCCTACCGGTAAATTTACAGTAATATCCACGCAAGTAAATCCGCAAGTACCGCACAG 11580
116420 TCCCTACCGGTAAATTTACAGTAATATCCACGCAAGTAAATCCGCAAGTACCGCACAG 116479
11581 AGGTGCACTGCTCGCAAGGCTCCGCGGCTCTTTATAGGCTAAATGGCCCTCCCA 11640
116480 AGGTGCACTGCTCGCAAGGCTCCGCGGCTCTTTATAGGCTAAATGGCCCTCCCA 116539
11641 AATGTTACTATGTTTACTATATGCAACCATATATCAATATATGATATGATATGATATGATATG 11700
116540 AATGTTACTATGTTTACTATATGCAACCATATATCAATATATGATATGATATGATATGATATG 116599
11701 GGGCAACGGCGGCGGCTCCACCGGCTCCACCGGCTCCACCGGCTCCACCGGCTCCACCGGCTCC 11760
116600 GGGCAACGGCGGCGGCTCCACCGGCTCCACCGGCTCCACCGGCTCCACCGGCTCCACCGGCTCC 116659
11761 TCCCGACGAATACGGGGGGCGAGATGTCGGGGGGCGGCTGGCATTTGGCAATATTTCCA 11820
116660 TCCCGACGAATACGGGGGGCGAGATGTCGGGGGGCGGCTGGCATTTGGCAATATTTCCA 116719
11821 GCATTTCACAGGGGCGACGAGGCTCCAGGCTACCGGGGATTTCCCAACATCATCCAGCG 11880
116720 GCATTTCACAGGGGCGACGAGGCTCCAGGCTACCGGGGATTTCCCAACATCATCCAGCG 116779
11881 CATTAAGGTTGGTGGTGGCTCCATCTGCGGGATTTCCCAACATCATCCAGCG 11940
116780 CATTAAGGTTGGTGGTGGCTCCATCTGCGGGATTTCCCAACATCATCCAGCG 116839
11941 TGCATTACAGTGGGAGCTGAGGCTGGCTCCAGAGAGAGTGGCTGGCTGGTGGTGA 12000
116840 TGCATTACAGTGGGAGCTGAGGCTGGCTCCAGAGAGAGTGGCTGGCTGGTGGTGA 116899
12001 GGGAGTTCCTTAATTAATTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 12060
116900 GGGAGTTCCTTAATTAATTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 116959
12061 GAGGACAGGGGCGGAGCTAGTACGTGGGGGAGCCCTTAACGGGGATTAATTAATTAATTAAT 12120
116960 GAGGACAGGGGCGGAGCTAGTACGTGGGGGAGCCCTTAACGGGGATTAATTAATTAATTAAT 117019
12121 AACTATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 12180
117020 AACTATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 117079
12181 TACAGGCTGTAGTTTGTATATGAGTACAGGCTGAGTACATTAATTAATTAATTAATTAATTAAT 12240
117080 TACAGGCTGTAGTTTGTATATGAGTACAGGCTGAGTACATTAATTAATTAATTAATTAATTAAT 117139
12241 TACAGGCTGTAGTTTGTATATGAGTACAGGCTGAGTACATTAATTAATTAATTAATTAATTAAT 12300
117140 TACAGGCTGTAGTTTGTATATGAGTACAGGCTGAGTACATTAATTAATTAATTAATTAATTAAT 117199
12301 GGGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 12360
117200 GGGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 117259
12361 TCATACATGAGGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 12420
117260 TCATACATGAGGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 117319
12421 TGGAGTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 12480
117320 TGGAGTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 117379
12481 AATCCTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 12540
117380 AATCCTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 117439
12541 AATCCTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 12600
117440 AATCCTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 117499
12601 TACCATGGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 12660
117500 TACCATGGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 117559
12661 GTAAACAAACCCCACTCGGATTTGGCTGCTGTTTGGCCCAACGAGCGAGAAATTC 12720
117560 GTAAACAAACCCCACTCGGATTTGGCTGCTGTTTGGCCCAACGAGCGAGAAATTC 117619
12721 CCTGATGACAGGCGGACTGSCCAATGTTTTCGAGCATTTTGTATGACAGACGCGCC 12780
117620 CCTGATGACAGGCGGACTGSCCAATGTTTTCGAGCATTTTGTATGACAGACGCGCC 117679
12781 GGCATTCGCAACCGAATTCGGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 12840
117680 GGCATTCGCAACCGAATTCGGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 117739
12841 GCGCGCGGGGTTTATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 12900
117740 GCGCGCGGGGTTTATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 117799
12901 GCGCGCGGGGTTTATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 12960
117800 GCGCGCGGGGTTTATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 117859
12961 GCGCGCGGGGTTTATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 13020
117860 GCGCGCGGGGTTTATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 117919
13021 GCGCATATGAGTGGATGGGAGCGGCGGAGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 13080
117920 GCGCATATGAGTGGATGGGAGCGGCGGAGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 117979
13081 GCGCGCAAGAGCGGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAG 13140
117980 GCGCGCAAGAGCGGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAG 118039
13141 CAGTGTGACCGCGGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAG 13200
118040 CAGTGTGACCGCGGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAG 118099
13201 AATTCACAGGTTTCTCATATGAGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAG 13260
118100 AATTCACAGGTTTCTCATATGAGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAG 118159
13261 TCGGATGACCGCGGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAG 13320
118160 TCGGATGACCGCGGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAG 118219
13321 TCGGATGACCGCGGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAG 13380
118220 TCGGATGACCGCGGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAG 118279
13381 CATGTGACATTTTCAATGAGACCGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAG 13440
118280 CATGTGACATTTTCAATGAGACCGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAG 118339

QY	13441	GGTGAATGTTCTGATGACCGCCGCTTAACGTTTGCAGCGGTGTACGCGGAACATAATTCT	13500
Db	118340	GGTGAATGTTCTGATGACCGCGGCTTAACGTTTGCAGCGGTGTACGCGGAACATAATTCT	118399
QY	13501	CCCCGGCTCCGAGCGCCGGGGCCGGGAGCCGAGTGGGTTATTAAAGTTACGTAAGG	13560
Db	118400	CCCCGGCTCCGAGCGCCGGGGCCGGGAGCCGAGTGGGTTATTAAAGTTACGTAAGG	118459
QY	13561	ATTAAATTTTAAATCACTACACCCCTTAAATGTCCGGCTCGCCCTGCGGCACGCTGACGGC	13620
Db	118460	ATTAAATTTTAAATCACTACACCCCTTAAATGTCCGGCTCGCCCTGCGGCACGCTGACGGC	118519
QY	13621	GGCGGTTTCGACCCATTGACCGCATCTCTGGTGCCGGGCAGAGCGCCGCGCAAGG	13680
Db	118520	GGCGGTTTCGACCCATTGACCGCATCTCTGGTGCCGGGCAGAGCGCCGCGCAAGG	118579
QY	13681	TGCGATCGCGGGGTGTGACCCACCGCGTGGGAGAAACCCCTCGGTTCCGTTGCTTGTGC	13740
Db	118580	TGCGATCGCGGGGTGTGACCCACCGCGTGGGAGAAACCCCTCGGTTCCGTTGCTTGTGC	118639
QY	13741	TGCGGTCCCTGGCCCTTGCCACCGGGGATGTCTTGTGACACTTTCGCCGTGAGAA	13800
Db	118640	TGCGGTCCCTGGCCCTTGCCACCGGGGATGTCTTGTGACACTTTCGCCGTGAGAA	118699
QY	13801	TAGACAGAGAGTGCCTCCGCAACATCATCGACGGGGTTGCCGTGGTGAACGGGAGCGG	13860
Db	118700	TAGACAGAGAGTGCCTCCGCAACATCATCGACGGGGTTGCCGTGGTGAACGGGAGCGG	118759
QY	13861	CCGCTTGGGTGGTGAAGTGTGCAGCGGTGGGCGGTATGACCCCGCAACGCGAGGGGCGG	13920
Db	118760	CCGCTTGGGTGGTGAAGTGTGCAGCGGTGGGCGGTATGACCCCGCAACGCGAGGGGCGG	118819
QY	13921	CTGGGCGGAAATTTTCCCGAAGACGGCGCCGCGCTTGGCGGCGGCTTCCCTCCCCA	13980
Db	118820	CTGGGCGGAAATTTTCCCGAAGACGGCGCCGCGCTTGGCGGCGGCTTCCCTCCCCA	118879
QY	13981	ACGACCCCTAATTTGGTTTAAATTGTTATTTAAAGTCGCCGTGTGTTTGTGTGACGGG	14040
Db	118880	ACGACCCCTAATTTGGTTTAAATTGTTATTTAAAGTCGCCGTGTGTTTGTGTGACGGG	118939
QY	14041	CTTAAGCGTGTGCACCTGTGTGGAGAGATCCCGGTGCGATGCGCCGCTCCGACCTCG	14100
Db	118940	CTTAAGCGTGTGCACCTGTGTGGAGAGATCCCGGTGCGATGCGCCGCTCCGACCTCG	118999
QY	14101	GTGACGCTGCCGAGCGTGCACCTGTGTTGGTTGTCTATCCCATGTCGCGCATCCCCCA	14160
Db	119000	GTGACGCTGCCGAGCGTGCACCTGTGTTGGTTGTCTATCCCATGTCGCGCATCCCCCA	119059
QY	14161	TCTTATTTTCCCGGACGAGCAACATTAACGTACAGTCGTTTGTGAAGAAATTAATGCTTTT	14220
Db	119060	TCTTATTTTCCCGGACGAGCAACATTAACGTACAGTCGTTTGTGAAGAAATTAATGCTTTT	119119
QY	14221	TTTATTTTGTGAACCCGCAACGCGATACAGTCTCGCCCTTTCACCCGTTGTTTGT	14280
Db	119120	TTTATTTTGTGAACCCGCAACGCGATACAGTCTCTCGCCCTTTCACCCGTTGTTTGT	119179
QY	14281	TACACGCCCCCTTGTGGGGCGGGACCGGGCTTAAACGGGGTGGGTTGGCGGCCACGACT	14340
Db	119180	TACACGCCCCCTTGTGGGGCGGGACCGGGCTTAAACGGGGTGGGTTGGCGGCCACGACT	119239
QY	14341	TGGCCACGTCGGGCTGTGAGAGAGCGGCTGTGACGACGTATTAAACATATGTATGTGAGG	14400
Db	119240	TGGCCACGTCGGGCTGTGAGAGAGCGGCTGTGACGACGTATTAAACATATGTATGTGAGG	119299
QY	14401	GGCTTACCAAGGCGCCCTTTTTCATTTTGGAGAAGCACCGAAAAAGTGGGAGCATGGT	14460
Db	119300	GGCTTACCAAGGCGCCCTTTTTCATTTTGGAGAAGCACCGAAAAAGTGGGAGCATGGT	119359
QY	14461	TGCGGCTTGACCAAGCTGTGTGCCCCGTTAGAAAAACTAAATTTTTCACGTCCCTTTCTG	14520
Db	119360	TGCGGCTTGACCAAGCTGTGTGCCCCGTTAGAAAAACTAAATTTTTCACGTCCCTTTCTG	119419

QY	14521	ACAGCTGGGGTCAATGGAGACATCAGGTGTTTGTATGGACCTAAAGTAACTCTGGGCTGG	14580
Db	119420	AGAGCTGGGGTCAATGAGAGACATCAGGTGTTTGTATGGACCTAAAGTAACTCTGGGCTGG	119475
QY	14581	ACCGAGCCTCTCGATTAATAATCCACGCTCTAGTAAAAAAAAGTGGAGACACAGGTCCA	14640
Db	119480	ACCGAGCCTCTCGATTAATAATCCACGCTCTAGTAAAAAAAAGTGGAGACACAGGTCCA	119535
QY	14641	ATCGCCCAACGAGAAAACACGGCCTCCAGCAACACGGAGGGGAATACGGGTTTCTCAG	14700
Db	119540	ATCGCCCAACGAGAAAACACGGCCTCCAGCAACACGGAGGGGAATACGGGTTTCTCAG	119599
QY	14701	TTGAGGGGCGACAGCCCGTTTGCAAAACCCCTCGGGGCTATGCTGGAGCCGGCGGGTCAA	14760
Db	119600	TTGAGGGGCGACAGCCCGTTTGCAAAACCCCTCGGGGCTATGCTGGAGCCGGCGGGTCAA	119655
QY	14761	AAAGCCACAGCAACGGCCTCTGCTGTGCTGCTAGTCTAGTGGGCGACCCACCTCAAC	14820
Db	119660	AAAGCCACAGCAACGGCCTCTGCTGTGCTGCTAGTCTAGTGGGCGACCCACCTCAAC	119713
QY	14821	GCTTATGCGGGAACATGGGTCCGGTCCGGGCTCGCCGACACCCCTCTTACCTACCTA	14880
Db	119720	GCTTATGCGGGAACATGGGTCCGGTCCGGGCTCGCCGACACCCCTCTTACCTACCTA	119779
QY	14881	GAGCGTTTATTAATACAGACGAAACCGCGGCGCTTACTTAAATGTGTCTTGCTCAAT	14940
Db	119780	GAGCGTTTATTAATACAGACGAAACCGCGGCGCTTACTTAAATGTGTCTTGCTCAAT	119833
QY	14941	TCCCGGAAGGTGTGGCAACCGACTCGGGGGGGCGCGGAGGGTTGGCGGCGAAAGCCG	15000
Db	119840	TCCCGGAAGGTGTGGCAACCGACTCGGGGGGGCGCGGAGGGTTGGCGGCGAAAGCCG	119899
QY	15001	ACGGCCTCCGCCAATCTGGCCGGAGGCGGCGCACGCGGACCGAGGCTTAAACAGCGCGCAG	15060
Db	119900	ACGGCCTCCGCCAATCTGGCCGGAGGCGGCGCACGCGGACCGAGGCTTAAACAGCGCGCAG	119959
QY	15061	GGGGCCGCCACCAAGGAGCGGGGCGAABACCGCGGCTGACGATGCTTTGTGA	15120
Db	119960	GGGGCCGCCACCAAGGAGCGGGGCGAABACCGCGGCTGACGATGCTTTGTGA	120019
QY	15121	ACAGACTCCACCACTGGCTGTGAAGGGCAAAAGCTGCTTTGTGAAGCGGCTTTTA	15180
Db	120020	ACAGACTCCACCACTGGCTGTGAAGGGCAAAAGCTGCTTTGTGAAGCGGCTTTTA	120077
QY	15181	AACAGGGTGGGCCGATGCGCTCCGTTGGTAAAGCGGCTCTAGTTTCCACCTTAAAGCC	15240
Db	120080	AACAGGGTGGGCCGATGCGCTCCGTTGGTAAAGCGGCTCTAGTTTCCACCTTAAAGCC	120139
QY	15241	TTAAGGATGATTTTTCTGTGTTCACTAAATCCGCCAGGAAAAATCTCTCCGCGCGCAA	15300
Db	120140	TTAAGGATGATTTTTCTGTGTTCACTAAATCCGCCAGGAAAAATCTCTCCGCGCGCAA	120199
QY	15301	AAGCATAAAAAGGGGCGCTTGAAGAAGATTCAGTCTCTATCTTGCCGGCTTAAAAATGA	15360
Db	120200	AAGCATAAAAAGGGGCGCTTGAAGAAGATTCAGTCTCTATCTTGCCGGCTTAAAAATGA	120259
QY	15361	CAGGGGCGCCCGACGCTCTGAAAACCCCGACGGGGATGCTGGACACTCTAGTAGCGA	15420
Db	120260	CAGGGGCGCCCGACGCTCTGAAAACCCCGACGGGGATGCTGGACACTCTAGTAGCGA	120313
QY	15421	TCCAGAATACTAAGGGCAGTGGGAAAAAGCTAGCATCCGCTGTGTGGGCGCTTGGCACAA	15480
Db	120320	TCCAGAATACTAAGGGCAGTGGGAAAAAGCTAGCATCCGCTGTGTGGGCGCTTGGCACAA	120377
QY	15481	GACCCGATCCACGTCCCCCAAGTAATCTCCGATGCCACACGTCACCTCCGTTTGTATGTC	15540
Db	120380	GACCCGATCCACGTCCCCCAAGTAATCTCCGATGCCACACGTCACCTCCGTTTGTATGTC	120439
QY	15541	CCATAGCAGGCGGTGGATGTTTACAAAGAGAGCTCTTGGGGCGAGGAGTTAGAGAGGGCC	15600
Db	120440	CCATAGCAGGCGGTGGATGTTTACAAAGAGAGCTCTTGGGGCGAGGAGTTAGAGAGGGCC	120499
QY	15601	CGGTCTGTGTACAGGACGGGGTCAATGTGCCGTGGGGCACTGGGGCCAAACAGACCATT	15660

D	120500	CGGTCCTGTACAGACGGGGTCAATGTCGGGTGGGCACTGGGCAACAGAACCATTT	120559	D	121580	TGAGTCGGGCGGGATTGCGAGAGGGGAGAGACGTGGCGTTGGCATTTGTGGCGGTCC	121633
Q	15661	GTCAAGCAGAGTAAGAAAGCGATATPAAGTCTACCTCGGGCTCAGGAGGCTTAATAC	15720	Q	16741	AGGTAGTCGGGAGGGGCGAAGACAGTCGAGAGCTCAGCGGCTTCAGGTAGTCGTGTG	16800
D	120560	GTCAAGCAGAGTAAGAAAGCGATATPAAGTCTACCTCGGGCTCAGGAGGCTTAATAC	120619	D	121640	AGGTAGTCGGGAGGGGCGAAGACAGTCGAGAGCTCAGCGGCTTCAGGTAGTCGTGTG	121699
Q	15721	GAAGTCGGGCTTAACACAAACTCTCTGTCGTATGTCGGCTCCACACTGTCCTCA	15780	Q	16801	CGATGCTTGAAGAAACGACGAAGCGCTGTTATGGGAGTAGATTAATGACAGACGGCG	16860
D	120620	GAAGTCGGGCTTAACACAAACTCTCTGTCGTATGTCGGCTCCACACTGTCCTCA	120679	D	121700	CGATGCTTGAAGAAACGACGAAGCGCTGTTATGGGAGTAGATTAATGACAGACGGCG	121759
Q	15781	TGTCCTGTGACAGTTCACGCCCTGCTGTCCCGGAAACGGCGGACTAGATGCAACCGGA	15840	Q	16861	TGCAGTAGTAGGGGCGCGGGGCTGTGACGGGGGATGATGTGGGGCGCAATGCAGCGG	16920
D	120680	TGTCCTGTGACAGTTCACGCCCTGCTGTCCCGGAAACGGCGGACTAGATGCAACCGGA	120739	D	121760	TGCAGTAGTAGGGGCGCGGGGCTGTGACGGGGGATGATGTGGGGCGCAATGCAGCGG	121819
Q	15841	AGCGGCTGTTCATTTAAGTGAAGTACAGAGCGGGGCAATTTGGCCAACAGTGAAGCGTTT	15900	Q	16921	GGATCGCGGGGACGACACCTGACGTGTTTGAAGTGAACAGCCCTGAAGCTTAACCGCGC	16980
D	120740	AGCGGCTGTTCATTTAAGTGAAGTACAGAGCGGGGCAATTTGGCCAACAGTGAAGCGTTT	120799	D	121820	GGATCGCGGGGACGACACCTGACGTGTTTGAAGTGAACAGCCCTGAAGCTTAACCGCGC	121879
Q	15901	CCTGAGCTGGGGTTTTACCTGGCAGAGCGCACTGGTCTGTTGGCAGCGCGCGGGGGG	15960	Q	16981	AGACCGCTTGGCGGCGCGCTTGAAGATCCCAACAGATGACGAGTCAACCGCTGACC	17040
D	120800	CCTGAGCTGGGGTTTTACCTGGCAGAGCGCACTGGTCTGTTGGCAGCGCGCGGGGGG	120859	D	121880	AGACCGCTTGGCGGCGCGCTTGAAGATCCCAACAGATGACGAGTCAACCGCTGACC	121939
Q	15961	ATTTTATTTAGTGTGAATTTGGCAGTCTCTGTCCATGCGACTATGCTGGCTGGAATG	16020	Q	17041	TGATGCGACACCTTTGGGATGACCCGTCCTGGATTCGGTGGGCGGCTTCCGATCC	17100
D	120860	ATTTTATTTAGTGTGAATTTGGCAGTCTCTGTCCATGCGACTATGCTGGCTGGAATG	120919	D	121940	TGATGCGACACCTTTGGGATGACCCGTCCTGGATTCGGTGGGCGGCTTCCGATCC	121999
Q	16021	GGGGGCGGATGGTGAATGTCTGTCACCGGCGACGGGCTTTTGAAGGCGCTTTGGCGGT	16080	Q	17101	GTGCGCTTGTTCGACACCGCGGCACTTGGCGGCTGATGTTGTTGGAAGGGGGGCGC	17160
D	120920	GGGGGCGGATGGTGAATGTCTGTCACCGGCGACGGGCTTTTGAAGGCGCTTTGGCGGT	120979	D	122000	GTGCGCTTGTTCGACACCGCGGCACTTGGCGGCTGATGTTGTTGGAAGGGGGGCGC	122059
Q	16081	TCCGCGGCTTTGACAGAACACCCGTAATGCAAAAAAGCGGGATGACGGGACTGCGACGTGC	16140	Q	17161	GGGTGCGGCGGCTGGGCGGGCGGCGAGCGCCGCTGCGCGCTCCCGGCGCTGTTCTCT	17220
D	120980	TCCGCGGCTTTGACAGAACACCCGTAATGCAAAAAAGCGGGATGACGGGACTGCGACGTGC	121039	D	122060	GGGTGCGGCGGCTGGGCGGGCGGCGAGCGCCGCTGCGCGCTCCCGGCGCTGTTCTCT	122119
Q	16141	GTCCGGCAAAACGGGACGCGTGAATGCTTAATCCCGGAAACGTGAGGCACTTGTCCAG	16200	Q	17221	AGTGGCGCGGCTTCCGCAATGTCCCTGACAGAACTTCCGACACCGGCTGTCCCATAC	17280
D	121040	GTCCGGCAAAACGGGACGCGTGAATGCTTAATCCCGGAAACGTGAGGCACTTGTCCAG	121099	D	122120	AGTGGCGCGGCTTCCGCAATGTCCCTGACAGAACTTCCGACACCGGCTGTCCCATAC	122179
Q	16201	GCGATACAGTAATAGGGGTCTGATTACAAAAGATGACTCCGTGACACACCGGGCCCG	16260	Q	17281	TATGCGGAGACGATGTGCGGGCTGCGCCACATGTTGCGGCTTACTGCGGTGTAATAAC	17340
D	121100	GCGATACAGTAATAGGGGTCTGATTACAAAAGATGACTCCGTGACACACCGGGCCCG	121159	D	122180	TATGCGGAGACGATGTGCGGGCTGCGCCACATGTTGCGGCTTACTGCGGTGTAATAAC	122239
Q	16261	CCGAGGGGGGCGACCTCGGGTCCCAATACCTAGCTAATAACTTCTCTGTGGGGGGA	16320	Q	17341	GGCAGATTAAGTAGTGGCCCTTTCAGACGCCGACACGCTGAGGGCGCGACGACGA	17400
D	121160	CCGAGGGGGGCGACCTCGGGTCCCAATACCTAGCTAATAACTTCTCTGTGGGGGGA	121219	D	122240	GGCAGATTAAGTAGTGGCCCTTTCAGACGCCGACACGCTGAGGGCGCGACGACGA	122299
Q	16321	TTTTCCTGGGTACCTTCTCTCTGTATGAGGATACGATGGAATGGGATGCGCGCG	16380	Q	17401	ACCTATGTTTATGTCGATTTGCGATTTGTCGCTGAGTGGCGGCGTAATTTGATCTGCC	17460
D	121220	TTTTCCTGGGTACCTTCTCTCTGTATGAGGATACGATGGAATGGGATGCGCGCG	121279	D	122300	ACCTATGTTTATGTCGATTTGCGATTTGTCGCTGAGTGGCGGCGTAATTTGATCTGCC	122359
Q	16381	GCGCGGGGGGCGCGGGGGCGCGCGGTGCTGCTGCCCTCCCTCTTGTCTCTG	16440	Q	17461	GCGCAGCATTTGACCGCTTATGATGGCGCGACAGCGCCGTTAACCCGACGAGCACCGACG	17520
D	121280	GCGCGGGGGGCGCGGGGGCGCGCGGTGCTGCTGCCCTCCCTCTTGTCTCTG	121339	D	122360	GCGCAGCATTTGACCGCTTATGATGGCGCGACAGCGCCGTTAACCCGACGAGCACCGACG	122419
Q	16441	TTTGTCTTTCAGAGACTTCGTCCTGTGTGGAGTTGTGACTGTGCACTCTGAGAGTAAACA	16500	Q	17521	CGGTTTATGTTTCTGCTATTAACGTTTATTAATCCGTGGCCGATTTGGGTGGCAG	17580
D	121340	TTTGTCTTTCAGAGACTTCGTCCTGTGTGGAGTTGTGACTGTGCACTCTGAGAGTAAACA	121399	D	122420	CGGTTTATGTTTCTGCTATTAACGTTTATTAATCCGTGGCCGATTTGGGTGGCAG	122479
Q	16501	AGGAACCTCTCGGACGCGGGGTGGAACCCCAACCCCTACGCTAGCAGTGGGATGT	16560	Q	17581	TGTGTAACTCAACGGCGCGCGCGCCCTTACTTGTGCGCGGCGAACCAGGAAAGTCT	17640
D	121400	AGGAACCTCTCGGACGCGGGGTGGAACCCCAACCCCTACGCTAGCAGTGGGATGT	121459	D	122480	TGTGTAACTCAACGGCGCGCGCGCCCTTACTTGTGCGCGGCGAACCAGGAAAGTCT	122539
Q	16561	ATGAGCAGAAACGGGGTCTCTGGACGAGAGCGCGCGTGGGTGCTGTGTGCTGAC	16620	Q	17641	GTTCGCGCGCGACGCGGGGCTGTGACGGGGGATGATGTGGGGCGCAATGCAGCGG	17700
D	121460	ATGAGCAGAAACGGGGGCTCTCTGGACGAGAGCGCGCGTGGGTGCTGTGTGCTGAC	121519	D	122540	GTTCGCGCGCGACGCGGGGCTGTGACGGGGGATGATGTGGGGCGCAATGCAGCGG	122599
Q	16621	CGCCTGTTGCGTGTAGGGGATGGGCGCTGTGAAGCGTTGGCGATTGGGGTGTGCCGG	16680	Q	17701	CTGGGCTTGTGTCAGTGAATTCACACAGATGCGATGTGATGGGCGTGTGTCAACGTC	17760
D	121520	CGCCTGTTGCGTGTAGGGGATGGGCGCTGTGAAGCGTTGGCGATTGGGGTGTGCCGG	121579	D	122600	CTGGGCTTGTGTCAGTGAATTCACACAGATGCGATGTGATGGGCGTGTGTCAACGTC	122659
Q	16681	TGAGTCGGGCGGGATTGCGAGAGGGGCGAGACGTCGGCGTTGGCGATTGTGGCGGTCC	16740	Q	17761	ACTTGTTAACCCGTAATTCGGAATTCCTGTCCCGCGGCGCGGTAGCGCGCGGCGCTTA	17820
D	121580	TGAGTCGGGCGGGATTGCGAGAGGGGCGAGACGTCGGCGTTGGCGATTGTGGCGGTCC	121633	D	122660	ACTTGTTAACCCGTAATTCGGAATTCCTGTCCCGCGCGCGGTAGCGCGCGGCGCTTA	122719

OY	17821	GCCTTATATGCTGTGCGACGCATCTGAAACTCGAAAGCTGGCCATATATAACCCACGTAAT	17880
Db	122720	GCCTTATATGCTGTGCGACGCATCTGAAACTCGAAAGCTGGCCATATATAACCCACGTAAT	122779
OY	17881	GGCGTGGGTGTGCGGGCAACCTTTTGGAAAAAGATTATTTGGCCGCGGGTTTAAGCA	17940
Db	122780	GGCGTGGGTGTGCGGGCAACCTTTTGGAAAAAGATTATTTGGCCGCGGGTTTAAGCA	122839
OY	17941	CCAACACGACCGCTGCTTTTCATAATATGTGSGGAGGAATTACATTTAACGCTGCTGTG	18000
Db	122840	CCAACACGACCGCTGCTTTTCATAATATGTGSGGAGGAATTACATTTAACGCTGCTGTG	122899
OY	18001	CGAGCGCTTGCCACGSGTGTGCGTCCGCTCTTCAAAACGACATATGCGGGGTCCCGTCACT	18060
Db	122900	CGAGCGCTTGCCACGSGTGTGCGTCCGCTCTTCAAAACGACATATGCGGGGTCCCGTCACT	122959
OY	18061	CTACCGCGTCCCTGGGGGTGCGTGTTAACGACACCCACGACGCTTCTTATGCTACCTGGC	18120
Db	122960	CTACCGCGTCCCTGGGGGTGCGTGTTAACGACACCCACGACGCTTCTTATGCTACCTGGC	123019
OY	18121	AAAAACAGGAATCGCTTAATCCCGTTAACGTGGCCACATATAGTTCCGAAGCGGCACGG	18180
Db	123020	AAAAACAGGAATCGCTTAATCCCGTTAACGTGGCCACATATAGTTCCGAAGCGGCACGG	123079
OY	18181	TGTTTCAACCCCCCGTTTCCGCGGTAGGGTTGACATTTCCGACACAAAGTTGACAGAAACGA	18240
Db	123080	TGTTTCAACCCCCCGTTTCCGCGGTAGGGTTGACATTTCCGACACAAAGTTGACAGAAACGA	123139
OY	18241	CCCTGAAGTTTTTTTAAATGCGACCCGTGAGAGACGAGGGGTGTCACCTGTATCTTTTAACG	18300
Db	123140	CCCTGAAGTTTTTTTAAATGCGACCCGTGAGAGACGAGGGGTGTCACCTGTATCTTTTAACG	123199
OY	18301	CGTTTGGAGTGGGAAAGCGTGTGSGGAACCGCGCTGCTGAACGGTTTACGTCCCGCTGCCA	18360
Db	123200	CGTTTGGAGTGGGAAAGCGTGTGSGGAACCGCGCTGCTGAACGGTTTACGTCCCGCTGCCA	123259
OY	18361	TGTCGCTACAGTTTTTACCCTCCGATTAACCCGACGAGCTGCTGTGCGGGCCGAGACCA	18420
Db	123260	TGTCGCTACAGTTTTTACCCTCCGATTAACCCGACGAGCTGCTGTGCGGGCCGAGACCA	123319
OY	18421	GTCCCGCACCGTTCGGTCAACTGTGACCGCGGTGCTCCGCCGACGCTGTGCAACCACTGAAAG	18480
Db	123320	GTCCCGCACCGTTCGGTCAACTGTGACCGCGGTGCTCCGCCGACGCTGTGCAACCACTGAAAG	123379
OY	18481	TGTTTCCCGGGCCCAACGGAACAAACCTGTTGTGGGTGCTGTGCAACGTAACGTCGCTGG	18540
Db	123380	TGTTTCCCGGGCCCAACGGAACAAACCTGTTGTGGGTGCTGTGCAACGTAACGTCGCTGG	123439
OY	18541	ACCCCGAAGACCTTGAGAAACGCGACGTGCTGCTACATCATATAGCGGGTTTGGCCGCGG	18600
Db	123440	ACCCCGAAGACCTTGAGAAACGCGACGTGCTGCTACATCATATAGCGGGTTTGGCCGCGG	123499
OY	18601	CGGGGGCCCTGAGACCCCGGTTTTTGGAGTCCCTGGAAGGAGACCACTACGTGCTGG	18660
Db	123500	CGGGGGCCCTGAGACCCCGGTTTTTGGAGTCCCTGGAAGGAGACCACTACGTGCTGG	123559
OY	18661	GTGTGTGTGGACGCGCGCCCGCTTTTAAAGCATTTTTTAAACGGGTGTTTTTGTATAGGT	18720
Db	123560	GTGTGTGTGGACGCGCGCCCGCTTTTAAAGCATTTTTTAAACGGGTGTTTTTGTATAGGT	123619
OY	18721	CTATGTGAGCGCGCGCTGTCCCGGTGTCTAGTGTTTTTTTGCCCAGTAGTGTCTCAATG	18780
Db	123620	CTATGTGAGCGCGCGCTGTCCCGGTGTCTAGTGTTTTTTTGCCCAGTAGTGTCTCAATG	123679
OY	18781	ACAAATACAAATTTTGAAGCTGGCTTTTAAAGGTGGTTTTTGTGACACACTTCCTGTTGA	18840
Db	123680	ACAAATACAAATTTTGAAGCTGGCTTTTAAAGGTGGTTTTTGTGACACACTTCCTGTTGA	123739
OY	18841	ACTGCATACACCGGGGTGTCCGCCAGAAACCGCGTCTCCCTTATGTCCGCTCGCCCTC	18900
Db	123740	ACTGCATACACCGGGGTGTCCGCCAGAAACCGCGTCTCCCTTATGTCCGCTCGCCCTC	123799

QY	18901	CCAGAGCGAAGTGAAGATGGTTCCTGGGGCGTTTGGCGTTGAGAGAGTGGCGCATGT	18960
Db	123800	CCAGAGCGAAGTGAAGATGGTTCCTGGGGCGTTTGGCGTTGAGAGAGTGGCGCATGT	123859
QY	18961	TGCGGTACGGCGTCTGCAAAAGGCTCACCGGCTCTGTTTTTCTTTTGTGAGCAA	19020
Db	123860	TGCGGTACGGCGTCTGCAAAAGGCTCACCGGCTCTGTTTTTCTTTTGTGAGCAA	123919
QY	19021	CACATGAGACCCCTTGAACAAATTAACCTTAACCTCGATGATGATTTTCTGTACTATTC	19080
Db	123920	CACATGAGACCCCTTGAACAAATTAACCTTAACCTCGATGATGATTTTCTGTACTATTC	123979
QY	19081	GAATAGCTACAGTATTGACGACAAATATGTCTTACCTTTAGACAGGAATCCACGT	19140
Db	123980	GAATAGCTACAGTATTGACGACAAATATGTCTTACCTTTAGACAGGAATCCACGT	124039
QY	19141	GTGTGCGGTGACGGTGGTTTCCACACTACCGTTTATGCCATTTATATGCTTTTTATTTT	19200
Db	124040	GTGTGCGGTGACGGTGGTTTCCACACTACCGTTTATGCCATTTATATGCTTTTTATTTT	124099
QY	19201	TTGCATTTACGGTGTGGGAAACGGCTTGTCCTATATATTTTTTTAAATTTAAAGCGCT	19260
Db	124100	TTGCATTTACGGTGTGGGAAACGGCTTGTCCTATATATTTTTTTAAATTTAAAGCGCT	124159
QY	19261	CGCCAACTCTGTGATGTACTGATGAGCGTGTGTGTATCTCCCTGTTTCTGTGCGC	19320
Db	124160	CGCCAACTCTGTGATGTACTGATGAGCGTGTGTGTATCTCCCTGTTTCTGTGCGC	124219
QY	19321	GTCTGTTTGTTCACGTGGCTGTGTACGTGGCGCACAGATGCTCACGTCCGGAGCTG	19380
Db	124220	GTCTGTTTGTTCACGTGGCTGTGTACGTGGCGCACAGATGCTCACGTCCGGAGCTG	124279
QY	19381	CAAGTGGAAATCTTTTCTTTTACCTTACACGACTTTGGCGGTACATTTGSGTGTG	19440
Db	124280	CAAGTGGAAATCTTTTCTTTTACCTTACACGACTTTGGCGGTACATTTGSGTGTG	124339
QY	19441	TATCAGCCTTATCAGGTGCTGTATAGTGTGTTTCCCGCGCCCGTGGGTCAAGCACAGG	19500
Db	124340	TATCAGCCTTATCAGGTGCTGTATAGTGTGTTTCCCGCGCCCGTGGGTCAAGCACAGG	124399
QY	19501	GGCCTCCGGCTTTCTCTCGGTGTGTGTCTTTTAATGTGGCGCTGGCGTGTCTGCCAA	19560
Db	124400	GGCCTCCGGCTTTCTCTCGGTGTGTGTCTTTTAATGTGGCGCTGGCGTGTCTGCCAA	124459
QY	19561	CGCGAGCCTTATAGGAGGGCCGTCGCTACCCAGAGACCAAGCGATGGATGTACGTA	19620
Db	124460	CGCGAGCCTTATAGGAGGGCCGTCGCTACCCAGAGACCAAGCGATGGATGTACGTA	124519
QY	19621	AGATGCCGGGAGATATACCTCAACTGAGACTGAGATTCAGAACCAACAGCGCATCTG	19680
Db	124520	AGATGCCGGGAGATATACCTCAACTGAGACTGAGATTCAGAACCAACAGCGCATCTG	124579
QY	19681	CGGGTTTTTGGTTCCTGTTGGGCTGATGTGCTTTTTACGACTTACGTGTGATGTGT	19740
Db	124580	CGGGTTTTTGGTTCCTGTTGGGCTGATGTGCTTTTTACGACTTACGTGTGATGTGT	124639
QY	19741	TAAAGCACGAGGCGCCCAAAAAGGAGCGGTTAAGGGGTATATTGAGAGGTGTGTGT	19800
Db	124640	TAAAGCACGAGGCGCCCAAAAAGGAGCGGTTAAGGGGTATATTGAGAGGTGTGTGT	124699
QY	19801	GCTGTTTTTAATTTTTTGTGCGCCCTATACCTGTGCAACTTTTTTTGACACCCGTGTGAG	19860
Db	124700	GCTGTTTTTAATTTTTTGTGCGCCCTATACCTGTGCAACTTTTTTTGACACCCGTGTGAG	124759
QY	19861	GACCGGTTTTCTGGCCGAACGTGCTACCTCAGGGAGCTGATACAGCGCCAGTACACAT	124819
Db	124760	GACCGGTTTTCTGGCCGAACGTGCTACCTCAGGGAGCTGATACAGCGCCAGTACACAT	124879
QY	19921	ATGTCTCCCTGTACAGAGCATGTATAGCGGCTGTGTGCCATTCGTATTTCTGTGCTTGG	19980
Db	124820	ATGTCTCCCTGTACAGAGCATGTATAGCGGCTGTGTGCCATTCGTATTTCTGTGCTTGG	124879
QY	19981	GTCCTCTGTTTAGAGAAAGGTTTAGGGAATACCTGTGCTGTTTATAGTGTTTTTTCCACTTC	20040

D	124880	GTCTCTGTTAGAGAGGTTAGGGTACTGTGCTCGTTAGGGTTTTCACATTC	124939	D	125960	GTTGCACCCGTAAGTCTTCTGTAGAGTTCCGCGGGGCGTAACCTGGGCCCATGA	126019
Q	20041	AGGTAGTTATGAGACACTCAGCAGCACTGGTTGGATTGTTGTACTATTATTTTC	20100	Q	21121	GTACCACTGTTCTCCGAGAACGAGGTCCAGTTTGGCCGCCACCGAAGTAGAGGTGTGA	21180
D	124940	AGGTAGTTATGAGACACTCAGCAGCACTGGTTGGATTGTTGTACTATTATTTTC	124999	D	126020	GTACCACTGTTCTCCGAGAACGAGGTCCAGTTTGGCCGCCACCGAAGTAGAGGTGTGA	126079
Q	20101	ATTTTGTATCATTATTTTCAATTAAGCATCTGACCTCAGACCTTACTAGCTTTA	20160	Q	21181	ATAGACTTCATGCTTGTGTGTAGATGACATCTTCTTGACAGACCCCTCCGACCCAC	21240
D	125000	ATTTTGTATCATTATTTTCAATTAAGCATCTGACCTCAGACCTTACTAGCTTTA	125059	D	126080	ATAGACTTCATGCTTGTGTGTAGATGACATCTTCTTGACAGACCCCTCCGACCCAC	126139
Q	20161	CTGTCTGTTCTTATGACACAGAGAAACAGGAGCTGGAAGGCCACCGCCACCGGGAAC	20220	Q	21241	GGTGCCGACACAGGTGGCCGCGCAGTCAAGTTTGGCAGCGCTGGCGCAGCTCTGCGAC	21300
D	125060	CTGTCTGTTCTTATGACACAGAGAAACAGGAGCTGGAAGGCCACCGCCACCGGGAAC	125119	D	126140	GGTGCCGACACAGGTGGCCGCGCAGTCAAGTTTGGCAGCGCTGGCGCAGCTCTGCGAC	126199
Q	20221	TGTATGTCCGCAAGCTCGGCGGCGACGTACGCCCACTGCGAGGGGTGAACTCAGCGC	20280	Q	21301	GTCCTGGGGCTGGAATTTGCAAGATGACGCCCGGGGTTTGGACACCAACCCATCTGACGGG	21360
D	125120	TGTATGTCCGCAAGCTCGGCGGCGACGTACGCCCACTGCGAGGGGTGAACTCAGCGC	125179	D	126200	GTCCTGGGGCTGGAATTTGCAAGATGACGCCCGGGGTTTGGACACCAACCCATCTGACGGG	126259
Q	20281	GGGGTGCACAGGAGGAGCCAGTGGGGGCCCTCCGGTGAAGTATGGCGGCCACGCGCGA	20340	Q	21361	CGTTTCCCTGACGGGATGGGAATCTGTAGGGCTCGGTTACGGGCCACGGGCCATCTCGAT	21420
D	125180	GGGGTGCACAGGAGGAGCCAGTGGGGGCCCTCCGGTGAAGTATGGCGGCCACGCGCGA	125239	D	126260	CGTTTCCCTGACGGGATGGGAATCTGTAGGGCTCGGTTACGGGCCACGGGCCATCTCGAT	126319
Q	20341	GTTGGCAGACGGGTTGCGTGGTAGTGTGCTGCGCAACATCTCGGGGCGGCGTTGCCCT	20400	Q	21421	AGCGTTAACACCATGCTCCCTGCTGCGTGAAGTGTGGCCGGAACACCAAGACCCCGGGA	21480
D	125240	GTTGGCAGACGGGTTGCGTGGTAGTGTGCTGCGCAACATCTCGGGGCGGCGTTGCCCT	125299	D	126320	AGCGTTAACACCATGCTCCCTGCTGCGTGAAGTGTGGCCGGAACACCAAGACCCCGGGA	126379
Q	20401	GTTGTAGTTCAGGGCGATGCGCTGCTGTGTAGATGTGCTCCTGACATGGCGTCCGCGG	20460	Q	21481	GAGCAGGGCCCTGTTAGCATGAAGAGTTGGCCAGAGTGTGCTGCTGAACCTCGGTAG	21540
D	125300	GTTGTAGTTCAGGGCGATGCGCTGCTGTGTAGATGTGCTCCTGACATGGCGTCCGCGG	125359	D	126380	GAGCAGGGCCCTGTTAGCATGAAGAGTTGGCCAGAGTGTGCTGCTGAACCTCGGTAG	126439
Q	20461	GTTATTCACAGCCCAAGTACCGCGCGCTGTGGGCCACCTCGGAGAGACAGGCCCCGAAGAAC	20520	Q	21541	GGTGGGACATCGGAAAGACACAGGAGTGTCAAAAGTGTGATCCCTGGGTTACAGTGGGGCAC	21600
D	125360	GTTATTCACAGCCCAAGTACCGCGCGCTGTGGGCCACCTCGGAGAGACAGGCCCCGAAGAAC	125419	D	126440	GGTGGGACATCGGAAAGACACAGGAGTGTCAAAAGTGTGATCCCTGGGTTACAGTGGGGCAC	126499
Q	20521	CCTAAACATGATGCTATGCTGTGGGGATGTGAGAGTTTACGACAGGACATCTGTG	20580	Q	21601	GGGGAAGGACACAGCAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATG	21660
D	125420	CCTAAACATGATGCTATGCTGTGGGGATGTGAGAGTTTACGACAGGACATCTGTG	125479	D	126500	GGGGAAGGACACAGCAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATG	126559
Q	20581	GTTCCCTGATGCTTCTCTCAAGTGTGATGTCCCACTGGTGGGGGTTTGGGTCGGG	20640	Q	21661	CCTGGAACATTCCTCGGCGGTGCGCTGATGATGATGATGATGATGATGATGATGATGATG	21720
D	125480	GTTCCCTGATGCTTCTCTCAAGTGTGATGTCCCACTGGTGGGGGTTTGGGTCGGG	125539	D	126560	CCTGGAACATTCCTCGGCGGTGCGCTGATGATGATGATGATGATGATGATGATGATGATG	126619
Q	20641	CGTGTGTAGGGGCTCTCTAGAGACCGAGCGCCCGCAGAGATGTGAAACCCCAATCTC	20700	Q	21721	TACCGTGTAGTGTGTGGGTGGCGCTGATGATGATGATGATGATGATGATGATGATGATG	21780
D	125540	CGTGTGTAGGGGCTCTCTAGAGACCGAGCGCCCGCAGAGATGTGAAACCCCAATCTC	125599	D	126620	TACCGTGTAGTGTGTGGGTGGCGCTGATGATGATGATGATGATGATGATGATGATGATG	126679
Q	20701	CCCGCAGCATAGTGAATGTATCCGCTCGGCGGAAGAGCCATTAAGGCCCCCATAGCA	20760	Q	21781	GGCCGACATGATGGCAAGTGTATGCTCAAGTGTCTGCAATAGTTCTTTCAGGCAAAACAG	21840
D	125600	CCCGCAGCATAGTGAATGTATCCGCTCGGCGGAAGAGCCATTAAGGCCCCCATAGCA	125659	D	126680	GGCCGACATGATGGCAAGTGTATGCTCAAGTGTCTGCAATAGTTCTTTCAGGCAAAACAG	126739
Q	20761	CCCGAGGCTGTTGAGAAAGCCATGATCGCGCATCGGGCCCCCAGTGTCTTCGAT	20820	Q	21841	TGTGTCTGACAGAGCCAGGCTGTGCTGCTCCGCGTTCCAAACGACGAGCGCTCAG	21900
D	125660	CCCGAGGCTGTTGAGAAAGCCATGATCGCGCATCGGGCCCCCAGTGTCTTCGAT	125719	D	126740	TGTGTCTGACAGAGCCAGGCTGTGCTGCTCCGCGTTCCAAACGACGAGCGCTCAG	126799
Q	20821	GGCCAGGTTTCCACGATGGTGTAGACCGGAGATCCCGGAGATGTTCCTCTCTTAAG	20880	Q	21901	CGTGTGTGCTGTAGAGCGCGACGCTGTGTAGATGATGATGATGATGATGATGATGATGATG	21960
D	125720	GGCCAGGTTTCCACGATGGTGTAGACCGGAGATCCCGGAGATGTTCCTCTCTTAAG	125779	D	126800	CGTGTGTGCTGTAGAGCGCGACGCTGTGTAGATGATGATGATGATGATGATGATGATGATG	126859
Q	20881	GTCGTGTGTGAGACGCGCGCAGCTGGAACCCGAGTGTGTGAAGCGGCGCATCAGCGC	20940	Q	21961	GGCGTATCTTCGCGCCCACTGCGCGCTGTGTATGCGCATCTGTATGCTGTCTCCATTAAG	22020
D	125780	GTCGTGTGTGAGACGCGCGCAGCTGGAACCCGAGTGTGTGAAGCGGCGCATCAGCGC	125839	D	126860	GGCGTATCTTCGCGCCCACTGCGCGCTGTGTATGCGCATCTGTATGCTGTCTCCATTAAG	126919
Q	20941	CCTGGGAGCGGGGCAACGGGGGTGACCAAGCGGCGCACTGTGGCGGCTCGACGGCGT	21000	Q	22021	CACGCACTGTCCGACCCACCGGTTCTGTGCTCCCTGCGCTGTGGTGAACCAAGCTTCTGGGCT	22080
D	125840	CCTGGGAGCGGGGCAACGGGGGTGACCAAGCGGCGCACTGTGGCGGCTCGACGGCGT	125899	D	126920	CACGCACTGTCCGACCCACCGGTTCTGTGCTCCCTGCGCTGTGGTGAACCAAGCTTCTGGGCT	126979
Q	21001	TGCAAAACAGTACAGTCTGTTCTGTGAAAACCTGGGGAAGTGGCCACAGTGTGTG	21060	Q	22081	AACCAAGCGTCCGTCGCGGCTGCGCTGTGTATGCGCATCTGTATGCTGTCTCCATTAAG	22140
D	125900	TGCAAAACAGTACAGTCTGTTCTGTGAAAACCTGGGGAAGTGGCCACAGTGTGTG	125959	D	126980	AACCAAGCGTCCGTCGCGGCTGCGCTGTGTATGCGCATCTGTATGCTGTCTCCATTAAG	127039
Q	21061	GTTGCACCCGTAAGTCTTCTGTAGATCTTGGCGGGCGTGAACCTGGGCCCATTA	21120	Q	22141	CGCATCTGTCTCCTTAAACACGACGATGTGTTGTGAACAATGTGTATGTGACAGCGGCGC	22200
				D	127040	CGCATCTGTCTCCTTAAACACGACGATGTGTTGTGAACAATGTGTATGTGACAGCGGCGC	127099

OY	22201	GGCCAGGGGTCCTTGGACCTGTGACCTGTGAACCAAGTCCGTTGGAGATCTGTCCACGTG	22260
Db	127100	GGCCAGGGGGTCCCACTTGTGGCACTGTGTGAGCCAGAGTCCGTGTGGAGCATCTGTCCACGTG	127159
OY	22261	TCGGGTGACAAACTCTTTGTCGCCAACCGTGGACATGACACAGATGATGTGACACCGGA	22320
Db	127160	TCGGGTGACAAACTCTTTGTCGCCAACCGTGGACATGACACAGATGATGTGACACCGGA	127219
OY	22321	GGCCAGGGGTAATAGGCCCACTGCGTGGCGAGGGGTGCTTTGGCCACCATCTCCAG	22380
Db	127220	GGCCAGGGGTAATAGGCCCACTGCGTGGCGAGGGGTGCTTTGGCCACCATCTCCAG	127279
OY	22381	TTCTTTCTGGGGCACCAGCAGATTGGAGGAAACGGGGTCTGCTCGAACCACAAATTCG	22440
Db	127280	TTCTTTCTGGGGCACCAGCAGATTGGAGGAAACGGGGTCTGCTCGAACCACAAATTCG	127339
OY	22441	GATGACTTCGGGCCGATGTTGGGTGTCTGATTCGCCACAGCTCCCGGGTTCCACAGCTCCAG	22500
Db	127340	GATGACTTCGGGCCGATGTTGGGTGTCTGATTCGCCACAGCTCCCGGGTTCCACAGCTCCAG	127399
OY	22501	GTCGTTCCAGAACTCAATTCCACAGCTTTCCGACGTTTTCCCAAGACGGCGAAAGGCA	22560
Db	127400	GTCGTTCCAGAACTCAATTCCACAGCTTTCCGACGTTTTCCCAAGACGGCGAAAGGCA	127459
OY	22561	TCGCGAGATGGGTGGGGCCCTTCATGAGCATCCAAAGGGGCCGGTTCCGGGTCGGTGC	22620
Db	127460	TCGCGAGATGGGTGGGGCCCTTCATGAGCATCCAAAGGGGCCGGTTCCGGGTCGGTGC	127519
OY	22621	GCGGGGGAGACGGCCAAAGACACGACGACAGGACGATTGAGAAACTTTGTAACTAGAT	22680
Db	127520	GCGGGGGAGAGCGCCAAAGACACGACGACAGGACGATTGAGAAACTTTGTAACTAGAT	127579
OY	22681	GTCGTTCCAGGTTTCCCGTAGAGATGTCGCGGTGGCGGTCAGTTGGCTCAGAAATGGTTGG	22740
Db	127580	GTCGTTCCAGGTTTCCCGTAGAGATGTCGCGGTGGCGGTCAGTTGGCTCAGAAATGGTTGG	127639
OY	22741	TGGAAGCTGAGAGACAAAGAGGCGGAGCGCCGCCCGCGAGACAGGAGCTCCACAGTGGCC	22800
Db	127640	TGGAAGCTGAGAGACAAAGAGGCGGAGCGCCGCCCGCGAGACAGGAGCTCCACAGTGGCC	127699
OY	22801	GATGACAGAGCGGGTCTATGGGGCCGATTAATGCTGTGTAATAGGGGCCCTTCCAAAT	22860
Db	127700	GATGACAGAGCGGGTCTATGGGGCCGATTAATGCTGTGTAATAGGGGCCCTTCCAAAT	127759
OY	22861	CTCGTAAGCCACAGCGAAGCTTTGGGTATGCGGGTAAATACCTGGGGCCTCCCCAGTA	22920
Db	127760	CTCGTAAGCCACAGCGAAGCTTTGGGTATGCGGGTAAATACCTGGGGCCTCCCCAGTA	127819
OY	22921	AAGGAGCGCTGTGTCATGCGCTCAACGGGTTCAAAAGACCCAAAGACAGATGATAG	22980
Db	127820	AAGGAGCGCTGTGTCATGCGCTCAACGGGTTCAAAAGACCCAAAGACAGATGATAG	127879
OY	22981	CTGACTGAATAAAGACTCTCTGAGAAATGTGATGCTTGAGGACAGCAGATTAACGGGA	23040
Db	127880	CTGACTGAATAAAGACTCTCTGAGAAATGTGATGCTTGAGGACAGCAGATTAACGGGA	127939
OY	23041	TGTGTGTGTAATACGTTCCGCTGCTGGTGGCGCTGTGAGCGTTTAAAGAAAGCC	23100
Db	127940	TGTGTGTGTAATACGTTCCGCTGCTGGTGGCGCTGTGAGCGTTTAAAGAAAGCC	127999
OY	23101	ACCGAGGACAGCGCGCGGGTGGCGGACAGTGTGCGCATGAGAGTGTGGCTGTGTGT	23160
Db	128000	ACCGAGGACAGCGCGCGGGTGGCGGACAGTGTGCGCATGAGAGTGTGGCTGTGTGT	128059
OY	23161	AATAGCTTGTGGCGTGGCGAGAAATAGCCCTCACTGACGCGCTGATGGCTTAAATCC	23220
Db	128060	AATAGCTTGTGGCGTGGCGAGAAATAGCCCTCACTGACGCGCTGATGGCTTAAATCC	128119
OY	23221	ACACAGGCGCATCTGATTTGGCCCCCGGGCAGCAGCGTGGCATGGACAGATGTTTTG	23280
Db	128120	ACACAGGCGCATCTGATTTGGCCCCCGGGCAGCAGCGTGGCATGGACAGATGTTTTG	128179

QY	23282I	CAGGCGACCTGACACCTGTCTGAAATGGCCGCTGTGCAGGTGTGTAAATGAATCAGCTATATGTG	23340
Db	128180	CAGGCGACCTGACACCTGTCTGAAATGGCCGCTGTGCAGGTGTGTAAATGAATCAGCTATATGTG	128233
QY	23341I	GCTTAACGTTTTGCGACGCGAGGCGCTGTGAAAAAGCAGCTGTGTAGCTCTGCGGGCCATGAC	23400
Db	128240	GCTTAACGTTTTGCGACGCGAGGCGCTGTGAAAAAGCAGCTGTGTAGCTCTGCGGGCCATGAC	128299
QY	23401I	GGCGTATCTGGACACCGTATAGCTGTGTGCGTTGAGAGCCCTGCACGGCCAGCGGTAAATAT	23460
Db	128300	GGCGTATCTGGACACCGTATAGCTGTGTGCGTTGAGAGCCCTGCACGGCCAGCGGTAAATAT	128355
QY	23461I	GTTCGCTGTGTAAAGGGAGACATCAACCGCGCGCATATTTGGGTCTCTCTGGCGACAGCTCT	23520
Db	128360	GTTCGCTGTGTAAAGGGAGACATCAACCGCGCGCATATTTGGGTCTCTCTGGCGACAGCTCT	128411
QY	23521I	CCAGGCGGTGAGATTGCAAATGTCAACCGGGAGCTGGCCCTGCAGGGGACATCAATATTTCAC	23580
Db	128420	CCAGGCGGTGAGATTGCAAATGTCAACCGGGAGCTGGCCCTGCAGGGGACATCAATATTTCAC	128477
QY	23581I	TAGTGTGCCAAAGTGTCAAGGCGGCCCAAGGTGCCCGGGGTACCCGATCGGCGACAAACCG	23640
Db	128480	TAGTGTGCCAAAGTGTCAAGGCGGCCCAAGGTGCCCGGGGTACCCGATCGGCGACAAACCG	128533
QY	23641I	TCTGTGCTGGCAGCTCAGATGTCTGCCACCTCTAACCGCAAGTTCTATGAGGCGCCT	23700
Db	128540	TCTGTGCTGGCAGCTCAGATGTCTGCCACCTCTAACCGCAAGTTCTATGAGGCGCCT	128599
QY	23701I	GTCCTCTAAGGCACTGGCACTTTTCGGCTAAATCTGTGTGTAAGGTGGCGATCAGGTCGG	23760
Db	128600	GTCCTCTAAGGCACTGGCACTTTTCGGCTAAATCTGTGTGTAAGGTGGCGATCAGGTCGG	128655
QY	23761I	GCCATTAGGCGAGGAGTATAGTATGATGAGCCCTGTGAGAGTCCGGCGACCGAGTTTCCAGAG	23820
Db	128660	GCCATTAGGCGAGGAGTATAGTATGATGAGCCCTGTGAGAGTCCGGCGACCGAGTTTCCAGAG	128711
QY	23821I	TGCATTAATTAAACAGAGGCGCCAGANAGATGCAGATACGCCACGCTGGGTGCTCATC	23880
Db	128720	TGCATTAATTAAACAGAGGCGCCAGANAGATGCAGATACGCCACGCTGGGTGCTCATC	128777
QY	23881I	GTCGTTCTCAAGGTATCAGAGGGGGGTTCACAAAGCCAAATTAATTCATCTAAACGA	23940
Db	128780	GTCGTTCTCAAGGTATCAGAGGGGGGTTCACAAAGCCAAATTAATTCATCTAAACGA	128833
QY	23941I	CTGTTCGCGCAACAGCGCCCAAAACACTTCTGTGCTCGAATGTGCATGAATTAAGCCCTC	24000
Db	128840	CTGTTCGCGCAACAGCGCCCAAAACACTTCTGTGCTCGAATGTGCATGAATTAAGCCCTC	128899
QY	24001I	CTCTTCGAGCTAAAGGGCTGCAGCGGCCACGAGAGGTTCTGTGCTGGGCCATATTTTGC	24060
Db	128900	CTCTTCGAGCTAAAGGGCTGCAGCGGCCACGAGAGGTTCTGTGCTGGGCCATATTTTGC	128955
QY	24061I	TAACTCTAAGCGCGCGCAAAAGCAAGGGGGGTTCATTAATGAGGCGATATAGGGTCTTT	24120
Db	128960	TAACTCTAAGCGCGCGCGCAAAAGCAAGGGGGGTTCATTAATGAGGCGATATAGGGTCTTT	129011
QY	24121I	AGGATATCGGTTGGGAGACCGCTCATGTTCATGAGACTTCAATATTAAATTATATGTTAGTTT	24180
Db	129020	AGGATATCGGTTGGGAGACCGCTCATGTTCATGAGACTTCAATATTAAATTATATGTTAGTTT	129077
QY	24181I	TGGGCACTTGGGAGTGTACACTTATACCTTCCCCATGTCCACAGTAATCACTTGACAGA	24240
Db	129080	TGGGCACTTGGGAGTGTACACTTATACCTTCCCCATGTCCACAGTAATCACTTGACAGA	129133
QY	24241I	TCCGCTCTCAACATCAATCAACACTGTTTGGGGGTGTGAGGTTACAGGTTAAGGGTGGAGG	24300
Db	129140	TCCGCTCTCAACATCAATCAACACTGTTTGGGGGTGTGAGGTTAAGGTTAAGGGTGGAGG	129199
QY	24301I	GGAATGTTAGGTGGCGCAACCAAGCAATACGTTCGCGGGCGGGAGGTGGAGGCTGTAAAC	24360
Db	129200	GGAATGTTAGGTGGCGCAACCAAGCAATACGTTCGCGGGCGGGAGGTGGAGGCTGTGTAAAC	129255
QY	24361I	CCAGAGATGTCACTTAACGCTGTGTTAGCGGATGCACAACTACCTCCGAAAGTGTGTCGT	24420

D	129260	CCAGAGTGTCTACCTTACGTTGGTAGCGATCGACAACCTACCTCCGAAATGTGCTCTGT	129319	D	130340	CAATAGCTATAAAAAAGAGTANGTAAATAGTCTATTAAGTATTAACATTAACAA	130399
Q	24421	TGATGATTTTGTGATAGGTAAACAGAAAGTTGTGAGAAAGTAACCTTATAGATGAC	24480	Q	25501	AAATTAATAAATTAAATACCTGTATTGTCGGTAACCTATAGAGTATGATTAAGGTG	25560
D	129320	TGATGATTTTGTGATAGGTAAACAGAAAGTTGTGAGAAAGTAACCTTATAGATGAC	129379	D	130400	AAATTAATAAATTAAATACCTGTATTGTCGGTAACCTATAGAGTATGATTAAGGTG	130459
Q	24481	CTCTGCTGAGCGCTGCGTGGGTGACAGCTGTGTTGTGATGAATGAACACTTCTCTGGGC	24540	Q	25561	TAAAGCTGTGTTGTGATGTTTCTGTTAATGATTAAGGTGTCACAGTGTCTAAATTA	25620
D	129380	CTCTGCTGAGCGCTGCGTGGGTGACAGCTGTGTTGTGATGAATGAACACTTCTCTGGGC	129439	D	130460	TAAAGCTGTGTTGTGATGTTTCTGTTAATGATTAAGGTGTCACAGTGTCTAAATTA	130519
Q	24541	GTTTCTGGGGTGGTGGTGTGTTCTACTAAGGAGCGCCAACTACACTTCTCTCTCC	24600	Q	25621	AAATTAATGTAGTATTATTTTAAAGTTATCTATTCAGTAATTCAAAGTTGT	25680
D	129440	GTTTCTGGGGTGGTGGTGTGTTCTACTAAGGAGCGCCAACTACACTTCTCTCTCC	129499	D	130520	AAATTAATGTAGTATTATTTTAAAGTTATCTATTCAGTAATTCAAAGTTGT	130579
Q	24601	CGTTACAGCCGTGAGCGGTTTCGTCGTACGCTTGTGAGGGGGTGTGCTGAACCTT	24660	Q	25681	GTCATACCTGCTGTAATTTGCAACCAAGATTCATTTCTTGTATGTTGTTTCC	25740
D	129500	CGTTACAGCCGTGAGCGGTTTCGTCGTACGCTTGTGAGGGGGTGTGCTGAACCTT	129559	D	130580	GTCATACCTGCTGTAATTTGCAACCAAGATTCATTTCTTGTATGTTGTTTCC	130639
Q	24661	GTTTGTGTAAACAATCCAGGTTAACCGGTAATGCACGCGGTCAAGGGGATTTGTAA	24720	Q	25741	CATAGCCACATTAACCATTAACCAACATGGGATTTAAATTAATCTGCAACGCGAT	25800
D	129560	GTTTGTGTGTAAACAATCCAGGTTAACCGGTAATGCACGCGGTCAAGGGGATTTGTAA	129619	D	130640	CATAGCCACATTAACCATTAACCAACATGGGATTTAAATTAATCTGCAACGCGAT	130699
Q	24721	CCATAAAGCCATTAATTAAGCTTACAAAGCATTTTGTGTAAAGTTGTATTTAGCC	24780	Q	25801	ACTTTGATTTTGTGAGTCCACATTAAGAAATGCGTAAGTAACAGTACCTATCCATGT	25860
D	129620	CCATAAAGCCATTAATTAAGCTTACAAAGCATTTTGTGTAAAGTTGTATTTAGCC	129679	D	130700	ACTTTGATTTTGTGAGTCCACATTAAGAAATGCGTAAGTAACAGTACCTATCCATGT	130759
Q	24781	CCAAAGTTTATACAAAGCGAACTACTTACGATTAAGTAATGAACCAACGCAAGAGA	24840	Q	25861	GTTCCCAACAAGACATGATGTTGTTTACTAGAAACAATTTTGGTGGTTTATPACA	25920
D	129680	CCAAAGTTTATACAAAGCGAACTACTTACGATTAAGTAATGAACCAACGCAAGAGA	129739	D	130760	GTTCCCAACAAGACATGATGTTGTTTACTAGAAACAATTTTGGTGGTTTATPACA	130819
Q	24841	TAACTACTGATTTCTGTTCCAAATGTTGCAATTTAAGAAATGAGAGATTAATTTGCC	24900	Q	25921	AAATTAATATGCTTGAAAAATTAACAACAAGCTTAATTTAAGGCCAATATCATAGTAA	25980
D	129740	TAACTACTGATTTCTGTTCCAAATGTTGCAATTTAAGAAATGAGAGATTAATTTGCC	129799	D	130820	AAATTAATATGCTTGAAAAATTAACAACAAGCTTAATTTAAGGCCAATATCATAGTAA	130879
Q	24901	CGCTGAGAAATGCTGGAATTAAGAGGGGCTATTTAACATGTGTACAGGTGAAAAAC	24960	Q	25981	AAACAATTAAACAGGTAAAGATTAACGCTTACCATTAAGTAATTAATGATATGCGATGC	26040
D	129800	CGCTGAGAAATGCTGGAATTAAGAGGGGCTATTTAACATGTGTACAGGTGAAAAAC	129859	D	130880	AAACAATTAAACAGGTAAAGATTAACGCTTACCATTAAGTAATTAATGATATGCGATGC	130939
Q	24961	TGTGAGTTTCACTTGTAGTACCCCTGCAAGTAACCCGCTAGAGTGTGCAAGCGGTG	25020	Q	26041	AATAGCACTACAGCTGTGTACCAAAATTAATCTGCTGCTCCAAAGGCCAATGCGATAGTAA	26100
D	129860	TGTGAGTTTCACTTGTAGTACCCCTGCAAGTAACCCGCTAGAGTGTGCAAGCGGTG	129919	D	130940	AATAGCACTACAGCTGTGTGTACCAAAATTAATCTGCTGCTCCAAAGGCCAATGCGATAGTAA	130999
Q	25021	TGTGTTGCAAGAACTACATCTTAATTTTAACTCTTAAAGGGGTTCTTGTAAATTAATTT	25080	Q	26101	AACACAATGCTGTGCAACCAAGTACCAAAATTAATTAAGTTTAATTTGCTAATTAATTA	26160
D	129920	TGTGTTGCAAGAACTACATCTTAATTTTAACTCTTAAAGGGGTTCTTGTAAATTAATTT	129979	D	131000	AACACAATGCTGTGCAACCAAGTACCAAAATTAATTAAGTTTAATTTGCTAATTAATTA	131059
Q	25081	AAGTTATGTTGCTTACATTAATTAATTCAGATAGTACATCCCAAAAAAGATATCCGAT	25140	Q	26161	TATTTCAATATGTTTAAATTAATTAATTCAGATAGTACATCCCAAAAAAGATATCCGAT	26220
D	129980	AAGTTATGTTGCTTACATTAATTAATTCAGATAGTACATCCCAAAAAAGATATCCGAT	130039	D	131060	TATTTCAATATGTTTAAATTAATTAATTCAGATAGTACATCCCAAAAAAGATATCCGAT	131119
Q	25141	AAAATCGTGTATGTGAAGTTTGCACAAATGCAGCGGTGAGTAGGCCCAAAAAATGA	25200	Q	26221	GAGTTAATGACCTGCTGCTGCTGATTAACATTAACAACTAATAGTTTCCATTAAGAG	26280
D	130040	AAAATCGTGTATGTGAAGTTTGCACAAATGCAGCGGTGAGTAGGCCCAAAAAATGA	130099	D	131120	GAGTTAATGACCTGCTGCTGCTGATTAACATTAACAACTAATAGTTTCCATTAAGAG	131179
Q	25201	TAAACCTTAATGAGCAAAATTTTATTAAGTACGTTTGTATACGCAAAATTAATTTAA	25260	Q	26281	AACACAATGCTGTGCAACCAAGTACCAAAATTAATTAAGTTTAATTTGCTAATTAATTA	26340
D	130100	TAAACCTTAATGAGCAAAATTTTATTAAGTACGTTTGTATACGCAAAATTAATTTAA	130159	D	131180	AACACAATGCTGTGCAACCAAGTACCAAAATTAATTAAGTTTAATTTGCTAATTAATTA	131239
Q	25261	ATTAATACTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	25320	Q	26341	GTTTGTGCAAAAGCTTATTAACCAAAAGCTTAATTAAGAAAGTTTGAAGTAACCAACTAC	26400
D	130160	ATTAATACTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	130219	D	131240	GTTTGTGCAAAAGCTTATTAACCAAAAGCTTAATTAAGAAAGTTTGAAGTAACCAACTAC	131299
Q	25321	GTAATCTGATTTGTGAGGAACTGTATGATGCAAGCAAGCGCTTGCAATTAACCA	25380	Q	26401	TCCAAATTAATAAAGATATAGCTACAGCAATTTTAAATTAATCAAACTGATTAATCAAG	26460
D	130220	GTAATCTGATTTGTGAGGAACTGTATGATGCAAGCAAGCGCTTGCAATTAACCA	130279	D	131300	TCCAAATTAATAAAGATATAGCTACAGCAATTTTAAATTAATCAAACTGATTAATCAAG	131359
Q	25381	ATAGGCAATGTTCCATATTCGATATTCGCCATGCAATTTTAAAGTGCACAGCAATTCAG	25440	Q	26461	TTAAGGGGAGTTTGAAGCTTTTAAAGGTGTTTAAATGCTTTTCCAGCAAACTCACT	26520
D	130280	ATAGGCAATGTTCCATATTCGATATTCGCCATGCAATTTTAAAGTGCACAGCAATTCAG	130339	D	131360	TTAAGGGGAGTTTGAAGCTTTTAAAGGTGTTTAAATGCTTTTCCAGCAAACTCACT	131419
Q	25441	CAATAGCTATTAATAAAGATATGTTAATAGTCTATTAAGTATTAATAAATTAATAA	25500	Q	26521	GAGTCAACAAGAGTTTGTGTGCGCCGCTACGGAATCTGCTTAATGCTGATTTTGT	26580
D				D	131420	GAGTCAACAAGAGTTTGTGTGCGCCGCTACGGAATCTGCTTAATGCTGATTTTGT	131479

OY	26561	TGGCACCACCAAGAAATCATGTGAAAAAGCAGAGTGGGAAATATTTGTTTGTTCGTTG	26640
Db	1314480	TGGCACCACCAAGAAATCATGTGAAAAAGCAGAGTGGGAAATATTTGTTTGTTCGTTG	1315399
OY	26641	GCGTGGATGCGTTGGAAACATTCCTGTTATTTGATGTTTGGGCCAAACGTGGAAAAATT	26700
Db	1315450	GCGTGGATGCGTTGGAAACATTCCTGTTATTTGATGTTTGGGCCAAACGTGGAAAAATT	1315999
OY	26701	AAGAGTTGTTATTTGAAAAATATTTTTTGGTAAACAAAACCATGTTTTAGTCCCAAGGAA	26760
Db	131600	AAGAGTTGTTATTTGAAAAATATTTTTTGGTAAACAAAACCATGTTTTAGTCCCAAGGAA	1316599
OY	26761	CATAAAATGTTTTATAGAAACATCCTGATGACAAATTTTGTGTTAGTAACTA	26820
Db	131660	CATAAAATGTTTTATAGAAACATCCTGATGACAAATTTTGTGTTAGTAACTA	1317199
OY	26821	AAAAATGTATGTTAAGGCGTTAGGCGTTAAGGCGCAAGGCGTTAAGGCGTTAAGGCGCA	26880
Db	131720	AAAAATGTATGTTAAGGCGTTAAGGCGTTAAGGCGCAAGGCGTTAAGGCGTTAAGGCGCA	1317799
OY	26881	AGCGGTTAAGGCGCAAGGCGTTAAGGCGCAAGGCGTTAAGGCGCAAGGCGTTA	26940
Db	131780	AGCGGTTAAGGCGCAAGGCGTTAAGGCGCAAGGCGTTAAGGCGCAAGGCGTTA	1318399
OY	26941	GGGCAAGGGGTAAAGGCAAGGGGTAAAGGCAAGGGGTAAAGGGGTAAAGGGCTAGG	27000
Db	131840	GGGCAAGGGGTAAAGGCGCAAGGGGTAAAGGGCAAGGGGTAAAGGGGTAAAGGGCTAGG	1318999
OY	27001	GGTAAAGGCTAAGGGGTAAAGGGCTAAGGGGTAGCTAAGGGGTAAAGGTTATAGT	27060
Db	131900	GGTAAAGGCTAAGGGGTAAAGGGCTAAGGGGTAGCTAAGGGGTAAAGGTTATAGT	1319599
OY	27061	GTAATAATATAGGCGCTAGCATTAATATGTCACATATTTTTTAAATTTGTTGTTCACTAA	27120
Db	131960	GTAATAATATAGGCGCTAGCATTAATATGTCACATATTTTTTAAATTTGTTGTTCACTAA	1320199
OY	27121	CAGCCATGCTGATTTAGATGAAGTTAAAGCTTCATATCAATATACAAAGTAAAGTAA	27180
Db	132020	CAGCCATGCTGATTTAGATGAAGTTAAAGCTTCATATCAATATATACAAAGTAAAGTAA	1320799
OY	27181	CCACAGCAATTTATACATATTTTACAAAAAGCAACCACTGGCCATGTAACTTACGC	27240
Db	132080	CCACAGCAATTTATACATATTTTACAAAAAGCAACCACTGGCCATGTAACTTACGC	1321399
OY	27241	TACCTTAAACGTACATACTGGGAGTAGAACCCAGAGGTAGTTAGAAATATACGGTAGTTA	27300
Db	132140	TACCTTAAACGTACATACTGGGAGTAGAACCCAGAGGTAGTTAGAAATATACGGTAGTTA	1321999
OY	27301	CAGAACTTTGCACTTCCTTAGAGCCAGCAGGGCTCTGCGGTTATTTAAACAAAGTTAAA	27360
Db	132200	CAGAACTTTGCACTTCCTTAGAGCCAGCAGGGCTCTGCGGTTATTTAAACAAAGTTAAA	1322599
OY	27361	GATTACTGAACCTTTAGGAAGTGCATATGGGTGCATATGTTTCCAAATAGGGCAAGGGTT	27420
Db	132260	GATTACTGAACCTTTAGGAAGTGCATATGGGTGCATATGTTTCCAAATAGGGCAAGGGTT	1323199
OY	27421	ACATAAACGTTGCGCTAGCGGCGGAGAGGCGCCGCGCGCGCGCGCGCGCGCGCG	27480
Db	132320	ACATAAACGTTGCGCTAGCGGCGGAGAGGCGCCGCGCGCGCGCGCGCGCGCGCGCG	1323799
OY	27481	GCGGCGCGCATTTTGGCGCCGGGGGCGAGGGTCCCGCGCGCGCCCGCGCGCGCGCG	27540
Db	132380	GCGGCGCGCATTTTGGCGCCGGGGGCGAGGGTCCCGCGCGCGCCCGCGCGCGCGCGCG	1324399
OY	27541	GGGCGCGCGCGCTCCCGCGGCTCCCGGCTCCCGGCTCCCGGCTCCCGGCGCGCGCGCG	27600
Db	132440	GGGCGCGCGCGCTCCCGCGGCTCCCGGCTCCCGGCTCCCGGCTCCCGGCGCGCGCGCG	1324999
OY	27601	GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTTTCGGGTTGCGGGGCGGGGGGT	27660
Db	132500	GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTTTCGGGTTGCGGGGCGGGGGGT	1325599

QY	27661	CCGCGGAGGGGCGCGGGGCGCGCCCGGGGTCGCGCTCCGCGGGGCCCGACATCCGGG	27720
Db	132560	CCGCGGGGGGGCGGGGGCGCGCCCGGGGTCGCGCTCCGCGGGGCCCGACATCCGGG	132611
QY	27721	AGCGCCCCGGTCCGGCGGAGCCCGGGGGGCGCGGCCCGGAGCGCCCGGGGCCGGGGC	27780
Db	132620	AGCGCCCCGGTCCGGCGGAGCCCGGGGGGCGCGGCCCGGAGCGCCCGGGGCCGGGGC	132677
QY	27781	CCCAAGCCGCGCGCGCGGCTCCGATGCGGGGCGCGCCCGCGCGGCATATGGCGTCC	27840
Db	132680	CCCAAGCGCGGGGCGCGGGGCTCCGATATCGGGGGGCGCGCCCGCGGCATATGGCGTCC	132733
QY	27841	TCGCGCGGCTCCCTCCCGACGCGCGCCCGAAAGTGTCTCCGCGCGCGCGGAGGG	27900
Db	132740	TCGCGCGGCTCCCTCCCGACGCGCGCCCGAAAGTGTCTCCGCGCGCGCGGAGGG	132799
QY	27901	GGGCGGGGGGCGGGGGGCGCTCGGGGGGGGCGCGGGCGGGGGGCGACAGAGGGCCCGGG	27960
Db	132800	GGGCGGGGGGCGGGGGGCGCTCGGGGGGGGCGCGGGCGGGGGGCGACAGAGGGCCCGGG	132855
QY	27961	AGAACGGGGGATCGGGAAAAACGGAGGGGAGCGGGGACAGAGGAGCGGCTGTCCGCTCT	28020
Db	132860	AGAACGGGGGATCGGGAAAAACGGAGGGGAGCGGGGAGACAGGGGACGGCGTGTCCGCTCT	132921
QY	28021	TGTGAGACACCGGGTACGGGCTGCTTCCTCTGTCCGCTGCGCTCTTGTGAGGGACAGTA	28080
Db	132920	TGTGAGACACCGGGTACGGGCTGCTTCCTCTGTCCGCTGCGCTCTTGTGAGGGACAGTA	132977
QY	28081	GGCGCTGTCTCGGCTGGCGCTGCTTGTCTAGGGGACAGTAAAGGCTGTGTGCGAGGGGAC	28140
Db	132980	GGCGCTGTCTCGGCTGGCGCTGCTTGTCTAGGGGACAGTAAAGGCTGTGTGCGAGGGGAC	133033
QY	28141	AGTAAAGGCTGTGCTCCGCTGCGGCTGCTTGTCTGAGAGGGACAGTAAAGGCTGTGCTTCT	28200
Db	133040	AGTAAAGGCTGTGCTCCGCTGCGGCTGCTTGTCTGAGAGGGACAGTAAAGGCTGTGCTTCT	133099
QY	28201	AGTAAAGGCTGTGCTGGGCTGCTTGTCTGTCCGCTGCGCTCTTGTGCTGCTGCTGGCC	28260
Db	133100	AGTAAAGGCTGTGCTGGGCTGCTTGTCTGTCCGCTGCGCTCTTGTGCTGCTGCTGGCC	133155
QY	28261	TGCTTGTCTCGGCTGGGCTGCTTGTGTGTGCTGCGGGCGCTGTGCTTGTGCTGGGCGC	28320
Db	133160	TGCTTGTCTCGGCTGGGCTGCTTGTGTGTGCTGCGGGCGCTGTGCTTGTGCTGGGCGC	133211
QY	28321	TGCTTGTCTCGGCTGGGCTGCTTGTGTGCTGCGGCGCTGTGCTGAGGGGACAGTA	28380
Db	133220	TGCTTGTCTCGGCTGGGCTGCTTGTGTGCTGCGGCGCTGTGCTGAGGGGACAGTA	133277
QY	28381	GGGCTGCTTGTCTGTAAAGGGGACGCTAGCGCTGTATGAGGGCTGCT	28440
Db	133280	GGGCTGCTTGTCTGTAAAGGGGACGCTAGCGCTGTATGAGGGCTGCT	133333
QY	28441	GGGCTGCTAGTAGGGCTGCTGGGCTGCTAGTAGGGCTGCTGGGCTGCTAGTAGGGCTGCT	28500
Db	133340	GGGCTGCTAGTAGGGCTGCTGGGCTGCTAGTAGGGCTGCTGGGCTGCTAGTAGGGCTGCT	133399
QY	28501	GGGCTGCTAGTAGGGGCTCGGGGCTGCTAGTAGGGCTGCTGGGAGCTAGTAGGGGCTGCT	28560
Db	133400	GGGCTGCTAGTAGGGGCTCGGGGCTGCTAGTAGGGCTGCTGGGAGCTAGTAGGGGCTGCT	133455
QY	28561	GGGCTGCTAGTAGGGCTGCTGGGCTGCTAGTAGGGCTGCTGGGCTGCTAGTAGGGCTGCT	28620
Db	133460	GGGCTGCTAGTAGGGGCTCGGGGCTGCTAGTAGGGCTGCTGGGCTGCTAGTAGGGCTGCT	133511
QY	28621	GGGCTGCTAGTAGGGCTGCTGGCTGCTGTGCTTGTGCTAGTAGGGGCGCTTCC	28680
Db	133520	GGGCTGCTAGTAGGGGCTCGCTGCTGCTTGTGCTTGTGCTAGTAGGGGCGCTTCC	133577
QY	28681	TGTCTACTAAGGGCTGTGTGAGCTGGGAGAAACAGATAGGGCTGCGCGGCGACATCTCGTGC	28740
Db	133580	TGTCTACTAAGGGCTGTGTGAGCTGGGAGAAACAGATAGGGCTGCGCGGCGACATCTCGTGC	133633
QY	28741	GAGGGGCTTCGAGGGGCGACAGAGACAGGGGACCGGGGCTGTCCCGCGCGCGGACCGC	28800

```

Db      133640 GAGGGGCTCCGAGGGCCAGACGAGACCGGGGCTCTCCCGCCGAGACCGC 133699
Oy      28801  CGGGCACCGCGCCAGATCT 28820
Db      133700 CGGGCACCGCGCCAGATCT 133719

RESULT 3
AA164291/c
ID  AA164291 standard; DNA; 128139 BP.
XX
AC  AA164291;
XX
DT  22-APR-2002 (first entry)
XX
DE  RRV genome nucleotide sequence.
XX
KM  RRV; rhesus rhadinovirus; japanese macaque virus; multiple sclerosis;
KM  JMHV; cytosstatic; antiasclmatic; antiallergic; dermatological;
KM  vulninary; gene therapy; leucopenia; thrombocytopaenia;
KM  inflammatory disease; asthma; allergy; dermatitis; virus; ds.
XX
OS  Macaca mulatta rhadinovirus 17577.
XX
FH  Key
FT  CDS
    Location/Qualifiers
    1353..2674
    /tag= a
    /product= "RRV R1"
    complement (2692..3258)
    /tag= b
    /product= "dihydrofolate reductase"
    /label= RRV_ORF2
    /note= "has similarity to Kaposi's sarcoma-associated
    virus (KSHV) open reading frame (ORF) 2"
    3676..5613
    /tag= c
    /product= "complement binding protein"
    /label= RRV_ORF4
    /note= "has similarity to KSHV ORF4"
    6045..9443
    /tag= d
    /product= "ssDNA binding protein"
    /label= RRV_ORF6
    /note= "has similarity to KSHV ORF6"
    9468..11528
    /tag= e
    /product= "transport protein"
    /label= RRV_ORF7
    /note= "has similarity to KSHV ORF7"
    11515..14004
    /tag= f
    /product= "glycoprotein B"
    /label= RRV_ORF8
    /note= "has similarity to KSHV ORF8"
    14122..17166
    /tag= g
    /product= "DNA polymerase protein"
    /label= RRV_ORF9
    /note= "has similarity to KSHV ORF9"
    17261..18511
    /tag= h
    /label= RRV_ORF10
    /note= "has similarity to KSHV ORF10"
    18520..19749
    /tag= i
    /label= RRV_ORF11
    /note= "has similarity to KSHV ORF11"
    complement (19921..20544)
    /tag= j
    /product= "RRV R2"
    /label= RRV_ORF
    /note= "has similarity to KSHV Interleukin (IL)-6 gene"
    FT

```

```

FT  CDS
    complement (20777..21778)
    /tag= k
    /product= "thymidylate synthase"
    /label= RRV_ORF70
    /note= "has similarity to KSHV ORF70"
    complement (22245..22592)
    /tag= l
    /product= "RRV R3"
    /note= "has similarity to KSHV R4 viral MIP gene"
    26846..27409
    /tag= m
    /product= "Bcl2-homologue"
    /label= RRV_ORF16
    /note= "has similarity to KSHV ORF16"
    complement (27515..29125)
    /tag= n
    /label= RRV_ORF17
    /note= "has similarity to KSHV ORF17"
    28998..29897
    /tag= o
    /label= RRV_ORF18
    /note= "has similarity to KSHV ORF18"
    complement (29905..31548)
    /tag= p
    /product= "tegument protein"
    /label= RRV_ORF19
    /note= "has similarity to KSHV ORF19"
    complement (31043..32095)
    /tag= q
    /label= RRV_ORF20
    /note= "has similarity to KSHV ORF20"
    32094..33767
    /tag= r
    /product= "thymidine kinase"
    /label= RRV_ORF21
    /note= "has similarity to KSHV ORF21"
    33754..35868
    /tag= s
    /product= "glycoprotein H"
    /label= RRV_ORF22
    /note= "has similarity to KSHV ORF22"
    complement (35865..37073)
    /tag= t
    /label= RRV_ORF23
    /note= "has similarity to KSHV ORF23"
    complement (37123..39321)
    /tag= u
    /label= RRV_ORF24
    /note= "has similarity to KSHV ORF24"
    39323..43459
    /tag= v
    /product= "major capsid protein"
    /label= RRV_ORF25
    /note= "has similarity to KSHV ORF25"
    43491..44408
    /tag= w
    /product= "capsid protein"
    /label= RRV_ORF26
    /note= "has similarity to KSHV ORF26"
    44433..45242
    /tag= x
    /label= RRV_ORF27
    /note= "has similarity to KSHV ORF27"
    45408..45683
    /tag= y
    /label= RRV_ORF28
    /note= "has similarity to KSHV ORF28"
    complement (45733..46779)
    /tag= z
    /label= RRV_ORF29b
    /note= "has similarity to KSHV ORF29b"
    46905..47135
    /tag= aa
    FT  CDS

```

```

FT /label- RRV_ORF30
FT /note- "has similarity to KSHV ORF30"
FT CDS
FT /tag- ab
FT /label- RRV_ORF31
FT /note- "has similarity to KSHV ORF31"
FT CDS
FT /tag- ac
FT /label- RRV_ORF32
FT /note- "has similarity to KSHV ORF32"
FT CDS
FT /tag- ad
FT /label- RRV_ORF33
FT /note- "has similarity to KSHV ORF33"
FT CDS
FT /tag- ae
FT /label- RRV_ORF29a
FT /note- "has similarity to KSHV ORF29a"
FT CDS
FT /tag- af
FT /label- RRV_ORF34
FT /note- "has similarity to KSHV ORF34"
FT CDS
FT /tag- ag
FT /label- RRV_ORF35
FT /note- "has similarity to KSHV ORF35"
FT CDS
FT /tag- ah
FT /product- "kinase"
FT /label- RRV_ORF36
FT /note- "has similarity to KSHV ORF36"
FT CDS
FT /tag- ai
FT /product- "alkaline exonuclease"
FT /label- RRV_ORF37
FT /note- "has similarity to KSHV ORF37"
FT CDS
FT /tag- aj
FT /label- RRV_ORF38
FT /note- "has similarity to KSHV ORF38"
FT CDS
FT /tag- ak
FT /product- "glycoprotein M"
FT /label- RRV_ORF39
FT /note- "has similarity to KSHV ORF39"
FT CDS
FT /tag- al
FT /product- "helicase/primase"
FT /label- RRV_ORF40
FT /note- "has similarity to KSHV ORF40"
FT CDS
FT /tag- am
FT /product- "helicase/primase"
FT /label- RRV_ORF41
FT /note- "has similarity to KSHV ORF41"
FT CDS
FT /tag- an
FT /product- "helicase/primase"
FT /label- RRV_ORF42
FT /note- "has similarity to KSHV ORF42"
FT CDS
FT /tag- ao
FT /product- "capsid protein"
FT /label- RRV_ORF43
FT /note- "has similarity to KSHV ORF43"

```

Query Match 0.1%; Score 33; DB 24; Length 128139;
 Best Local Similarity 100.0%; Pred. No. 0.00036;
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12644 ATATATATAGGAACTGTAAACAACCAAC 12676
 DB 18331 ATATATATAGGAACTGTAAACAACCAAC 18299

```

RESULT 4
AAC64754/C
ID AAC64754 standard; DNA; 133719 BP.
XX
XX AAC64754;
AC
XX 28-FEB-2001 (first entry)
DE
XX Macaca mulatta rhadinovirus 17577 (RRV) genome sequence SEQ ID NO:1.
XX
XX Macaca mulatta rhadinovirus 17577; RRV; rhesus macaque rhadinovirus;
XX genome; Kaposi's sarcoma-associated herpesvirus; KSHV; interleukin 6;
XX IL-6; macrophage inflammatory protein; MIP; diagnosis; vaccine;
XX cytostatic; anti-HIV; gene therapy; infection; Kaposi's sarcoma;
XX lymphoproliferative disorder; B-cell hyperplasia; lymphadenopathy;
XX splenomegaly; hypergammaglobulinemia; autoimmune haemolytic anaemia;
XX ds.
XX
XX Macaca mulatta rhadinovirus 17577.
XX
XX WO200028040-A2.
XX
XX 18-MAY-2000.
XX
XX 05-NOV-1999; 99WO-US26260.
XX
XX 06-NOV-1998; 98US-0107507.
XX 20-NOV-1998; 98US-0109409.
XX
XX (UYOR-) UNIV OREGON HEALTH SCI.
XX
XX Wong SW, Axthelm MK, Searles RP;
XX WPT. 2000-376552/32.
XX
XX New rhesus rhadno virus for producing non-human primate model useful
XX for testing potential treatments and efficacy of the candidate vaccine
XX for conditions associated with RRV infection
XX
XX Claim 2; Page 83-122; 141pp; English.
XX
XX The present invention describes a novel rhesus macaque rhadinovirus
XX called macaca mulatta rhadinovirus 17577 (RRV). AAC64754 represents the
XX RRV genome sequence, and AAB53123 to AAB53204 represent the proteins
XX encoded by the genome sequence. The present invention also specifically
XX claims the individual open reading frame (ORF) nucleotide sequences from
XX the genome which encode the individual proteins, but these sequences are
XX not given. A non-human animal infected with RRV can be used for testing
XX the efficacy of drug in the treatment of condition associated with
XX infection with RRV such as Kaposi's sarcoma, lymphoproliferative
XX disorders, B-cell hyperplasia, lymphadenopathy, splenomegaly,
XX hypergammaglobulinemia or autoimmune haemolytic anaemia, by
XX administering the drug to a immuno-compromised non-human primate
XX preferably Rhesus macaque monkey obtained by as a result of infection
XX by Simian Immunodeficiency Virus (SIV). RRV is useful for producing
XX non-human primate model for testing potential treatments for conditions
XX associated with RRV infection. It is also useful for testing the
XX efficacy of the candidate vaccine against RRV infection or conditions
XX associated with its infection by administering the vaccine to the
XX CC subject capable of infection with RRV, inoculating the subject with RRV
XX CC and observing the effect of vaccine. AAC64755 to AAC64765 and AAB53205
XX CC to AAB53213 represent sequence used in the exemplification of the
XX CC present invention.
XX
XX Sequence 133719 BP; 32746 A; 35648 C; 34521 G; 30804 T; 0 other;
SQ

```

Query Match 0.1%; Score 33; DB 21; Length 133719;
 Best Local Similarity 100.0%; Pred. No. 0.00036;
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12644 ATATATATAGGAACTGTAAACAACCAAC 12676
 DB 18331 ATATATATAGGAACTGTAAACAACCAAC 18299

DB 23911 ATATATATGGAGACTTGTAACAAACCCAC 23879

RESULT 5
AAC81583/c
ID AAC81583 standard; DNA; 3571 BP.
XX
XX AAC81583;
XX
XX 09-MAR-2001 (first entry)
XX
XX Mouse zvegf3 DNA, SEQ ID NO:34.
DE
XX
XX Mouse; zvegf3; zvegf4 fusion; growth factor homologue; VEGF/PDGF family;
KM murine; CUB domain; PDGF-like activity; mitogenic; osteogenic;
KM neovascularisation; tissue repair; proliferation; differentiation;
KM liver damage; neurodegenerative; Alzheimer's disease; multiple sclerosis;
KM periodontal disease; bone fracture; wound healing; vulnerrary; ischaemia;
KM immunomodulation; hepatic; ds.
XX
XX Mus musculus.
XX
XX WO200066736-A1.
XX
XX 09-NOV-2000.
XX
XX 03-MAY-2000; 2000MO-US40047.
XX
XX 03-MAY-1999; 99US-0304216.
XX 10-NOV-1999; 99US-0164463.
XX 04-FEB-2000; 2000US-0180169.
XX
XX (ZYMO) ZYMOGENETICS INC.
XX
XX Gilbert T, Hart CE, Sheppard PO, Gilbertson DG;
PI
PI WPI: 2000-687541/67.
DR P-PSDB; AAB48658.
XX
XX Growth factor homologs and the nucleic acids that encode them, useful
PT e.g. for treating liver damage, ischemia, multiple sclerosis and
PT Alzheimer's disease -
XX
XX Disclosure: Page 127-130; 143pp; English.

The invention relates to the human growth factor homologue zvegf4 (AAB48653), and nucleic acids encoding it (AAC81555). zvegf4 is a member of the PDGF (platelet-derived growth factor)/VEGF (vascular endothelial growth factor) family. zvegf4 has a growth factor domain (AAB48654) characterised by a PDGF cystine knot structure, and a CUB domain (AAB48655) which has a beta barrel structure. zvegf4 has PDGF-like activity, having mitogenic activity on fibroblasts, vascular smooth muscle cells and pericytes, and has also been shown to stimulate bone growth. The invention also relates to fusion proteins comprising human zvegf4 or fragments thereof, particularly human zvegf4/human zvegf3 fusions; expression constructs and host cells comprising human zvegf4 nucleic acids; the recombinant expression of human zvegf4; an antibody which binds to human zvegf4 or a fragment thereof; a method of activating a cell-surface PDGF receptor using a zvegf4-derived polypeptide; a method of modulating the proliferation, differentiation, migration or metabolism of bone cells, comprising exposing bone cells to zvegf4-derived polypeptides; and a method of detecting a genetic abnormality in the zvegf4 gene of a patient. zvegf4 proteins and derived fragments may be used to stimulate tissue development or repair, or cellular differentiation or proliferation. They are particularly used for the treatment or repair of liver damage, and may also be used to modulate neurite growth (e.g., in the treatment of Alzheimer's disease or multiple sclerosis). Due to their osteogenic activity, they may be used in the treatment of periodontal disease and fractures. They may also be used to enhance expansion and mobilisation of haematopoietic stem cells and endothelial precursor stem cells, which may be useful in the treatment of ischemia, in wound healing, and in the modulation of the immune system. The present sequence represents DNA encoding mouse

CC zvegf3.
XX
XX Sequence 3571 BP; 876 A; 935 C; 875 G; 885 T; 0 other;
SQ
Query Match 0.1%; Score 28; DB 21; Length 3571;
Best Local Similarity 100.0%; Pred. No. 0.081;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 16376 GCGCGCGCGCGCGCGCGCGCGCGCG 16403
DB 184 GCGCGCGCGCGCGCGCGCGCGCGCGCG 157

RESULT 6
AAA51527/c
ID AAA51527 standard; cDNA; 3571 BP.
XX
XX AAA51527;
AC
XX 26-SEP-2000 (first entry)
DT
XX
XX Murine vascular endothelial growth factor homologue, ZVEGF3 DNA.
DE
XX
XX Vascular endothelial growth factor; homologue; zvegf3; CUB domain;
KM Cystine knot; platelet-derived growth factor; PDGF; neuropilin;
KM chromosome 4q28.3; cytoskeletal; anti-psoriatic; anti-inflammatory;
KM anti-diabetic; ophthalmological; anti-rheumatic; anti-arthritic;
KM vulnerrary; ss.
XX
XX Mus musculus.
XX
XX
FH Key Location/Qualifiers
FT CDS 1049..2086
FT /tag= a
FT /product= ZVEGF3
XX
XX WO200034474-A2.
XX
XX 15-JUN-2000.
XX
XX 07-DEC-1999; 99MO-US28968.
XX
XX 07-DEC-1998; 98US-0207120.
XX 06-JUL-1999; 99US-0142576.
XX 21-OCT-1999; 99US-0161653.
XX 12-NOV-1999; 99US-0165255.
XX
XX (ZYMO) ZYMOGENETICS INC.
XX
XX Gao Z, Hart CE, Piddington CS, Sheppard PO, Shoemaker KE;
PI Gilbertson DG, West JW;
PI
XX
XX WPI: 2000-423420/36.
DR P-PSDB; AAY96861.
XX
XX Novel zvegf3 polypeptides and nucleotides encoding them useful for
PT stimulating growth of smooth muscle cells and fibroblasts comprising an
PT epitope bearing portion of a specific amino acid sequence
XX
XX Claim 30; Page 166-169; 173pp; English.

This DNA encodes murine ZVEGF3 a novel vascular endothelial growth factor homologue. Polypeptides comprising an epitope-bearing portion human or murine ZVEGF3 are claimed. The growth factors comprise a growth factor domain and a CUB domain (generic sequence motifs are shown in AAY96859 and AAY96860). The growth factor domain is characterized by an arrangement of cysteine residues and beta-strands that is characteristic of the "cystine knot" structure of the platelet-derived growth factor (PDGF) family. The CUB domain shows homology to CUB domains in neuropilins, human bone morphogenetic protein-1, porcine seminal plasma protein, bovine acidic seminal fluid protein and Xenopus laevis tolloid-like protein. Structural analysis and homology predict that ZVEGF3 polypeptides complex with a second polypeptide to form multimeric

CC proteins. The human zvegf3 gene has been mapped to chromosome 4q28.3.
CC ZVGF3 is useful for stimulating the growth of fibroblasts or smooth
CC muscle cells, for activating cell surface PDGF- α receptor and for
CC inhibiting PDGF- α receptor mediated cellular processes. ZVEGF3 is
CC useful for regulating (post-development) organ growth, regeneration and
CC maintenance, as well as tissue maintenance and repair processes. ZVEGF3
CC antagonists are useful for treating cancer, rheumatoid arthritis,
CC diabetic retinopathy, ischemic limb disease, peripheral vascular
CC disease, myocardial ischemia, vascular intimal hyperplasia,
CC atherosclerosis, wound healing, chronic liver disease and haemangioma
CC formation. ZVEGF3 can also be used to modulate neurite growth and
CC development of the nervous system, and for treating neurodegenerative
CC diseases.
CC XX
SQ Sequence 3571 BP; 876 A; 935 C; 875 G; 885 T; 0 other;
Query Match 0.1%; Score 28; DB 21; Length 3571;
Best Local Similarity 100.0%; Pred. No. 0.081;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 16376 GCGGGCGCGGGGGCGGGGGCGCG 16403
Db 184 GCGGGCGCGGGGGCGGGGGCGCGCG 157
RESULT 7
AAD04650/c
ID AAD04650 standard; DNA: 3571 BP.
AC AAD04650;
XX 04-JUL-2001 (first entry)
DT
DE Mouse zvegf3 DNA.
XX
XX Mouse; zvegf3 antagonist; cell proliferation; stellate cell activation;
KW extracellular matrix production; fibrosis; VEGF-R; PDGF-C;
KW platelet-derived growth factor; PDGF; vascular endothelial growth factor;
KW VEGF; mitogenic effect; therapy; keloid; scleroderma; fibrotic disorder;
KW chronic active hepatitis; fulminant viral hepatitis; amyloidosis;
KW diabetic nephropathy; alpha-1-antitrypsin deficiency; silicosis;
KW asbestosis; renal arteriosclerosis; post necrotic cirrhosis;
KW diabetic glomerulosclerosis; focal glomerulosclerosis; hyperostosis;
KW pulmonary hypertension; idiopathic pulmonary fibrosis; osteopetrosis;
KW bronchiolitis obliterans-organising pneumonia; transplant vasculopathy;
KW fibropoliferative disorder; ds.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT CDS 1049..2086
FT /tag= a
FT /product= "Mouse zvegf3 protein"
XX
XX WO200128586-A1.
XX
XX 26-APR-2001.
XX
XX 23-OCT-2000; 2000WO-US29270.
XX
XX 21-OCT-1999; 99US-0161653.
XX 12-NOV-1999; 99US-0165255.
XX 01-AUG-2000; 2000US-0222223.
XX
XX (ZYMO) ZYMOGENETICS INC.
XX
XX Glibertson DG;
XX
XX WPI; 2001-300278/31.
XX P-PSDB; AAE00998.
XX
XX Use of zvegf3 antagonist for reducing fibropoliferative disorder of
PT kidney, liver and bone, reducing extracellular matrix production,

PT treating fibrosis or reducing stellate cell activation in mammal -
XX
XX Example 2; Page 58-61; 70pp; English.
XX
CC The patent discloses materials and methods for reducing cell
CC proliferation or extracellular matrix production, treating fibrosis and
CC reducing stellate cell activation in a mammal. The method comprises
CC administering a composition containing a zvegf3 antagonist in combination
CC with a delivery vehicle. The zvegf3 is a protein that is structurally
CC related to platelet-derived growth factor (PDGF) and the vascular
CC endothelial growth factors (VEGF). The zvegf3 protein is also designated
CC as "VEGF-R" and "PDGF-C". The zvegf3 antagonist is useful to block the
CC mitogenic effects of zvegf3 and thereby to inhibit or prevent and treat
CC keloids, scleroderma, fibrotic disorders of liver such as chronic active
CC hepatitis, fulminant viral hepatitis, post necrotic cirrhosis and
CC alpha-1-antitrypsin deficiency, fibrotic disorders of the kidney such as
CC diabetic glomerulosclerosis, focal glomerulosclerosis, diabetic
CC nephropathy, amyloidosis and renal arteriosclerosis, fibrotic disorders
CC of the lung such as silicosis, asbestosis, idiopathic pulmonary fibrosis,
CC bronchiolitis obliterans-organising pneumonia and pulmonary hypertension,
CC fibrotic disorders of pancreas, fibropoliferative disorders of the
CC vasculature such as transplant vasculopathy and fibropoliferative
CC disorders of the bone such as osteopetrosis and hyperostosis.
CC The present sequence is mouse zvegf3 DNA.
CC XX
SQ Sequence 3571 BP; 876 A; 935 C; 875 G; 885 T; 0 other;
Query Match 0.1%; Score 28; DB 22; Length 3571;
Best Local Similarity 100.0%; Pred. No. 0.081;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 16376 GCGGGCGCGGGGGCGGGGGCGCGCG 16403
Db 184 GCGGGCGCGGGGGCGGGGGCGCGCGCG 157
RESULT 8
ABS68648/c
ID ABS68648 standard; cDNA: 3571 BP.
AC ABS68648;
XX
XX 19-NOV-2002 (first entry)
DT
DE Mouse cDNA encoding VEGF-like protein zvegf 3.
XX
XX ss; gene; VEGF; vascular endothelial growth factor; zvegf 3;
KW chromosome 3; cell proliferation; differentiation; metabolism;
KW migration; revascularisation; solid tumour; diabetic retinopathy;
KW psoriasis; rheumatoid arthritis; cancer; autoimmune disease;
KW inflammation; myocardial ischaemia; scleroderma; fibrosis; mouse;
KW glomerulosclerosis; atherosclerosis; skin wound; ulcer; burn;
KW skin grafting; female reproductive tract disorder; chronic liver disease;
KW ciliary disorder; heart failure; neurodegenerative disease;
KW multiple sclerosis; Parkinson's disease; Alzheimer's disease; stroke;
KW neurite outgrowth.
XX
OS Mus musculus.
XX
XX US6432673-B1.
XX
XX 13-AUG-2002.
XX
XX 07-DEC-1999; 99US-0457066.
XX
XX 07-DEC-1998; 98US-111173P.
XX 06-JUL-1999; 99US-142576P.
XX 21-OCT-1999; 99US-161653P.
XX 12-NOV-1999; 99US-165255P.
XX
XX (ZYMO) ZYMOGENETICS INC.
XX
XX Gao Z, Hart CE, Piddington GS, Sheppard PO, Shoemaker KE;
PI

PI Gilbertson DG, West JW;
 XX WPI, 2002-689759/74.
 DR P-PSDB; ABG92894.
 XX Novel polypeptide, designated zvegf3 useful for treating skin wounds,
 PT ulcers, burns, skin grafting, female reproductive tract disorders,
 PT Parkinson's disease, and Alzheimer's disease -
 XX
 PS Example 4; Column 97-104; 68pp; English.
 XX
 CC The invention relates to an isolated polypeptide, designated zvegf3
 CC (a vascular endothelial growth factor-like protein) of 111-136 amino acid
 CC residues in length and comprises the sequence appearing as ABG92889
 CC from amino acid residues 235-345. Also included are an isolated
 CC protein comprising a first polypeptide disulphide bonded to a second
 CC polypeptide, where each of the first and second polypeptides is from
 CC zvegf 3, and where the protein modulates cell proliferation,
 CC differentiation, metabolism or migration, the zvegf 3 encoding
 CC polynucleotides and zvegf 3 expression vectors and host cells.
 CC Zvegf 3 is useful as additives in tissue adhesives for promoting
 CC revascularisation of the healing tissue, for designing molecules that
 CC antagonise semaphorin-stimulated activities, including neurite growth,
 CC cardiovascular development, cartilage and limb development, and T and
 CC B-cell function, and for imaging tumours or other sites of abnormal cell
 CC proliferation and in gene therapy applications. The proteins are useful
 CC therapeutically to stimulate tissue development or repair, or cellular
 CC differentiation or proliferation, for stimulating the growth of
 CC fibroblast or smooth muscle cells, as molecular weight standards, as
 CC reagents in assays for determining circulatory level of the protein or as
 CC standards in the analysis of cell phenotype, for identifying inhibitors
 CC of their activity which are useful for reducing the growth of solid
 CC tumours, for treating diabetic retinopathy, psoriasis, Rheumatoid
 CC arthritis, various forms of cancers, autoimmune disease, inflammation,
 CC myocardial ischaemia, scleroderma, and reducing fibrosis, including scar
 CC formation, keloids, liver fibrosis, lung fibrosis (e.g. silicosis,
 CC asbestosis), kidney fibrosis (including diabetic nephropathy),
 CC glomerulosclerosis, atherosclerosis, skin wounds, ulcers, burns, skin
 CC grafting, and female reproductive tract disorders, chronic liver disease
 CC (hepatitis), cirrhosis, Reye's syndrome, Wilson's disease, circulatory
 CC disorders e.g. heart failure, hepatic or portal vein thrombosis, cardiac
 CC sclerosis, neurodegenerative diseases such as multiple sclerosis,
 CC Parkinson's disease, Alzheimer's disease, and for regenerating neurite
 CC outgrowths following strokes. The gene for mouse zvegf3 is located on
 CC chromosome 3. The present sequence encodes zvegf 3.
 XX
 SQ Sequence 3571 BP; 876 A; 935 C; 875 G; 885 T; 0 other;
 Query Match 0.1%; Score 28; DB 24; Length 3571;
 Best Local Similarity 100.0%; Pred. No. 0.081;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16376 GCGGGGCGGGGCGGGGCGCG 16403
 DB 184 GCGGGGCGGGGCGGGGCGCG 157

RESULT 9
 AAI72444/c
 ID AAI72444 standard; cDNA: 3571 BP.
 XX
 AC AAI72444;
 XX
 DT 16-MAY-2002 (first entry)
 XX
 DE Mouse zvegf3 coding sequence.
 XX
 KW Gene: human; mouse; zvegf3; zvegf4; platelet derived growth factor;
 KW PDGF; homolog; growth; bone; ligament; cartilage; proliferation;
 KW osteoblast; chondrocyte; bony defect; fracture; bone graft;
 KW implant; periodontal pocket; osteoclast; bone marrow stem cell;
 KW osteoporosis; ss.
 XX

OS Mus musculus.
 FH Key Location/Qualifiers
 FT CDS 1049..2086
 FT /*tag= a
 FT /product= "zvegf3"
 XX
 XX US2002004225-A1.
 XX
 PD 10-JAN-2002.
 XX
 XX 29-MAR-2001; 2001US-0823033.
 XX
 PR 07-DEC-1998; 98US-111173P.
 PR 06-JUL-1999; 99US-142576P.
 PR 21-OCT-1999; 99US-161653P.
 PR 12-NOV-1999; 99US-165255P.
 PR 31-MAR-2000; 2000US-193723P.
 PR 07-DEC-1999; 99US-0457066.
 XX
 PA (HART/) HART C E.
 PA (GILB/) GILBERTSON D G.
 PI Hart CE, Gilbertson DG;
 DR WPI, 2002-171026/22.
 DR P-PSDB; AAB47890.
 XX
 XX Promoting growth of bone, ligament or cartilage in a mammal, involves
 XX administering to the mammal a protein which comprises growth factor
 XX domain of zvegf3 protein, a homolog of platelet-derived growth factor
 XX -
 PS Disclosure; Page 16-19; 31pp; English.
 XX
 CC The sequences given in AAI72443-44 encode human and mouse zvegf3,
 CC respectively. zvegf3 is a platelet derived growth factor (PDGF) homolog
 CC and it was used in the method of the invention for promoting growth of
 CC bone, ligament or cartilage and stimulating proliferation of osteoblasts
 CC or chondrocytes in a mammal. The proteins used were preferably a dimeric
 CC protein of residues 235-345 of human zvegf3 or all of the mouse zvegf3
 CC protein, with a delivery vehicle. The method of the invention is useful
 CC for promoting growth of bone, ligament or cartilage in a mammal, where
 CC the composition is administered at a site of a bony defect, preferably
 CC a fracture, bone graft site, implant site, or periodontal pocket, and
 CC for stimulating proliferation of osteoblasts or chondrocytes in a
 CC mammal. It is further useful for promoting proliferation of osteoblasts,
 CC osteoclasts, chondrocytes or bone marrow stem cells, where the bone
 CC marrow stem cells are harvested from a patient prior to culture. The
 CC method is therefore useful for treating osteoporosis.
 XX
 SQ Sequence 3571 BP; 876 A; 935 C; 875 G; 885 T; 0 other;
 Query Match 0.1%; Score 28; DB 24; Length 3571;
 Best Local Similarity 100.0%; Pred. No. 0.081;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16376 GCGGGGCGGGGCGGGGCGCG 16403
 DB 184 GCGGGGCGGGGCGGGGCGCG 157

RESULT 10
 ABX93182/c
 ID ABX93182 standard; DNA: 3571 BP.
 XX
 AC ABX93182;
 XX
 DT 22-MAY-2003 (first entry)
 XX
 DE DNA encoding mouse growth factor homologue, zvegf3.
 XX
 KW Mouse; growth factor homologue; zvegf3; fibroblast; smooth muscle cell;
 KW

CC phenylmethyl sulphonyl fluoride. PACE 4 and 4.1 convert prorenin to
 CC renin in the human kidney, causing elevation of blood pressure.
 CC They can therefore be used to identify other inhibitors of their
 CC action and may also be used to inhibit blood coagulation.
 CC (Updated on 25-MAR-2003 to correct PN field.)

XX
 SQ Sequence 2218 BP; 534 A; 623 C; 623 G; 438 T; 0 other;

Query Match 0.1%; Score 27; DB 14; Length 2218;
 Best Local Similarity 100.0%; Pred. No. 0.23;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16377 GCGGGCGGGGGCGGGGGCGGGCGG 16403
 |||||

Db 242 GCGGGCGGGGGCGGGGGCGGGCGG 268

RESULT 12

AA594758
 ID AA594758 standard; DNA; 4361 BP.

XX
 AC AA594758;

DT 14-FEB-2002 (first entry)

XX Human DNA sequence #13 expressed during foam cell differentiation.

XX Human; foam cell differentiation; atherosclerosis; cerebral stroke;

KW cardiovascular disorder; coronary artery disease; gene therapy; ds.

XX Homo sapiens.

XX WO200177389-A2.

XX 18-OCT-2001.

PD 04-APR-2001; 2001WO-US11128.

XX 05-APR-2000; 2000US-195106P.

XX (INCY-) INCYTE GENOMICS INC.

XX Shiffman D, Somogyi R, Lawn R, Selhamer JJ, Porter GJ, Mikita T;
 PI Tai J;

XX WPI; 2002-010925/01.

XX Composition useful for diagnosis of conditions, disorders or diseases
 PT associated with atherosclerosis, comprises several polynucleotides that
 PT are differentially expressed in foam cell development -

XX Claim 1; Page 70-71; 315pp; English.

XX The present invention relates to the isolation of human polynucleotide
 CC sequences that are differentially expressed during foam cell
 CC differentiation. The polynucleotide sequences of the invention or a
 CC composition comprising these polynucleotides are useful as a high
 CC throughput method for detecting altered expression of one or more
 CC polynucleotides in a sample. The polynucleotides can be used in the
 CC diagnosis of disorders associated with foam cell development such as
 CC atherosclerosis, cerebral stroke, and cardiovascular disorders such as
 CC coronary artery disease. The polynucleotide sequences can also be used
 CC as PCR primers and probes. The polynucleotides of the invention are also
 CC useful in gene therapy. AA594746-AA595021 represent the human
 CC polynucleotide sequences of the invention which are differentially
 CC expressed during foam cell differentiation.

SQ Sequence 4361 BP; 1013 A; 1229 C; 1203 G; 916 T; 0 other;

Query Match 0.1%; Score 27; DB 24; Length 4361;
 Best Local Similarity 100.0%; Pred. No. 0.23;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16377 GCGGGCGGGGGCGGGGGCGGGCGG 16403
 |||||

Db 200 GCGGGCGGGGGCGGGGGCGGGGGCGG 226

RESULT 13

AA047927
 ID AA047927 standard; cDNA; 4403 BP.

XX
 AC AA047927;

DT 25-MAR-2003 (updated)

DT 24-MAR-1994 (first entry)

XX Paired basic amino acid converting enzyme (PACE) 4 gene.

XX Paired basic amino acid converting enzyme; PACE; prorenin; renin;
 KW hypertension; blood; coagulation; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

FT CDS 170..3079

FT /*tag= a

FT /product= PACE 4.

PN WO9318159-A2.

XX 16-SEP-1993.

XX 09-MAR-1993; 93WO-US02147.

XX 09-MAR-1992; 92US-0848629.

XX (CHIR) CHIRON CORP.

XX Barr PJ, Kiefer MC;

XX WPI; 1993-303473/38.

XX P-PSDB; AAR41662.

XX New polynucleotide encoding PACE endo-peptidase - used for e.g.
 PT reducing blood pressure

XX Claim 1; Figure 1; 81pp; English.

XX The mammalian endopeptidases PACE 4 and PACE 4.1 (an alternative
 CC form of PACE 4) are involved in the production of mature
 CC polypeptides from precursor polypeptides by cleavage at pairs of
 CC basic amino acids e.g. Lys-Arg, Lys-Lys and Arg-Arg. The enzymes
 CC are stimulated by the presence of calcium ions and inhibited by
 CC phenylmethyl sulphonyl fluoride. PACE 4 and 4.1 convert prorenin to
 CC renin in the human kidney, causing elevation of blood pressure.
 CC They can therefore be used to identify other inhibitors of their
 CC action and may also be used to inhibit blood coagulation.
 CC (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 4403 BP; 1016 A; 1253 C; 1214 G; 920 T; 0 other;

Query Match 0.1%; Score 27; DB 14; Length 4403;
 Best Local Similarity 100.0%; Pred. No. 0.23;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16377 GCGGGCGGGGGCGGGGGCGGGCGG 16403
 |||||

Db 242 GCGGGCGGGGGCGGGGGCGGGGGCGG 268

RESULT 14

ABN95905
 ID ABN95905 standard; DNA; 4403 BP.

XX
 AC ABN95905;

XX 13-AUG-2002 (first entry)
 DT XX
 DE Gene #2403 used to diagnose liver cancer.
 XX
 KW Gene: liver cancer; ds; hepatocellular carcinoma; hepatotropic;
 KW metastatic liver tumour; cytostatic; expression profile; disease state;
 KW disease progression; drug toxicity; drug efficacy; drug metabolism.
 XX
 OS Homo sapiens.
 XX
 PN WO200229103-A2.
 XX
 PD 11-APR-2002.
 XX
 PF 02-OCT-2001; 2001WO-US30589.
 XX
 PR 02-OCT-2000; 2000US-237054P.
 XX
 PA (GENE-) GENE LOGIC INC.
 XX
 PI Horne D, Alvares C, Peres-Da-Silva S, Vockley JG;
 XX
 DR WPI; 2002-426119/45.
 XX
 PT Diagnosing and detecting the progression of liver cancer,
 PT hepatocellular carcinoma or metastatic liver tumor in a patient,
 PT involves detecting the level of expression of two or more genes in a
 PT liver tissue sample -
 PS Claim 1: SEQ ID NO 2403; 298pp; English.
 XX
 CC The invention relates to a novel method for diagnosing and detecting the
 CC progression of liver cancer, hepatocellular carcinoma or metastatic liver
 CC tumor in a patient, and differentiating metastatic liver cancer from
 CC hepatocellular carcinoma in a patient, involving detecting the level of
 CC expression of two or more genes represented in ABN93503-ABN97455 in a
 CC tissue sample. The method of the invention has hepatotropic, and
 CC cytostatic activity. The method is useful for diagnosing and detecting
 CC the progression of liver cancer, hepatocellular carcinoma and metastatic
 CC liver carcinoma in a patient. The method is useful for identifying
 CC expression profiles which serve as useful diagnostic markers as well as
 CC markers that can be used to monitor disease states, disease progression,
 CC drug toxicity, drug efficacy and drug metabolism.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 4403 BP; 1016 A; 1252 C; 1214 G; 921 T; 0 other;
 XX
 Query Match 0.1%; Score 27; DB 24; Length 4403;
 Best local Similarity 100.0%; Pred. No. 0.23;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 16377 GCGGGCGCGGGGGCGGGGGCGCG 16403
 DB 242 GCGGGCGCGGGGGCGGGGGCGCG 268
 XX
 RESULT 15
 AAS94759/c
 ID AAS94759 standard; DNA; 3132 BP.
 XX
 AC AAS94759;
 XX
 DT 14-FEB-2002 (first entry)
 XX
 DE Human DNA sequence #14 expressed during foam cell differentiation.
 XX
 KW Human: foam cell differentiation; atherosclerosis; cerebral stroke;
 KW cardiovascular disorder; coronary artery disease; gene therapy; ds.
 XX
 OS Homo sapiens.

XX WO200177389-A2.
 PN XX
 PD 18-OCT-2001.
 XX
 PF 04-APR-2001; 2001WO-US11128..
 XX
 PR 05-APR-2000; 2000US-195106P.
 XX
 PA (INCY-) INCYTE GENOMICS INC.
 XX
 PI Shiffman D, Somogyi R, Lawn R, Sellhammer JJ, Porter GJ, Mikita T;
 PI Tai J;
 XX
 DR WPI; 2002-010925/01.
 XX
 PT Composition useful for diagnosis of conditions, disorders or diseases
 PT associated with atherosclerosis, comprises several polynucleotides that
 PT are differentially expressed in foam cell development -
 XX
 PS Claim 1: Page 71-72; 315pp; English.
 XX
 CC The present invention relates to the isolation of human polynucleotide
 CC sequences that are differentially expressed during foam cell
 CC differentiation. The polynucleotide sequences of the invention or a
 CC composition comprising these polynucleotides are useful as a high
 CC throughput method for detecting altered expression of one or more
 CC polynucleotides in a sample. The polynucleotides can be used in the
 CC diagnosis of disorders associated with foam cell development such as
 CC atherosclerosis, cerebral stroke, and cardiovascular disorders such as
 CC coronary artery disease. The polynucleotide sequences can also be used
 CC as PCR primers and probes. The polynucleotides of the invention are also
 CC useful in gene therapy. AAS94746-AAS95021 represent the human
 CC polynucleotide sequences of the invention which are differentially
 CC expressed during foam cell differentiation.
 XX
 SQ Sequence 3132 BP; 578 A; 924 C; 885 G; 700 T; 45 other;
 XX
 Query Match 0.1%; Score 26; DB 24; Length 3132;
 Best local Similarity 100.0%; Pred. No. 0.68;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 16378 CGGGCGGGGGCGGGGGCGGGGGCGCG 16403
 DB 2985 CGGGCGGGGGCGGGGGCGGGGGCGCG 2960
 XX
 RESULT 16
 ABV94750/c
 ID ABV94750 standard; cDNA; 2870 BP.
 XX
 AC ABV94750;
 XX
 DT 14-JAN-2003 (first entry)
 XX
 DE Human pancreatic cancer expressed cDNA SEQ ID NO 131.
 XX
 KW Human: pancreas; cancer; gene therapy; vaccine; immunostimulant;
 KW cytostatic; tumour; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200260317-A2.
 XX
 PD 08-AUG-2002.
 XX
 PF 30-JAN-2002; 2002WO-US02781.
 XX
 PR 30-JAN-2001; 2001US-265305P.
 PR 31-JAN-2001; 2001US-265682P.
 PR 09-FEB-2001; 2001US-267568P.
 PR 21-MAR-2001; 2001US-278651P.
 PR 28-APR-2001; 2001US-287112P.

PR 16-MAY-2001; 2001US-291631P.
 PR 12-JUL-2001; 2001US-305484P.
 PR 20-AUG-2001; 2001US-313999P.
 PR 27-NOV-2001; 2001US-333626P.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Benson DR, Kalos MD, Lodes MJ, Persing DH, Hepler WT, Jiang Y;
 XX
 DR WPI: 2002-627435/67.
 DR P-PSDB; ABP68605.
 XX
 PT New isolated polynucleotide and pancreatic tumor polypeptides, useful
 PT for diagnosing, preventing and/or treating cancer, particularly
 PT pancreatic cancer
 PS
 PS Claim 1; SEQ ID NO 131; 300pp + Sequence Listing; English.
 XX
 CC The invention relates to an isolated polynucleotide (I) comprising: (a)
 CC any of a group of over 4000 nucleotide sequences (ABV94628-ABV99145);
 CC (b) complements of (a); (c) sequences consisting of at least 20
 CC contiguous residues of (a); (d) sequences that hybridize to (a), under
 CC moderately stringent conditions; (e) sequences having at least 75% or 90%
 CC identity to (a); or (f) degenerate variants of (a). Polypeptides
 CC (ABP68596-ABP68637) encoded by (I) and oligonucleotide can be used to
 CC detect cancer in a patient and compositions comprising polypeptides and
 CC polynucleotides, antibodies, fusion proteins, T cell populations and
 CC antigen presenting cells expressing the polypeptide are useful in
 CC treating pancreatic cancer and stimulating an immune response. The
 CC polynucleotides can be used as probes or primers for nucleic acid
 CC hybridisation, in the design and preparation of ribozyme molecules for
 CC inhibiting expression of the tumor polypeptides and proteins in the
 CC tumour cells, in vaccines and for gene therapy.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 2870 BP; 704 A; 792 C; 725 G; 649 T; 0 other;
 QY
 Query Match 0.1%; Score 25; DB 24; Length 2870;
 Best Local Similarity 100.0%; Pred. No. 2;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 16379 GGGCGCGGGGGCGGGGGCGCG 16403
 2291 GGGCGCGGGGGCGGGGGCGCG 2267
 RESULT 17
 AAT97303/C
 ID AAT97303 standard; DNA; 2876 BP.
 XX
 AC AAT97303;
 XX
 DT 14-APR-1998 (first entry)
 XX
 DE Human plasminogen activator inhibitor DNA.
 XX
 KW plasminogen activator inhibitor type 1; PAI-1; human;
 KW elastase inhibitor; vitronectin; cell attachment;
 KW cell proliferation; emphysema; adult respiratory distress syndrome;
 KW acute lung inflammation; alpha 1-antitrypsin deficiency;
 KW cystic fibrosis; atopic dermatitis; pancreatitis;
 KW periodontal disease; arthritis; HIV; atherosclerosis; restenosis;
 KW neointima; fibrosis; wound healing; tumour; metastasis; psoriasis;
 KW thrombosis; angiogenesis; therapy; ds.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 76..1284
 FT /*tag- a
 FT sig_peptide 76..144

FT /*tag- b
 FT mat_peptide 145..1281
 FT /*tag- c
 XX
 XX WO9739028-A1.
 XX
 PD 23-OCT-1997.
 XX
 XX 11-APR-1997; 97WO-US06071.
 XX
 XX 12-APR-1996; 96US-0015299.
 PR
 XX (AMNA-) AMERICAN NAT RED CROSS.
 PA
 PI Lawrence DA, Stefansson SP;
 XX
 DR WPI: 1997-526399/48.
 DR P-PSDB; AAM31587.
 XX
 XX Plasminogen activator-inhibitor type I mutant inhibits elastase - or
 PT has high affinity for vitronectin, for therapeutic inhibition of
 PT elastase or vitronectin-mediated cell attachment, migration etc.
 PS
 PS Disclosure; Page 91-95; 144pp; English.
 XX
 CC This nucleotide sequence codes for wild-type human plasminogen
 CC activator inhibitor type (PAI-1) (see AAM31587). Novel mutants
 CC (see AAM56710-25) of the PAI-1 mature protein are claimed that
 CC inhibit elastase or other elastase-like proteases, or are
 CC inhibitors of vitronectin-dependent cell migration. The mutants
 CC are obtained by site-directed mutagenesis of the PAI-1 DNA sequence
 CC and expression in host cells, and have a range of therapeutic uses.
 CC
 SQ Sequence 2876 BP; 706 A; 793 C; 726 G; 651 T; 0 other;
 QY
 Query Match 0.1%; Score 25; DB 18; Length 2876;
 Best Local Similarity 100.0%; Pred. No. 2;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 16379 GGGCGCGGGGGCGGGGGCGCG 16403
 2297 GGGCGCGGGGGCGGGGGCGCG 2273
 RESULT 18
 AAS09460/C
 ID AAS09460 standard; CDNA; 2876 BP.
 XX
 AC AAS09460;
 XX
 DT 26-SEP-2001 (first entry)
 XX
 DE Human cDNA encoding Plasminogen activator inhibitor-1, PAI-1.
 XX
 KW Human; Plasminogen activator inhibitor-1; PAI-1; serpin;
 KW immobilised enzyme; cystic fibrosis; acute respiratory distress syndrome;
 KW ARDS; HIV infection; Human immunodeficiency virus; prostate cancer;
 KW TNF-mediated inflammation; benign prostatic hypertrophy; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 76..1284
 FT /*tag- a
 FT /product= "PAI-1"
 FT sig_peptide 76..138
 FT /*tag- b
 FT /note= "Alternative signal peptide"
 FT sig_peptide 76..143
 FT /*tag- c
 FT /note= "Alternative signal peptide"
 FT mat_peptide 139..1281
 FT /*tag- d

FT		/label= Mature_PAI_1 #1
FT		/note= "Both forms of the protein are detected in vivo"
FT	mat_peptide	144..1281
FT		/*tag-
FT		/label= Mature_PAI_1 #2
FT		/note= "Both forms of the protein are detected in vivo"
PX		
PX	W0200138560-A2.	
PX		
PX	31-MAY-2001.	
PX		
PX	22-NOV-2000; 2000WO-US32315.	
PF		
PX	22-NOV-1999; 99US-0167553.	
PR		
PA	(AMNA-) AMERICAN NAT RED CROSS.	
PI	Lawrence DA, Day D;	
PX		
DR	WPI: 2001-441438/47.	
XX	P-PADB: AAU04913.	
PT	Detecting a functionally active form of an enzyme in a biological sample comprises contacting an enzyme inhibitor immobilised on a solid substrate -	
PX		
PS	Disclosure; Fig 3; 69pp; English.	
XX		
CC	The sequence encodes human plasminogen activator inhibitor-1,	
CC	PAI-1, a serine protease inhibitor or serpin. The protein	
CC	is used to demonstrate the method of the invention which comprises	
CC	detecting a functionally active form of an enzyme in a biological	
CC	sample by contacting an enzyme inhibitor immobilised on a	
CC	solid substrate with the biological sample and measuring the binding of	
CC	the enzyme inhibitor to the active form of the enzyme by a detectable	
CC	label, where the enzyme inhibitor specifically forms a covalent bond or	
CC	binds with a dissociation constant of 1 x 10 ⁻⁹ M or less with the active	
CC	form of the enzyme. The present invention provides a sensitive method for	
CC	the detection of a functionally active form of an enzyme in a biological	
CC	sample. Human PAI-1 can be used to detect a number of enzymes including	
CC	tissue plasminogen activator, urokinase, thrombin, plasmin, neutrophil	
CC	elastase, pancreatic elastase, trypsin, chymotrypsin, cathepsin G and	
CC	prostate specific antigen and as such can be used in methods to diagnose	
CC	diseases such as cystic fibrosis, acute respiratory distress syndrome	
CC	(ARDS), HIV infection, TNF-mediated inflammation, prostate cancer and	
CC	benign prostatic hypertrophy.	
XX		
SQ	Sequence 2876 BP; 706 A; 793 C; 726 G; 651 T; 0 other:	
	Query Match	0.1%; Score 25; DB 22; Length 2876;
	Best Local Similarity	100.0%; Pred. No. 2;
	Matches	25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	16379 GGCGGCGGGGGCGGGGGCGGC 16403	
Db	2297 GGCGGCGGGGGCGGGGGCGGC 2273	
RESULT 19		
AAH02917/c		
ID	AAH02917 standard: DNA; 2876 BP.	
XX	AAH02917;	
AC		
DT	15-JUN-2001 (first entry)	
DE	Human shear stress-response coding sequence SEQ ID NO: 87.	
XX		
KW	Human: shear stress-response protein; vascular disease;	
XX	arteriosclerosis; da.	
OS	Homo sapiens.	
XX		

```

PN WO200125427-A1.
PD 12-APR-2001.
XX
XX 02-OCT-2000; 2000WO-JP06840.
PF
XX 01-OCT-1999; 99JP-0280976.
PR
XX (KYOW) KYOWA HAKKO KOGYO KK.
PA (NOJII/) NOJIMA H.
PI Nojima H, Yoshisue H, Odayashi M, Ota T, Kawabata A, Sakurada K;
    Kuga T, Sekine S, Nakamura Y, Sugano S;
DR WPI: 2001-266308/27.
XX P-PSDB: AAB90794.
XX
XX DNA sequences, proteins encoded by them and antibodies against them
PT useful in diagnosis and treatment of vascular disease caused by
PT arteriosclerosis -
PI
XX Claim 20; Page 472-476; 678pp; Japanese.
XX
XX The present invention provides the protein and coding sequences of a
CC number of human shear stress response proteins. These are useful in the
CC diagnosis, treatment and screening of vascular diseases caused by
CC arteriosclerosis, including heart failure, post-PICA stenosis and
CC hypertension.
XX
SQ Sequence 2876 BP; 706 A; 793 C; 726 G; 651 T; 0 other:

Query Match          0.1%; Score 25; DB 22; Length 2876;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      16379 GGGCGGCGGGGGCGGGCGGGCGGC 16403
        |||||||
Db       2297 GGGCGCGGGGGCGCGGGGGCGGC 2273

RESULT 20
ABV77991/C
ID ABV77991 standard; DNA; 2876 BP.
XX
XX ABV77991;
AC
XX
XX 12-NOV-2002 (first entry)
DT
XX
XX Hypoxia-regulated protein coding sequence #11.
DE
XX
XX Cytostatic; vasotropic; tranquiliser; antiatherosclerotic; gene therapy;
XX antiinflammatory; vulnary; gynecological; ophthalmological; vaccine;
XX hypoxia; tumorigenesis; angiogenesis; apoptosis; cancer;
XX ischaemic condition; reperfusion injury; retinopathy; neonatal stress;
XX precleptmia; athrosclerosis; inflammatory condition; wound healing;
XX inflammation; erythropoiesis; hair loss; human; gene; ds.
XX
XX Homo sapiens.
OS
XX
XX WO200246465-A2.
XX
XX 13-JUN-2002.
PD
XX
XX 10-DEC-2001; 2001WO-GB05458.
PF
XX
XX 08-DEC-2000; 2000GB-0030076.
PR 08-FEB-2001; 2001GB-0003156.
PR 25-OCT-2001; 2001GB-0025666.
XX
XX (OXFO-) OXFORD BIOMEDICA UK LTD.
XX
XX White J, Mundy CR, Ward NR, Krige D, Kingsman SM, Harris RA;
PI Rayner WN;
```

XX WPI: 2002-627238/67.
XX
XX Identifying a gene involved in disease for treating hypoxia-regulated
PT conditions, comprises comparing the transcriptome/proteome of two cell
PT types under different conditions and identifying a differentially
PT regulated gene -
XX
XX Claim 37: Page 338; 538pp; English.
XX
XX The present invention relates to methods for identifying genes and
CC proteins that are implicated in a specific disease or physiological
CC condition. The method comprises comparing the transcriptome/proteome of a
CC specialised cell type implicated in a disease or condition with that of a
CC second specialised cell type, under two experimental conditions, and
CC identifying a gene that is differentially regulated in the two
CC specialised cell types under experimental conditions. ABV7873-ABV78116
CC and ABP5061-ABP5257 were identified using the methods of the invention.
CC The coding sequences and proteins are useful for treating a disease in a
CC patient, for manufacture of a medicament for treating hypoxia-regulated
CC conditions, and for regulating tumorigenesis, angiogenesis, apoptosis,
CC biological response to hypoxia conditions, or hypoxic-associated
CC pathology in a patient. The coding sequences and proteins are also useful
CC for monitoring the therapeutic treatment of a disease or physiological
CC condition, such as cancer, ischaemic conditions, reperfusion injury
CC retinopathy, neonatal stress, preeclampsia, atherosclerosis, inflammatory
CC conditions, wound healing, inflammation, erythropoiesis or hair loss.
XX
SQ Sequence 2876 BP; 706 A; 793 C; 726 G; 651 T; 0 other;

Query Match 0.1%; Score 25; DB 24; Length 2876;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16379 GGGCGCGGGGGCGGGGGCGCG 16403
DB 2297 GGGCGCGGGGGCGGGGGCGCG 2273
|||||
RESULT 21
AAN80253/C
ID AAN80253 standard; cDNA; 2944 BP.
XX
AC AAN80253;
XX
DT 25-MAR-2003 (updated)
DT 16-OCT-1990 (first entry)
XX
XX Insert of lambda 3 encoding beta-PAI protein.
DE
XX Endothelial plasminogen activator inhibitor; ss.
KW
XX Homo sapiens.
OS
XX
FH Key 1.1156 Location/Qualifiers
FT CDS
FT sig_peptide 1.112 /tag= a
FT mat_peptide 13..1153 /tag= b
FT product= beta-PAI /tag= c
FT polyA_signal 2916..2921 /tag= d
FT polyA_signal 1998..2003 /tag= e
FT
FT
XX W08801273-A.
PN
XX
PD 25-FEB-1988.
XX
PF 19-AUG-1987; 87WO-US02053.
XX

PR 19-AUG-1986; 86US-0897990.
XX
XX (SCRI) SCRIPPS CLINIC & RES FOUND.
PA (LOSK/) LOSKUTOFF D J.
XX
XX Loskutoff DJ, NY T, Sawdey M;
PI
XX
XX WPI: 1988-063992/09.
DR
XX P-PSDB; AAP82007.
XX
XX Diagnostic assays for tissue - and urokinase-type plasminogen
PT inhibitor - and pure, recombinant human endothelial plasminogen
PT activator inhibitor.
XX
XX Claim 1; Fig 22; 100pp; English.
XX
XX The lambda 3 clone DNA or plasmid pPAI3 can be used to produce the
CC t-PA inhibitor by recombinant DNA technology. The protein can
CC be used in a solid phase assay for detection of endothelial PAI,
CC and as an immunogen to raise antibodies for use as receptor molecules
CC in other assay systems.
CC See also AAP80252-54.
CC (Updated on 25-MAR-2003 to correct PA field.)
XX
SQ Sequence 2944 BP; 734 A; 784 C; 728 G; 698 T; 0 other;

Query Match 0.1%; Score 25; DB 9; Length 2944;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16379 GGGCGCGGGGGCGGGGGCGCG 16403
DB 2165 GGGCGCGGGGGCGGGGGCGCG 2141
|||||
RESULT 22
AAS94905/C
ID AAS94905 standard; DNA; 3171 BP.
XX
AC AAS94905;
XX
DT 14-FEB-2002 (first entry)
DT
XX
XX Human DNA sequence #160 expressed during foam cell differentiation.
DE
XX Human; foam cell differentiation; atherosclerosis; cerebral stroke;
XX cardiovascular disorder; coronary artery disease; gene therapy; ds.
KW
XX Homo sapiens.
OS
XX
PN W0200177389-A2.
PN
XX 18-OCT-2001.
PD
XX 04-APR-2001; 2001WO-US11128.
PE
XX 05-APR-2000; 2000US-195106P.
PR
XX (INCY-) INCYTE GENOMICS INC.
XX
XX Shiffman D, Somogyi R, Lawn R, Sellhammer J, Porter GJ, Mikita T;
PI Tal J;
PI
XX
XX WPI: 2002-010925/01.
DR
XX
XX Composition useful for diagnosis of conditions, disorders or diseases
PT associated with atherosclerosis, comprises several polynucleotides that
PT are differentially expressed in foam cell development -
XX
XX Claim 1; Page 215; 315pp; English.
XX
XX The present invention relates to the isolation of human polynucleotide
CC sequences that are differentially expressed during foam cell

CC bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with
 CC bisulphite, of genes associated with tumour suppression and
 CC oncogenes having a sequence taken from 536 (actually 533 since
 CC numbers 408, 458 and 500 are missing from the sequence listing) sequences
 CC (5s) and sequences complementary to (5s). The nucleic acid may be a
 CC peptide nucleic acid-oligomer (PNA) of at least 9 nucleotides and may
 CC form part of a set of probes for detecting the cytosine methylation state
 CC and/or single nucleotide polymorphisms and also to be used in an
 CC array for analysing diseases associated with CPG dinucleotides e.g.
 CC cancers and tumours. The probes can also be used in a method for
 CC ascertaining genetic and/or epigenetic parameters for the diagnosis
 CC and/or therapy of existing diseases or the predisposition to specific
 CC diseases, by analysing cytosine methylations. The parameters may be
 CC compared to another set of genetic and/or epigenetic parameters, the
 CC differences serving as basis for diagnosis and/or prognosis events which
 CC are disadvantageous to patients. The present sequence is one of the
 CC 533 genomic sequences derived from tumour suppressor genes and
 CC oncogenes. Sequences with even numbered Seq ID numbers are the
 CC complementary sequence of the corresponding odd numbered sequence (e.g.
 CC ID 2 and ID1, ID 536 and ID 535, except for those whose partner sequence
 CC is missing).
 CC Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic
 CC format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

CC Sequence 7309 BP; 1739 A; 181 C; 1806 G; 3583 T; 0 other;

CC Query Match 0.1%; Score 25; DB 22; Length 7309;

CC Best Local Similarity 100.0%; Pred. No. 1.9;
 CC Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 25487 AAACATTTAAACAAATTTAAAAA 25511

DB 7011 AAACATTTAAACAAATTTAAAAA 6987

RESULT 25

ABK34011/C
 ID ABK34011 standard; DNA; 7309 BP.

AC ABK34011;

DT 18-JUN-2002 (first entry)

XX Human DNA for staging of Astrocytomas, complement, #49.

XX Human; ds; astrocytoma; cytosstatic; staging; cysteine methylation; CPG;

KW bisulphite; brain tissue; MALDI; ESI; electron spray mass spectrometry;
 KM matrix assisted laser desorption/ionization mass spectrometry.

XX Homo sapiens.

OS WO200202808-A2.

PN 10-JAN-2002.

PD 02-JUL-2001; 2001WO-EP07538.

PE 30-JUN-2000; 2000DE-1032529.

PR 01-SEP-2000; 2000DE-1043826.

XX (EPIC-) EPIGENOMICS AG.

PA Olek A, Plepenbrock C, Berlin K;

PI WPI; 2002-171649/22.

XX Novel chemically modified genomic DNA sequences, useful in the
 PT characterisation, classification, differentiation, grading, staging,
 PT treatment and/or diagnosis of astrocytomas or predisposition to
 PT astrocytomas
 XX

PS Claim 1; SEQ ID No 98; 37bp; English.

XX The invention relates to a nucleic acid comprising a sequence (I) of at
 CC least 18 bases in length of a segment of chemically pre-treated genomic
 CC DNA which has any one of the sequences of (ABK33919-ABK34032) or its
 CC complement. Also included are an oligonucleotide or peptide nucleic
 CC acid (or set thereof) of at least 9 nucleotides which hybridises to (I),
 CC primers for (I), probes for detecting cytosine methylation or single-
 CC nucleotide polymorphisms (SNP) in (I), an array of oligomers
 CC or peptide nucleic acids for analysing diseases associated with the
 CC methylation states of the Cpg dinucleotides of (I). The array is useful
 CC for determining genetic and/or epigenetic parameters, classification,
 CC differentiation, grading, staging, treatment and/or diagnosis of
 CC astrocytomas, or the predisposition to astrocytomas by analysing cytosine
 CC methylations, involves obtaining a biological sample containing genomic
 CC DNA, extracting the genomic DNA, converting cytosine bases which are
 CC unmethylated at the 5-position, in the genomic DNA sample, to uracil or
 CC another base which is dissimilar to cytosine in terms of hybridisation
 CC behaviour, by chemical treatment and amplifying chemically pre-treated
 CC genomic DNA fragments using the array and a polymerase, where the
 CC amplification carries a detectable label. The method further involves
 CC identifying methylation status of one or more cytosine positions, and
 CC analysing methylation status of the cytosine positions by reference to
 CC one or more data sets. The genomic DNA is chemically treated by using a
 CC bisulphite, hydrogen sulphide or disulphite. The amplification
 CC step amplifies DNA which is of particular interest in astrocytoma or
 CC brain tissue, based on the specific genomic methylation status of brain
 CC tissues, as opposed to background DNA. The amplification carries a
 CC fluorescent label or radionuclide. Optionally, the labels of the
 CC which are detected in a mass spectrometer. The fragments of chemically
 CC pre-treated genomic DNA to be amplified, have a single positive or
 CC negative charge for a better detectability in the mass spectrometer.
 CC Preferably, the amplification or fragments of the amplification are
 CC detected by matrix assisted laser desorption/ionization mass spectrometry
 CC (MALDI) or using electron spray mass spectrometry (ESI). The
 CC present sequence is one of the chemically pre-treated reference DNA
 CC samples of the invention.
 CC Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic
 CC format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

CC Sequence 7309 BP; 1739 A; 181 C; 1806 G; 3583 T; 0 other;

CC Query Match 0.1%; Score 25; DB 24; Length 7309;

CC Best Local Similarity 100.0%; Pred. No. 1.9;
 CC Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 25487 AAACATTTAAACAAATTTAAAAA 25511

DB 7011 AAACATTTAAACAAATTTAAAAA 6987

RESULT 26

ABL33817/C
 ID ABL33817 standard; DNA; 7309 BP.

AC ABL33817;

DT 26-MAR-2002 (first entry)

XX Human immune system associated gene SEQ ID NO: 1790.

XX Human; immune system disease; cytosine methylation; antiasthmatic;
 KW antiarteriosclerotic; antianaemic; cytosstatic; nootropic;

KW neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
 KW antineumatic; antiarthritic; antidiabetic; antipsoriatic;

KW antineumatic; cancer; eye disease; arteriosclerosis; anaemia;
 KW acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;

KW neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
 KW gene; ds.

XX

OS Homo sapiens.
XX WO200200928-A2.
XX 03-JAN-2002.
XX 02-JUL-2001; 2001WO-EP07537.
XX 30-JUN-2000; 2000DE-1032529.
XX 01-SEP-2000; 2000DE-1043826.
XX (EPIC-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI: 2002-130909/17.
XX Nucleic acid comprising fragment of chemically modified gene, useful
XX for diagnosis and treatment of diseases associated with abnormal
XX cytosine methylation -
XX Claim 1; SEQ ID NO 1790; 32pp + Sequence Listing; German.
XX The present invention provides a number of human immune system associated
XX genes which are modified by the methylation of cytosines. The sequences
XX can be used in the diagnosis and treatment of immune system disorders,
XX including eye diseases such as retinopathy, neovascular glaucoma and
XX macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid
XX leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,
XX rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
XX diseases. The present sequence is a gene of the invention.
XX
SQ Sequence 7309 BP; 1739 A; 181 C; 1806 G; 3583 T; 0 other;
Query Match 0.1%; Score 25; DB 24; Length 7309;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 25487 AAACATTAAACAAATTATAAAAA 25511
DB 7011 AAACATTAAACAAATTATAAAAA 6987
RESULT 27
ABN95599/C
ID ABN95599 standard; DNA: 17509 BP.
XX ABN95599;
AC
XX 13-AUG-2002 (first entry)
DT
XX Gene #2097 used to diagnose liver cancer.
DE
XX Gene; liver cancer; ds; hepatocellular carcinoma; hepatotropic;
XX metastatic liver tumour; cytosolic; expression profile; disease state;
XX disease progression; drug toxicity; drug efficacy; drug metabolism.
XX Homo sapiens.
XX WO200229103-A2.
XX 11-APR-2002.
XX 02-OCT-2001; 2001WO-US30589.
XX 02-OCT-2000; 2000US-237054P.
XX (GENE-) GENE LOGIC INC.
XX Horne D, Alvares C, Peres-Da-Silva S, Vockley JG;
XX WPI: 2002-426119/45.
XX

PT Diagnosing and detecting the progression of liver cancer,
PT hepatocellular carcinoma or metastatic liver tumor in a patient,
PT involves detecting the level of expression of two or more genes in a
PT liver tissue sample -
PS Claim 1; SEQ ID NO 2097; 298pp; English.
XX The invention relates to a novel method for diagnosing and detecting the
XX progression of liver cancer, hepatocellular carcinoma or metastatic liver
XX tumor in a patient, and differentiating metastatic liver cancer from
XX hepatocellular carcinoma in a patient, involving detecting the level of
XX expression of two or more genes represented in ABN93503-ABN97455 in a
XX tissue sample. The method of the invention has hepatotropic, and
XX cytosolic activity. The method is useful for diagnosing and detecting
XX the progression of liver cancer, hepatocellular carcinoma and metastatic
XX liver carcinoma in a patient. The method is useful for identifying
XX expression profiles which serve as useful diagnostic markers as well as
XX markers that can be used to monitor disease states, disease progression,
XX drug toxicity, drug efficacy and drug metabolism.
XX Note: The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pcl_sequences.
SQ Sequence 17509 BP; 4974 A; 4406 C; 4386 G; 3743 T; 0 other;
Query Match 0.1%; Score 25; DB 24; Length 17509;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 16379 GGGCGGGGGGGCGGGGGGGCGG 16403
DB 14507 GGGCGGGGGGGCGGGGGGGCGG 14483
RESULT 28
ABK32842/C
ID ABK32842 standard; DNA: 2307 BP.
XX ABK32842;
AC
XX 23-APR-2002 (first entry)
DT
XX DNA encoding human homologue of MPT1 antifungal target.
DE
XX antifungal; fungal gene transcription; RPP34; POP3; TFA2; NAB2;
XX MPT1; MTR2; BOS1; POL30; RSA2; SOR1; MTW1; TFB1; SPC98; BPR2; RAA1;
XX GCD7; SKI6; NRP1; LCP5; NCE103; ECO1; ORC2; CNS1; YPD1; TIM10; SRB4;
XX yeast; fungus; ds; gene.
XX Homo sapiens.
XX WO200202055-A2.
XX 10-JAN-2002.
XX 28-JUN-2001; 2001WO-US20592.
XX 29-JUN-2000; 2000US-215164P.
XX 10-AUG-2000; 2000US-224457P.
XX (ANAD-) ANADYS PHARM INC.
XX Moore J, Buurman ET, Desilva T, Harris S, Komarnitsky S;
XX Mendillo M, Moore D, McCoy M, Sanderson K, Haq T, Zhu S, Long F;
XX Davidov E, Thompson CM;
XX WPI: 2002-147962/19.
XX P-PSDB; AAU82954.
XX Screening candidate antifungal compound for interaction with essential
XX protein, modulation of essential protein activity, binding to essential
XX protein, by contacting protein with test compound and determining
XX effects -
PT

XX disclosure; Figure 80; 522pp; English.

XX
XX
XX The invention describes a method of screening a candidate antifungal
CC compound for interaction with essential proteins (EP) or for modulation
CC of EP activity e.g. fungal gene transcription. The proteins tested in the
CC invention include RPL34, POP3, TFA2, NAB2, MPT1, MPT2, BOS1, POL30, RSA2,
CC SOT1, MTR1, TPE1, SPC98, BFR2, RNAL, GCD7, SKI6, NIT1, LCP9, NCE103,
CC ECOL1, ORC2, CEN1, YPD1, TIM10 and SRB4 from *S. cerevisiae*, *C. albicans*
CC and human homologues. The method involves contacting a culture with one
CC or more test compounds and determining the effects on the growth or
CC viability of the culture of cells which preferably comprises fungal cells
CC or yeast cells. Preferably the identified compounds interact with, or
CC modulate (preferably inhibit) activity of *C. albicans* EP. The inhibitor
CC compounds identified by the method are useful for preventing or
CC inhibiting fungal, particularly *C. albicans* growth in culture or in a
CC mammal. The antifungal agents interact with essential fungal elements
CC that can be used to treat fungal infection by preventing the growth and
CC preferentially killing the fungi, but does not inhibit the biological
CC activity of mammalian homologues. This sequence encodes a target protein
CC used to test the antifungal compounds, described in the method of the
CC invention.

XX
SQ Sequence 2307 BP; 359 A; 969 C; 724 G; 255 T; 0 other;

XX
XX
XX Query Match 0.1%; Score 23; DB 24; Length 2307;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16373 CGCGCGCGCGCGCGCGCG 16395
|||||
DB 756 CGCGCGCGCGCGCGCGCG 734

RESULT 29
ABX08754
ID ABX08754 standard; cDNA; 6816 BP.

XX
AC ABX08754;
XX
DT 21-JAN-2003 (first entry)
XX
DE Angiogenesis-associated human polynucleotide sequence #16.
XX
KW Human; angiogenesis-associated transcript; angiogenesis;
KW angiogenesis-associated disease; cancer; cytostatic; gene therapy;
KW gene; ss.
XX
OS Homo sapiens.
XX
PN WO200279492-A2.
XX
PD 10-OCT-2002.
XX
PF 14-FEB-2002; 2002WO-US04915.
XX
PR 14-FEB-2001; 2001US-0784356.
PR 22-FEB-2001; 2001US-0791390.
PR 19-APR-2001; 2001US-285475P.
PR 03-AUG-2001; 2001US-310025P.
PR 13-NOV-2001; 2001US-350666P.
PR 29-NOV-2001; 2001US-334244P.
XX
PA (EOSB-) EOS BIOTECHNOLOGY INC.
XX
PI Murray R, Glynn R, Watson SR, Aziz N;
XX
DR WPI: 2003-040681/03.
XX
P-PSDB; AB003471.
XX
PT Detecting angiogenesis-associated transcript in a cell for diagnosing
PT and treating cancer by contacting a sample with a polynucleotide that
PT exhibits changes in expression level as a function of time in tissue

PT undergoing angiogenesis -
XX
XX
XX Example 2; Page 193-195; 291pp; English.

XX
XX The present invention relates to methods and compositions for
CC detecting an angiogenesis-associated transcript in a cell in
CC a patient. The method involves contacting a biological sample from
CC the patient with a polynucleotide that selectively hybridises to a
CC sequence at least 80% identical to any of the angiogenesis-associated
CC human polynucleotide sequences given in the specification. These
CC angiogenesis-associated polynucleotide sequences comprise genes that
CC exhibit changes in expression levels as a function of time in tissue
CC undergoing angiogenesis. The method and the polynucleotide sequences
CC of the invention are useful for diagnosing and treating angiogenesis
CC and angiogenesis-associated diseases e.g. cancer. The polynucleotide
CC sequences are also useful in the gene therapy of such disorders. The
CC angiogenesis-associated proteins encoded by the polynucleotide
CC sequences are useful as a vaccine for therapeutic and prophylactic
CC immunisation. ABX08739-ABX08853 represent angiogenesis-associated
CC polynucleotide sequences.

XX
SQ Sequence 6816 BP; 1852 A; 1702 C; 1736 G; 1526 T; 0 other;

XX
XX
XX Query Match 0.1%; Score 23; DB 25; Length 6816;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16379 GGGCGCGCGCGCGCGCGCG 16401
|||||
DB 2802 GGGCGCGCGCGCGCGCGCG 2824

RESULT 30
ABL70224/C
ID ABL70224 standard; DNA; 7752 BP.

XX
AC ABL70224;
XX
DT 01-JUL-2002 (first entry)
XX
DE Chemically treated cell signalling DNA sequence complementary to#57.
XX
KW Cell signalling; cytosine methylation; cell signalling disease;
KW cancer; tumour; cytostatic; ds.
XX
OS Unidentified.
XX
PN WO200202807-A2.
XX
PD 10-JAN-2002.
XX
PF 29-JUN-2001; 2001WO-EP07471.
XX
PR 30-JUN-2000; 2000DE-1032529.
PR 01-SEP-2000; 2000DE-1043826.
XX
PA (EPIC-) EPIDENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI: 2002-154758/20.
XX
PT Nucleic acid, useful for diagnosis and therapy of diseases associated
PT with cell signalling e.g. cancer, comprises chemically modified genomic
PT sequences of genes associated with cell signalling -
XX
XX
XX Claim 1; SEQ ID NO 114; 24pp+sequence listing; English.

XX
XX The invention relates to a nucleic acid comprising a sequence of at least
CC 18 bases of a segment of chemically pretreated DNA of genes associated
CC with cell signalling. The activity of the modified sequences of the
CC invention may be described as cytostatic. The object of the invention is
CC to provide the chemically modified DNA of genes associated with cell

FT	CDS		complement (123808..127296)
FT		/tag= n	
FT		/product=	immediate early protein
XX			
XX	PN	W09804576-A1.	
XX	PD		
XX	PE	05-FEB-1998.	
XX	PF	22-JUL-1997;	97WO-US13346.
XX	PR	29-NOV-1996;	96US-0757669.
XX	PR	25-JUL-1996;	96US-0686243.
XX	PR	25-JUL-1996;	96US-0686349.
XX	PR	25-JUL-1996;	96US-0686350.
XX	PR	25-JUL-1996;	96US-0687253.
XX	PR	05-SEP-1996;	96US-0688814.
XX	PR	10-OCT-1996;	96US-0708678.
XX	PR	13-NOV-1996;	96US-0728323.
XX	PR	13-NOV-1996;	96US-0747887.
XX	PA	(UYCO) UNIV COLUMBIA NEW YORK.	
XX	PI	Bohenzky RA, Chang Y, Edelman IS, Moore PS, Russo JJ;	
XX	DR	WP1; 1998-130615/12.	
XX	PT	New nucleic acid encoding Kaposi's sarcoma associated herpes virus	
XX	PT	proteins - useful for, e.g. detecting levels of HHV8 in, and	
XX	PT	preparation of vaccines for treatment of, HIV patients	
XX	PS	Example 2; Page 135-203; 230pp; English.	
CC	CC	This sequence represents the long unique region and terminal repeat of	
CC	CC	the Kaposi's sarcoma-associated herpes virus (KSHV). KSHV is also known	
CC	CC	as human herpes virus 8 (HHV8). This sequence contains the DNAs of the	
CC	CC	invention which encode KSHV polypeptides selected from: (a) viral	
CC	CC	macrophage inflammatory protein (MIP) II; (b) viral interleukin-6 (IL-6);	
CC	CC	(c) viral IRF 1; (d) complement-binding protein; glycoproteins B, M or L;	
CC	CC	(e) capsid protein IV encoded by ORF5; and (e) immediate early protein	
CC	CC	encoded by ORF73. Labelled probes for the nucleic acid, proteins encoded	
CC	CC	by it, and antibodies (Ab) specific for the proteins are useful for	
CC	CC	detecting HHV8, specifically for diagnosis of Kaposi's sarcoma, in body	
CC	CC	fluids or tissue samples. HHV8 infections can be treated with antisense	
CC	CC	or triplex forming molecules or agents that bind specifically to the	
CC	CC	protein. Ab may be used for prophylaxis or treatment of HHV8 infection,	
CC	CC	while the protein can be used in protective vaccines. Ab may also be used	
CC	CC	to differentiate between lymphomas, and HHV8 may be implicated in many	
CC	CC	other lymphoproliferative diseases such as lymphomas, leukaemia,	
CC	CC	splenomegaly and mycosis fungoides. Cells and animals containing the	
CC	CC	nucleic acid are useful for drug screening. HHV8-derived peptides can be	
CC	CC	used as targets for antiviral drugs, e.g. dihydrofolate reductase gene	
CC	CC	can be inhibited with methotrexate. These can also be used to determine	
CC	CC	the immune status of a patient infected with HIV. HHV8 derived protein	
CC	CC	viral MIP III may be used as an anti-inflammatory agent for,	
CC	CC	e.g. treating rheumatoid arthritis. This sequence is stated as containing	
CC	CC	81 open reading frames.	
SQ	Sequence	137507 BP; 32579 A; 37795 C; 35758 G; 31375 T; 0 other:	
OY	Query Match	0.1%; Score 23; DB 19; Length 137507;	
DB	Best Local Similarity	100.0%; Pred. No. 14;	
	Matches	23; Conservative 0; Mismatches 0; Indels 0; Gaps 0	
		5460 GTTTTAAATACAGACTAGTT 5482	
		114702 GTTTTAAATACGACAGTAGTT 114724	
RESUL.F 33			
ID	ABK97604		
XX	ABK97604 standard; cDNA; 1044 BP.		

[illegible]

KW Human; digestive system antigen; gene therapy; cancer; appendicitis;
KW ulcerative colitis; infection; Hirschsprung's disease; chronic colitis;
KW digestive system disorder; Meckel's diverticulum; ds.
XX Homo sapiens.
XX WO200155314-A2.
PD 02-AUG-2001.
XX 17-JAN-2001; 2001WO-US01324.
XX 31-JAN-2000; 2000US-0179065.
XX 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226686.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229309.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 08-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.

PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239335.
PR 13-OCT-2000; 2000US-0239337.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 06-DEC-2000; 2000US-0256719.
PR 08-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.

PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249267.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251088.
PR 05-DEC-2000; 2000US-0251988.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251866.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
XX
XX WPI: 2001-502630/55.
XX
XX Polynucleotides encoding digestive system antigens, useful for
PT diagnosing, treating, preventing and/or prognosing disorders of the
PT digestive system, particularly cancer and cancer metastases -
XX
XX
PS Disclosure: SEQ ID NO 4077; 986pp; English.
XX
XX The present invention provides the protein and coding sequences of a
CC number of human digestive system antigens. These can be used in the
CC diagnosis, treatment and prevention of digestive system disorders,
CC including cancer, Meckel's diverticulum, bacterial or parasitic
CC infections, appendicitis, Hirschsprung's disease, chronic colitis or
CC ulcerative colitis. The present sequence is a genomic DNA fragment
CC encoding a digestive system antigen of the invention.
XX
SQ Sequence 3024 BP; 760 A; 753 C; 763 G; 748 T; 0 other;

Query Match 0.1%; Score 22; DB 22; Length 3024;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9722 CAAAGGCACATATATTTTTTTT 9743
|||||
DB 928 CAAAGGCACATATATTTTTTTT 907
RESULT 36
AA157831
ID AA157831 standard; cDNA; 4176 BP.
XX
XX AA157831;
AC
XX
XX 22-OCT-2001 (first entry)
DE Human polynucleotide SEQ ID NO 34.
XX
XX Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia; ss.
XX
XX Homo sapiens.
OS
XX WO200153312-A1.
PN
XX 26-JUL-2001.
PD
XX 26-DEC-2000; 2000WO-US34263.
PF
XX 21-JAN-2000; 2000US-0488725.
PR 25-APR-2000; 2000US-0552317.
PR 09-JUL-2000; 2000US-0598042.
PR 19-JUL-2000; 2000US-0620312.
PR 03-AUG-2000; 2000US-0639450.
PR 14-SEP-2000; 2000US-0662191.
PR 19-OCT-2000; 2000US-0693036.
PR 29-NOV-2000; 2000US-0727344.
XX
XX (HSE-) HSEQ INC.
XX
XX Tang YF, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;
XX
XX WPI: 2001-442253/47.
DR P-PSDB; AAM36675.
XX
XX Novel nucleic acids and polypeptides, useful for treating disorders
PT such as central nervous system injuries -
XX
XX
PS Claim 1; SEQ ID NO 34; 10078pp; English.
XX
XX The invention relates to human nucleic acids (AA157798-AA161369) and
CC the encoded polypeptides (AAM36642-AAM42213) with nootropic,
CC immunosuppressant and cytostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: Immune system suppression,
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukemias and
CC C.N.S disorders.
CC Note: The sequence data for this patent did not form part of the printed
CC specification.
XX
SQ Sequence 4176 BP; 668 A; 1320 C; 1591 G; 597 T; 0 other;

Query Match 0.1%; Score 22; DB 22; Length 4176;

Best Local Similarity 100.0%; Pred. No. 46;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 27465 GCGCCGCGCGCGCGCGCGCC 27486
DB 1749 GCGCCGCGCGCGCGCGCGCC 1770
RESULT 37
ABAI5786/c
ID ABAI5786 standard; DNA: 13334 BP.
XX
AC ABAI5786;
XX
DT 23-JAN-2002 (first entry)
XX
DE Human nervous system related polynucleotide SEQ ID NO 8117.
XX
KW Human; neurotropic; neuroprotective; cytoskeletal; dermatological; virucide;
KW immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnereary;
KW antiparkinsonian; antistroke; antianaemic; antiarthritic; cancer;
KW antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;
KW antiallergic; antidiabetic; antileuc; anticonvulsant; antifungal;
KW antiparasitic; cardiac; immune disorder; cardiovascular disorder;
KW neurological disease; infection; neurotropic; gene therapy; vaccine; ds.
XX
OS Homo sapiens.
XX
PN WO200159063-A2.
XX
PD 16-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01334.
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0186874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226868.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227099.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.

PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 21-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234497.
PR 25-SEP-2000; 2000US-0234498.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235634.
PR 27-SEP-2000; 2000US-0235636.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.

XX Ryan JW;
PI WPI: 2002-394128/42.
XX P-PSDB; AAE22737.
DR Novel genomic polynucleotide from human chromosome-7 encoding snare
XX YKT6, liver glucokinase, adipocyte enhancer binding protein polymerase
PT delta small subunit useful in gene therapy for treating e.g. diabetes,
PT cancer -
XX
PS Claim 1; Page 5-21; 94pp; English.
XX
CC The present invention relates to novel genomic polynucleotide from human
CC chromosome 7 encoding human snare YKT6, liver glucokinase (AEP: D-hexose
CC 6-phosphotransferase), adipocyte enhancer binding protein (AEBP1) and DNA
CC directed 50 kpa regulatory subunit (POLD2). Sequences of the invention
CC are used to prevent, treat or ameliorate a medical condition. Antisense
CC oligonucleotides specific for snare YKT6 are useful for inhibiting cell
CC growth and in particular to treat or prevent tumour growth. Glucokinase
CC and AEBP are useful for treating hyperglycaemia. Genomic sequences of
CC the invention are useful for gene therapy e.g., SNARE YKT6 is useful to
CC modulate or prevent cell apoptosis and treat disorder such as virus-
CC induced lymphocyte depletion (AIDS-acquired immune deficiency syndrome),
CC cell death in neurodegenerative disorders (e.g., Alzheimer's disease,
CC Parkinson's disease, ALS (amyotrophic lateral sclerosis), retinitis
CC pigmentosa, spinal muscular atrophy and various forms of cerebellar
CC degeneration), cell death in blood cell disorders resulting from the
CC deprivation of growth factors (anaemia associated with chronic disease,
CC aplastic anaemia, chronic neutropenia and myelodysplastic syndromes)
CC and disorders arising from acute loss of blood flow such as stroke and
CC myocardial infarctions. Glucokinase gene is useful for treating diabetes
CC mellitus. AEBP is useful in modulating or inhibiting adipogenesis and
CC in treating obesity, diabetes mellitus or osteopenic disorders. POLD2 is
CC useful in treating defects in DNA repair such as xeroderma pigmentosum,
CC progeria and ataxia telangiectasia. The present sequence is human snare
CC YKT6 genomic DNA.
XX
SQ Sequence 38997 BP; 10813 A; 9678 C; 9403 G; 9103 T; 0 other;
Query Match 0.1%; Score 22; DB 24; Length 38997;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2543 GAGTACCCCAATCCTCCAC 2564
DB 14535 GAGTACCCCAATCCTCCAC 14556
|||||
|||||

RESULT 39
ABK99972
ID ABK99972 standard; DNA; 157875 BP.
XX
AC ABK99972;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human CADPKL genomic DNA.
XX
KM Human; calcium/calmodulin-dependent protein kinase-like gene; CADPKL; ds;
KM gene; neuropsychiatric disorder; attention deficit disorder; ADD;
KM schizoaffective disorder; bipolar disorder; unipolar affective disorder;
KM schizophrenia; adolescent conduct disorder; pharmacogenomics;
KM fingerprinting; paternity testing; antidepressant; neuroleptic.
XX
OS Homo sapiens.
XX
PN WO200254939-A2.
XX
PD 18-JUL-2002.
XX
PF 07-JAN-2002; 2002MO-US00367.
XX

PR 09-JAN-2001; 2001US-0757300.
PR 23-AUG-2001; 2001US-0935464.
XX
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Meyer JW, Barrington-Martin R, Parker A;
XX WPI: 2002-590643/63.
XX
DR New variants of calcium/calmodulin-dependent protein kinase-like
XX nucleic acids and polypeptides, useful for diagnosing and treating
PT neuropsychiatric disorders e.g. schizophrenia, schizoaffective
PT disorder, and bipolar disorder -
XX
PS Claim 1; Page 119-200; 223pp; English.
XX
XX The invention relates to a nucleic acid comprising a polymorphic region
CC of a Calcium/calmodulin-dependent protein kinase-like gene (CADPKL)
CC allelic variant, and the polypeptide it encodes. CADPKL allelic variants
CC are useful in determining whether a subject has or is at risk of
CC developing a neuropsychiatric disorder, such as schizophrenia, attention
CC deficit disorder (ADD), schizoaffective disorder, bipolar disorder,
CC unipolar affective disorder and adolescent conduct disorder. The
CC polypeptides, polynucleotides, antibodies and modulators of the CADPKL
CC allelic variants are useful for diagnosing or treating these
CC neuropsychiatric disorders. The polypeptides may be used to raise
CC antibodies to a CADPKL polypeptide. The nucleic acids may be used as
CC probes or primers, in pharmacogenomics for designing therapies for the
CC disorders, and in fingerprinting for detection of different individuals
CC with the same species (e.g. paternity testing). This sequence represents
CC human CADPKL genomic DNA of the invention.
XX
SQ Sequence 157875 BP; 44403 A; 35734 C; 34322 G; 43416 T; 0 other;
Query Match 0.1%; Score 22; DB 24; Length 157875;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 28643 CTGGCTGCTGCTGCTGCT 28664
DB 80030 CTGGCTGCTGCTGCTGCT 80051
|||||
|||||

RESULT 40
AB223704
ID AB223704 standard; CDNA; 254366 BP.
XX
AC AB223704;
XX
DT 21-MAR-2003 (first entry)
XX
DE Human phosphatase genomic DNA #SEQ ID 3.
XX
KM Human; phosphatase; enzyme; chromosome 12; colon adenocarcinoma;
KM placenta; gene therapy; single nucleotide polymorphism; SNP;
KM gene; ds.
XX
XX Homo sapiens.
XX
XX
FH Key
FH variation
FT Location/Qualifiers
FT replace(36..37,A)
FT /tag= a
FT /standard_name= "single nucleotide polymorphism"
FT replace(1414, A,C)
FT /tag= b
FT /standard_name= "single nucleotide polymorphism"
FT replace(1743,C)
FT /tag= c
FT /standard_name= "single nucleotide polymorphism"
FT replace(2766,A)
FT /tag= d
FT /standard_name= "single nucleotide polymorphism"
FT replace(3155,T)
FT variation

```
FT      /*tag- e  
FT      /standard_name="single nucleotide polymorphism"  
FT      replace(5816,A)  
FT      /*tag- f  
FT      /standard_name="single nucleotide polymorphism"  
FT      replace(6074,T)  
FT      /*tag- g  
FT      /standard_name="single nucleotide polymorphism"  
FT      replace(9550,C)  
FT      /*tag- h  
FT      /standard_name="single nucleotide polymorphism"  
FT      replace(9644,G)  
FT      /*tag- i  
FT      /standard_name="single nucleotide polymorphism"  
FT      replace(16630,G)  
FT      /*tag- j  
FT      /standard_name="single nucleotide polymorphism"  
FT      replace(17957,A)  
FT      /*tag- k  
FT      /standard_name="single nucleotide polymorphism"  
FT      replace(18299,G)  
FT      /*tag- l  
FT      /standard_name="single nucleotide polymorphism"  
FT      replace(23521,G)  
FT      /*tag- m  
FT      /standard_name="single nucleotide polymorphism"  
FT      replace(28463,A)  
FT      /*tag- n  
FT      /standard_name="single nucleotide polymorphism"  
FT      replace(35221,T)  
FT      /*tag- o  
FT      /standard_name="single nucleotide polymorphism"  
FT      replace(41813,G)  
FT      /*tag- p  
FT      /standard_name="single nucleotide polymorphism"  
FT      replace(41957,T)  
FT      /*tag- q  
FT      /standard_name="single nucleotide polymorphism"  
FT      replace(42599,T)  
FT      /*tag- r  
FT      /standard_name="single nucleotide polymorphism"  
FT      replace(47819,A)  
FT      /*tag- s  
FT      /standard_name="single nucleotide polymorphism"  
FT      replace(51990..51991,A)  
FT      /*tag- t  
FT      /standard_name="single nucleotide polymorphism"  
FT      replace(51992,T)  
FT      /*tag- u  
FT      /standard_name="single nucleotide polymorphism"  
FT      replace(51992..51993,T)  
FT      /*tag- v  
FT      /standard_name="single nucleotide polymorphism"  
FT      replace(52788,A)  
FT      /*tag- w  
FT      /standard_name="single nucleotide polymorphism"  
FT      replace(55029,C)  
FT      /*tag- x  
FT      /standard_name="single nucleotide polymorphism"  
FT      replace(60776,T)  
FT      /*tag- y  
FT      /standard_name="single nucleotide polymorphism"  
FT      replace(61193,G)  
FT      /*tag- z  
FT      /standard_name="single nucleotide polymorphism"  
FT      replace(63994,T)  
FT      /*tag- aa  
FT      /standard_name="single nucleotide polymorphism"  
FT      replace(63244,T)  
FT      /*tag- ab  
FT      /standard_name="single nucleotide polymorphism"  
FT      replace(65053,T)  
FT      /*tag- ac  
FT      /standard_name="single nucleotide polymorphism"  
FT      replace(68460,A)  
FT      /*tag- ad  
FT      /standard_name="single nucleotide polymorphism"  
FT      replace(69326,G)  
FT      /*tag- ae  
FT      /standard_name="single nucleotide polymorphism"  
FT      replace(73039,G)  
FT      /*tag- af  
FT      /standard_name="single nucleotide polymorphism"  
FT      replace(73084,G)  
FT      /*tag- ag  
FT      /standard_name="single nucleotide polymorphism"  
FT      replace(75205,A)  
FT      /*tag- ah  
FT      /standard_name="single nucleotide polymorphism"  
FT      replace(75491,C)  
FT      /*tag- ai  
FT      /standard_name="single nucleotide polymorphism"  
FT      replace(75962,T)  
FT      /*tag- aj  
FT      /standard_name="single nucleotide polymorphism"  
FT      replace(82853,A)  
FT      /*tag- ak  
FT      /standard_name="single nucleotide polymorphism"  
FT      replace(82930,C)  
FT      /*tag- al  
FT      /standard_name="single nucleotide polymorphism"  
FT      replace(86505,C)  
FT      /*tag- am  
FT      /standard_name="single nucleotide polymorphism"  
FT      replace(95970,A)  
FT      /*tag- an  
FT      /standard_name="single nucleotide polymorphism"  
FT      replace(95970..95971,A)  
FT      /*tag- ao  
FT      /standard_name="single nucleotide polymorphism"  
FT      replace(96524,T)  
FT      /*tag- ap  
FT      /standard_name="single nucleotide polymorphism"  
FT      replace(100868,A)  
FT      /*tag- aq  
FT      /standard_name="single nucleotide polymorphism"  
FT      replace(102246,G)  
FT      /*tag- ar  
FT      /standard_name="single nucleotide polymorphism"  
FT      replace(107335,T)  
FT      /*tag- as  
FT      /standard_name="single nucleotide polymorphism"  
FT      replace(107921,T)  
FT      /*tag- at  
FT      /standard_name="single nucleotide polymorphism"  
FT      replace(110413,T)  
FT      /*tag- au  
FT      /standard_name="single nucleotide polymorphism"  
FT      replace(111600,G)  
FT      /*tag- av  
FT      /standard_name="single nucleotide polymorphism"  
FT      replace(114518,C)  
FT      /*tag- aw  
FT      /standard_name="single nucleotide polymorphism"  
FT      replace(114614,T)  
FT      /*tag- ax  
FT      /standard_name="single nucleotide polymorphism"  
FT      replace(124665,A)  
FT      /*tag- ay  
FT      /standard_name="single nucleotide polymorphism"  
FT      replace(125409,A)  
FT      /*tag- az  
FT      /standard_name="single nucleotide polymorphism"  
FT      replace(129447,A)  
FT      /*tag- ba  
FT      /standard_name="single nucleotide polymorphism"
```

```
FT variation replace(135139,G)
FT /tag= db
FT /standard_name= "single nucleotide polymorphism"
FT variation replace(148111,T)
FT /tag= bc
FT /standard_name= "single nucleotide polymorphism"
FT variation replace(200822,G)
FT /tag= bd
FT /standard_name= "single nucleotide polymorphism"
FT variation replace(207967,G)
FT /tag= be
FT /standard_name= "single nucleotide polymorphism"
FT variation replace(213624,C)
FT /tag= bf
FT /standard_name= "single nucleotide polymorphism"
FT variation replace(215753,G)
FT /tag= bg
FT /standard_name= "single nucleotide polymorphism"
FT variation replace(216081,A)
FT /tag= bh
FT /standard_name= "single nucleotide polymorphism"
FT variation replace(218692,T)
FT /tag= bi
FT /standard_name= "single nucleotide polymorphism"
FT variation replace(218705,G)
FT /tag= bj
```

Query Match 0.1%; Score 22; DB 25; Length 254366;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
OY 25240 AACGCAAAATTAATTTAA 25261
Db 244415 AACGCAAAATTAATTTAA 244436
```

RESULT 41

```
AAF22305
ID AAF22305 standard; DNA; 1082138 BP.
XX
AC AAF22305;
XX
DT 20-MAR-2001 (first entry)
XX
DE Arabidopsis thaliana chromosome 4 centromere.
XX
KW Centromere; michromosome; vector; ds.
XX
OS Arabidopsis thaliana.
XX
PN WO200055325-A2.
XX
PD 21-SEP-2000.
XX
PF 17-MAR-2000; 2000WO-US07392.
XX
PR 18-MAR-1999; 99US-0125219.
PR 01-APR-1999; 99US-0127409.
PR 18-MAY-1999; 99US-0134770.
PR 13-SEP-1999; 99US-0153584.
PR 17-SEP-1999; 99US-0154603.
XX
PA (UYCH-) UNIV CHICAGO.
PI Preuss D, Copenhaver G, Keith K;
XX
DR WPI; 2000-587529/55.
XX
PT Recombinant DNA construct comprising a plant centromere, useful for
PT producing stably inherited michrosomes which can serve as vectors for
PT the construction of transgenic plant and animal cells.
PS Claim 68; Page 977-1388; 1449pp; English.
```

```
XX
CC The present invention relates to a recombinant DNA construct of a plant
CC (Arabidopsis thaliana) centromere. The constructs are useful for
CC producing stably inherited michrosomes which can serve as vectors for
CC the construction of transgenic plant and animal cells expressing
CC selected proteins such as hormones, enzymes, interleukins, clotting
CC factors, cytokines, antibodies, and growth factors.
XX
SQ Sequence 1082138 BP; 348775 A; 194404 C; 195515 G; 343444 T; 0 other;
```

Query Match 0.1%; Score 22; DB 21; Length 1082138;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
OY 25246 AAAATTAATTTAAATAATA 25267
Db 637773 AAAATTAATTTAAATAATA 637794
```

RESULT 42

```
AAH42781/C
ID AAH42781 standard; cDNA; 414 BP.
XX
AC AAH42781;
XX
DT 01-OCT-2001 (first entry)
XX
DE Nucleotide sequence of cancer associated gene KIA0160.
XX
KW Cancer associated gene; prostate cancer; stomach cancer;
KW oesophageal cancer; cancer; vaccine; ss.
XX
OS Homo sapiens.
XX
PN WO200153524-A2.
XX
PD 26-JUL-2001.
XX
PF 18-JAN-2001; 2001WO-GB00188.
XX
PR 18-JAN-2000; 2000GB-0000993.
XX
PA (UYNO-) UNIV NOTTINGHAM TRENT.
XX
PI Rees RC, Li G, Mian S;
XX
DR WPI; 2001-476121/51.
XX
PT Use of cancer-associated genes and their products in detecting,
PT monitoring, treating or preventing cancer, specifically prostate
PT cancer, and in developing DNA-based vaccines that promote anti-tumor
PT responses
```

Claim 1; Page 18; 43pp; English.

AAH42781-AAH42846 represent the nucleotide sequences of cancer associated genes, identified using SEREX (Serological Identification of Antigens by Recombinant Expression Cloning). The genes are overexpressed in prostate cancer, and some are overexpressed in other cancers such as stomach cancer and oesophageal cancer. The nucleic acids are useful for detecting and monitoring cancer, particularly prostate cancer. They are particularly useful in the treatment or prevention of cancer, in producing DNA-based vaccines against prostate cancer or that promote anti-tumor immune responses, and to raise antibodies. The expression of genes and detection of their protein products and/or peptides may be used to monitor disease progression during therapy, or as a prognostic indicator of initial disease status of the patient.

Sequence 414 BP; 101 A; 102 C; 132 G; 79 T; 0 other;

Query Match 0.1%; Score 21; DB 22; Length 414;
Best Local Similarity 100.0%; Pred. No. 1,4e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12956 GCCACCGCGCGGACCCCG 12976
|||||
DB 62 GCCACCGCGCGGACCCCG 42

RESULT 43
ABQ41636
ID ABQ41636 standard; DNA: 597 BP.
XX
AC ABQ41636:
XX
DT 12-JUL-2002 (first entry)
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 28227.
XX
KW Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
KW drug; side effect; cancer; central nervous system; cardiovascular;
KW gastrointestinal; respiratory system; single nucleotide polymorphism;
KW SNP; cell differentiation; ds.
XX
OS Homo sapiens.
XX
PN WO200218632-A2.
XX
PD 07-MAR-2002.
XX
PF 01-SEP-2001; 2001WO-EP10074.
XX
PR 01-SEP-2000; 2000DE-1043826.
XX
PR 05-SEP-2000; 2000DE-1044543.
XX
PA (EPIC-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K, Guetig D;
XX
DR WPI; 2002-371829/40.
XX
PT Determining the degree of cytosine methylation in genomic DNA, useful
PT for diagnosis and prognosis, comprises selective hybridization of
PT amplicons from chemically treated DNA -
XX
PS Claim 12: 56bp + Sequence Listing; 56bp; German.
XX
CC This invention describes a novel method for determining the degree of
CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a
CC genomic sample of DNA. The sample is treated chemically to convert
CC cytosine (C) but not methylated C, to uracil, then part of the genomic
CC DNA that contains the target C is amplified to form a labeled amplicon.
CC The amplicon is hybridised to two classes, each with at least one
CC member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers
CC and the degree of hybridisation to both classes is determined from the
CC label on the amplicon. From the ratio of labels hybridised to the two
CC classes of oligomers, the degree of methylation is calculated. The method
CC is used: (i) for diagnosis and/or prognosis of side effects of
CC therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders
CC of the central nervous, cardiovascular, gastrointestinal and respiratory
CC systems etc., particularly by detecting mutations or single nucleotide
CC polymorphisms (SNP's); and (ii) for differentiation of cell or tissue
CC types and for investigating cell differentiation. The method allows the
CC methylation status of many C residues to be determined simultaneously.
CC ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the
CC method for determining the degree of cytosine methylation described in
CC the disclosure of the invention.
XX
SQ Sequence 597 BP; 48 A; 87 C; 217 G; 245 T; 0 other;

Query Match 0.1%; Score 21; DB 24; Length 597;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 16383 GCGGGGCGCGGGGCGCG 16403
|||||

DB 413 GCGGGGCGCGGGGCGCG 433

RESULT 44
ABQ41637/C
ID ABQ41637 standard; DNA: 597 BP.
XX
AC ABQ41637:
XX
DT 12-JUL-2002 (first entry)
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 28228.
XX
KW Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
KW drug; side effect; cancer; central nervous system; cardiovascular;
KW gastrointestinal; respiratory system; single nucleotide polymorphism;
KW SNP; cell differentiation; ds.
XX
OS Homo sapiens.
XX
PN WO200218632-A2.
XX
PD 07-MAR-2002.
XX
PF 01-SEP-2001; 2001WO-EP10074.
XX
PR 01-SEP-2000; 2000DE-1043826.
XX
PR 05-SEP-2000; 2000DE-1044543.
XX
PA (EPIC-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K, Guetig D;
XX
DR WPI; 2002-371829/40.
XX
PT Determining the degree of cytosine methylation in genomic DNA, useful
PT for diagnosis and prognosis, comprises selective hybridization of
PT amplicons from chemically treated DNA -
XX
PS Claim 12: 56bp + Sequence Listing; 56bp; German.
XX
CC This invention describes a novel method for determining the degree of
CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a
CC genomic sample of DNA. The sample is treated chemically to convert
CC cytosine (C) but not methylated C, to uracil, then part of the genomic
CC DNA that contains the target C is amplified to form a labeled amplicon.
CC The amplicon is hybridised to two classes, each with at least one
CC member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers
CC and the degree of hybridisation to both classes is determined from the
CC label on the amplicon. From the ratio of labels hybridised to the two
CC classes of oligomers, the degree of methylation is calculated. The method
CC is used: (i) for diagnosis and/or prognosis of side effects of
CC therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders
CC of the central nervous, cardiovascular, gastrointestinal and respiratory
CC systems etc., particularly by detecting mutations or single nucleotide
CC polymorphisms (SNP's); and (ii) for differentiation of cell or tissue
CC types and for investigating cell differentiation. The method allows the
CC methylation status of many C residues to be determined simultaneously.
CC ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the
CC method for determining the degree of cytosine methylation described in
CC the disclosure of the invention.
XX
SQ Sequence 597 BP; 245 A; 217 C; 87 G; 48 T; 0 other;

Query Match 0.1%; Score 21; DB 24; Length 597;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 16383 GCGGGGCGCGGGGCGCG 16403
|||||

DB 185 GCGGGGCGCGGGGCGCG 165

RESULT 45
AAK77708
ID AAK77708 standard; DNA; 607 BP.
XX
AC AAK77708;
XX
DT 07-NOV-2001 (first entry)
XX
DE Human Immune/haematopoietic antigen genomic sequence SEQ ID NO:32520.
XX
KW Human; Immune; haematopoietic; immune/haematopoietic antigen; cancer;
XX cytostatic; gene therapy; vaccine; metastasis; ds.
OS Homo sapiens.
XX
PN WO200157182-A2.
XX
PD 09-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01354.
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0188874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226868.
PR 23-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.

PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 13-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249246.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249266.
PR 17-NOV-2000; 2000US-0249267.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.


```

PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 11-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
XX
XX WPI; 2001-483426/52.
XX
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
XX useful for preventing, diagnosing and/or treating cancers and
XX metastasis -
XX
XX PS Disclosure; SEQ ID NO 32520; 3071bp + Sequence Listing; English.
XX
XX CC AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)
XX amino acid sequences given in AAK82170 to AAK91921. (I) have cytostatic
XX activity, and can be used in gene therapy and vaccine production. (I)
XX proteins and polynucleotides may be used in the prevention, diagnosis and
XX treatment of diseases associated with inappropriate (I) expression. For
XX example, they may be used to treat disorders associated with decreased
XX expression by rectifying mutations or deletions in a patient's genome
XX that affect the activity of (I) by expressing inactive proteins or to
XX supplement the patient's own production of (I). Additionally, (I)
XX polynucleotides may be used to produce the secreted (I), by inserting
XX the nucleic acids into a host cell and culturing the cell to express the
XX protein. (I) proteins and polynucleotides may be used to prevent,
XX diagnose and treat immune/hematopoietic-related diseases, especially
XX cancers and cancer metastases of hematopoietic-derived cells. AAK64703
XX to AAK87694 represent human immune/hematopoietic antigen genomic
XX sequences from the present invention. AAK54942 to AAK54950 and AAK82169
XX represent sequences used in the exemplification of the present invention.
XX
XX SO Sequence 607 BP; 192 A; 127 C; 123 G; 165 T; 0 other;

```

```

Query Match          0.1%; Score 21; DB 22; Length 607;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

OY 12632 AATGAAATATATATATATATA 12652
    |||||||||||||||||||
DB 60 AATGAAATATATATATATATATA 80

```

```

Search completed: September 30, 2003, 03:05:17
Job time : 6377 secs

```

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 29, 2003, 10:19:43 ; Search time 7579 Seconds
(Without alignments)
12466.068 Million cell updates/sec

Title: US-09-831-000-1_COPY_1_35000
 Perfect score: 35000

Sequence: 1 gatcgggaaaaacgcgagggg.....cagctaaccacacatttag 35000

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 2552756 seqs, 1349719017 residues

word size :

Total number of hits satisfying chosen parameters: 5105512

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

Post-processing: Listing first 45 summaries

Database : N_Geneseq_19Jun03:*

1:	/SIDSL/gcgdata/genseq/genseqn-emb1/NA1980.DAT *
2:	/SIDSL/gcgdata/genseq/genseqn-emb1/NA1961.DAT *
3:	/SIDSL/gcgdata/genseq/genseqn-emb1/NA1982.DAT *
4:	/SIDSL/gcgdata/genseq/genseqn-emb1/NA1983.DAT *
5:	/SIDSL/gcgdata/genseq/genseqn-emb1/NA1984.DAT *
6:	/SIDSL/gcgdata/genseq/genseqn-emb1/NA1985.DAT *
7:	/SIDSL/gcgdata/genseq/genseqn-emb1/NA1986.DAT *
8:	/SIDSL/gcgdata/genseq/genseqn-emb1/NA1987.DAT *
9:	/SIDSL/gcgdata/genseq/genseqn-emb1/NA1988.DAT *
10:	/SIDSL/gcgdata/genseq/genseqn-emb1/NA1989.DAT *
11:	/SIDSL/gcgdata/genseq/genseqn-emb1/NA1990.DAT *
12:	/SIDSL/gcgdata/genseq/genseqn-emb1/NA1991.DAT *
13:	/SIDSL/gcgdata/genseq/genseqn-emb1/NA1992.DAT *
14:	/SIDSL/gcgdata/genseq/genseqn-emb1/NA1993.DAT *
15:	/SIDSL/gcgdata/genseq/genseqn-emb1/NA1994.DAT *
16:	/SIDSL/gcgdata/genseq/genseqn-emb1/NA1995.DAT *
17:	/SIDSL/gcgdata/genseq/genseqn-emb1/NA1996.DAT *
18:	/SIDSL/gcgdata/genseq/genseqn-emb1/NA1997.DAT *
19:	/SIDSL/gcgdata/genseq/genseqn-emb1/NA1998.DAT *
20:	/SIDSL/gcgdata/genseq/genseqn-emb1/NA1999.DAT *
21:	/SIDSL/gcgdata/genseq/genseqn-emb1/NA2000.DAT *
22:	/SIDSL/gcgdata/genseq/genseqn-emb1/NA2001.DAT *
23:	/SIDSL/gcgdata/genseq/genseqn-emb1/NA2001B.DAT *
24:	/SIDSL/gcgdata/genseq/genseqn-emb1/NA2002.DAT *
25:	/SIDSL/gcgdata/genseq/genseqn-emb1/NA2003.DAT *

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysts of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	35000	100.0	133719	21	AAIC64754	Macca mulatta Rha
2	29420	84.1	128139	24	AAI164291	RRV genome nucleot
3	624	1.8	624	21	AAIC64764	RRV interleukin 6
4	348	1.0	348	21	AAIC64765	RRV macrophage in
5	201	0.6	630	24	AAI164294	RRV nucleotide se
6	107	0.3	406	24	AAI164295	JMHV ORF17 nucleot
7	107	0.3	487	24	ABA97190	JMHV ORF17 nucleot
8	74	0.2	358	24	AAI164298	JMHV ORF7 nucleotit

C	10	71	0.2	4.66	24	AA164293
C	9	71	0.2	5.24	24	AA164293
C	11	70	0.2	3.14	24	ABA87131
C	12	59	0.2	3.30	24	ABA87194
C	13	58	0.2	6.81	24	ABA87192
C	14	51	0.1	4.88	24	AA164300
C	15	40	0.1	3.89	24	ABA87193
C	16	40	0.1	6.30	24	AA164286
C	17	37	0.1	5.24	24	AA164289
C	18	33	0.1	1.28139	24	AA164291
C	19	33	0.1	1.33719	21	AAC64754
C	20	29	0.1	2.511	18	AA151553
C	21	29	0.1	3.5100	20	AA173802
C	22	29	0.1	1.37507	19	AA151941
C	23	26	0.1	5.36	18	AA151545
C	24	26	0.1	6.51	23	AA849565
C	25	26	0.1	1.1024	25	ABZ83266
C	26	26	0.1	1.536	24	ABO82701
C	27	26	0.1	1.536	24	ABR80458
C	28	26	0.1	1.536	24	ABR33355
C	29	26	0.1	3.298	14	AA184648
C	30	26	0.1	3.298	24	AA594945
C	31	26	0.1	3.612	18	AA184697
C	32	26	0.1	1.8556	22	AA131109
C	33	26	0.1	1.8556	22	AA131109
C	34	26	0.1	1.8556	24	ABN95092
C	35	26	0.1	1.8556	24	ABK33344
C	36	26	0.1	1.8556	24	ABL62854
C	37	26	0.1	1.8556	24	ABL63078
C	38	26	0.1	1.8556	24	ABL67927
C	39	24	0.1	5.35	24	AB183559
C	40	24	0.1	1.539	23	AA849600
C	41	24	0.1	1.692	22	ABA09660
C	42	24	0.1	3.422	23	AA849559
C	43	23	0.1	3.24	19	AA152505
C	44	23	0.1	5.42	24	ABO30241
C	45	23	0.1	5.42	24	ABO30241

ALIGNMENTS

RESULT 1

ID AAC64754 standard; DNA; 133719 BP.

AAC64754 ;

DT 28-FEB-2001 (first entry)

DE Macaca mulatta rhadinovirus 17577 (RRV) genome sequence SEQ ID NO:1

KW genome; mullata; rhadinovirus 15577; RVV; rheus; macque; rhadinovirus;
KW macoma; kaposti's sarcoma-associated herpesvirus; KSHV; interileukin 6;
KW IL-6; macrophage inflammatory protein; MIP; diagnosis; vaccine;
KW cytostatic; anti-HIV; gene therapy; infection; kaposi's sarcoma;
KW lymphoproliferative disorder; B-cell hyperplasia; lymphadenopathy;
KW splenomegaly; hypergammaglobulinlaemia; autoimmune haemolytic anaemia;
KW ds.

OS Macaca mulatta rhadinovirus 17577.

PN WO200028040-A2

PD 18-MAY-2000.

PF 05-NOV-1999; 99WO-US26260.

PR	06-NOV-1998;	98US-0107507.
PR	20-NOV-1998;	98US-0109409.

PA (UYOR-) UNIV OREGON HEALTH SCI.

XX

QY 1621 CAACACGCGAGTAAACATCGATTTTCGGGTAAAGCTACCGCCCTCACGGCTCCAG 1680
DB 1621 CAACACGCGAGTAAACATCGATTTTCGGGTAAAGCTACCGCCCTCACGGCTCCAG 1680
QY 1681 AACGGCTCTCTTCATACGGGTATACCTACGGCAATTAACACAGGGTATTAAGTGTACT 1740
DB 1681 AACGGCTCTCTTCATACGGGTATACCTACGGCAATTAACACAGGGTATTAAGTGTACT 1740
QY 1741 CTGTGGAACGCTTAAGTAACGCTGTCTTCAATTTAAAGGTACAGCGGTCAACA 1800
DB 1741 CTGTGGAACGCTTAAGTAACGCTGTCTTCAATTTAAAGGTACAGCGGTCAACA 1800
QY 1801 ACGGTACTACAAACAATACATACATTTGTGTTAACAGAAAACAGAGGAGCATTT 1860
DB 1801 ACGGTACTACAAACAATACATACATTTGTGTTAACAGAAAACAGAGGAGCATTT 1860
QY 1861 TCTGTCTGCGTTTATTGGGAATGAAAAATTTCTATCTCAGACAAATTAATGTGTTTTA 1920
DB 1861 TCTGTCTGCGTTTATTGGGAATGAAAAATTTCTATCTCAGACAAATTAATGTGTTTTA 1920
QY 1921 CTTCATTTACCTTTAAACCTTAACACGACATTCCTCAATGAGTACATTTTAAATACG 1980
DB 1921 CTTCATTTACCTTTAAACCTTAACACGACATTCCTCAATGAGTACATTTTAAATACG 1980
QY 1981 GGCATAATACAAACAAGCTAGTGTACAAACATCCTGAAAACACTAGTTGTCTCTGTC 2040
DB 1981 GGCATAATACAAACAAGCTAGTGTACAAACATCCTGAAAACACTAGTTGTCTCTGTC 2040
QY 2041 CCGTTTTTTCTATTGGCGTTTTTAAACAGTATTTGCAATATCTGTAATATGTGTGTTAT 2100
DB 2041 CCGTTTTTTCTATTGGCGTTTTTAAACAGTATTTGCAATATCTGTAATATGTGTGTTAT 2100
QY 2101 TTCAATATACGCTGACAGAGACCTGTAATCATCACTAATAGTATGCAAGCCAGACAA 2160
DB 2101 TTCAATATACGCTGACAGAGACCTGTAATCATCACTAATAGTATGCAAGCCAGACAA 2160
QY 2161 GCTACATTTCAACCCCTCCATTAATCAGCGTTCCAACTACTAATGAATGTAGTCCATACCT 2220
DB 2161 GCTACATTTCAACCCCTCCATTAATCAGCGTTCCAACTACTAATGAATGTAGTCCATACCT 2220
QY 2221 ACAGAAATGCTCATCAGAGAGAGATTTGAAGAACTACCAACACACACAGTGA 2280
DB 2221 ACAGAAATGCTCATCAGAGAGAGATTTGAAGAACTACCAACACACAGTGA 2280
QY 2281 CTGATTTCTGCTGTCATTAATTTACTTTACTTGAAGTGAAGAAATGTAGCCATGAGACCGC 2340
DB 2281 CTGATTTCTGCTGTCATTAATTTACTTTACTTGAAGTGAAGAAATGTAGCCATGAGACCGC 2340
QY 2341 AGGAAAACACAATTAAGCAAGTTATGCAACAGTATGATGATGTGGTTGTAAGAAATATAG 2400
DB 2341 AGGAAAACACAATTAAGCAAGTTATGCAACAGTATGATGATGTGGTTGTAAGAAATATAG 2400
QY 2401 AACCAACATCATATGAGGATTAATGTTGAGCACATGAGCATATAGTACTATAATCCCA 2460
DB 2401 AACCAACATCATATGAGGATTAATGTTGAGCACATGAGCATATAGTACTATAATCCCA 2460
QY 2461 ATTTAATTTACTACAGTGCATTAATATGGAAGAAAGTATGAGTATTAATTAATCCCA 2520
DB 2461 ATTTAATTTACTACAGTGCATTAATATGGAAGAAAGTATGAGTATTAATTAATCCCA 2520
QY 2521 TAGAAAAATCAATATCATGATTAATTAATGAGAAATTTAGATCACAAATGAGTAAATCAT 2580
DB 2521 TAGAAAAATCAATATCATGATTAATTAATGAGAAATTTAGATCACAAATGAGTAAATCAT 2580
QY 2581 TAAATGATTTAAATGATTAAGACAAATATGATGTTGATTAATTAATTAATTAATTAAT 2640
DB 2581 TAAATGATTTAAATGATTAAGACAAATATGATGTTGATTAATTAATTAATTAATTAAT 2640
QY 2641 TTTTAAATTTAAACATTAACAAATTAAGACGATTTTGTGTAATCACTTTATTTATTT 2700
DB 2641 TTTTAAATTTAAACATTAACAAATTAAGACGATTTTGTGTAATCACTTTATTTATTT 2700

QY 2701 AAAATTTTTTCATATACCTGAACCTTAATTAATTTCAATTTCCCTCAAGTTGTATC 2760
DB 2701 AAAATTTTTTCATATACCTGAACCTTAATTAATTTCAATTTCCCTCAAGTTGTATC 2760
QY 2761 TTTGCCCGGTATCTCTGATTAACATGAGTATTTCCGTAAATTAATTTGATGAAAAATAC 2820
DB 2761 TTTGCCCGGTATCTCTGATTAACATGAGTATTTCCGTAAATTAATTTGATGAAAAATAC 2820
QY 2821 ATCAACAATCAAAACCTCCATTAATGCGCGTAAATATATGTTTAAAGGACACTTATAT 2880
DB 2821 ATCAACAATCAAAACCTCCATTAATGCGCGTAAATATATGTTTAAAGGACACTTATAT 2880
QY 2881 AAGAACACTCTCAATAACAGATTTTCTCAATAACCAAGACCGGTAAATTTGTTCTTT 2940
DB 2881 AAGAACACTCTCAATAACAGATTTTCTCAATAACCAAGACCGGTAAATTTGTTCTTT 2940
QY 2941 TAGTTTGTATTTGTCTATTAAGAAATTAACGCATCGTCTAGCGTTCTCGTACAGAGTGC 3000
DB 2941 TAGTTTGTATTTGTCTATTAAGAAATTAACGCATCGTCTAGCGTTCTCGTACAGAGTGC 3000
QY 3001 TCCGTTGCGGTGTCAGTAAATTCCTGCTCAAAATTAATTAATTTCTGTCACAGAG 3060
DB 3001 TCCGTTGCGGTGTCAGTAAATTCCTGCTCAAAATTAATTAATTTCTGTCACAGAG 3060
QY 3061 GCGCTTCTTTTACAGGATGAAAAACATGTTCTTTTCCCATTAATTAACACATTTCTTT 3120
DB 3061 GCGCTTCTTTTACAGGATGAAAAACATGTTCTTTTCCCATTAATTAATTAACACATTTCTTT 3120
QY 3121 ACCTAACACGATGCGGTAGACGTCATTTTCTGAATAATACATATTTGTTCTTAAGTA 3180
DB 3121 ACCTAACACGATGCGGTAGACGTCATTTTCTGAATAATACATATTTGTTCTTAAGTA 3180
QY 3181 CGGCCAAGCATTTGTCGTTTTTACCAATTCCTTAATTTGTCATACACGACATGCA 3240
DB 3181 CGGCCAAGCATTTGTCGTTTTTACCAATTCCTTAATTTGTCATACACGACATGCA 3240
QY 3241 GTTAACCTTAATGTCATGTTTATGTTTACCACTGACGCGTTTAAACAGAGATTTTCA 3300
DB 3241 GTTAACCTTAATGTCATGTTTATGTTTACCACTGACGCGTTTAAACAGAGATTTTCA 3300
QY 3301 CAATTAATAACAAATTAACCCACGTCACATGTAATTTACTTAATGTAATGTAATGTAAT 3360
DB 3301 CAATTAATAACAAATTAACCCACGTCACATGTAATTTACTTAATGTAATGTAATGTAAT 3360
QY 3361 TAGTTAATCATATTCGTTTACATTAATGAGCAAAACGAAAAATGTTACCTGTATAG 3420
DB 3361 TAGTTAATCATATTCGTTTACATTAATGAGCAAAACGAAAAATGTTACCTGTATAG 3420
QY 3421 CCTACCTTGTGTTGATGATTTATGTTTACAAATGAAAAATTAATTAATTAATTAAT 3480
DB 3421 CCTACCTTGTGTTGATGATTTATGTTTACAAATGAAAAATTAATTAATTAATTAAT 3480
QY 3481 TTTTACGTAACAAATTAATGTAATTAATACAGTATGTTTATGTTGCTACAAACACA 3540
DB 3481 TTTTACGTAACAAATTAATGTAATTAATACAGTATGTTTATGTTGCTACAAACACA 3540
QY 3541 ATGTTTGCATTAAGCACTTAATGTTAGAGAGCTTCAATCTTAATTTATTTATTAAT 3600
DB 3541 ATGTTTGCATTAAGCACTTAATGTTAGAGAGCTTCAATCTTAATTTATTTATTAAT 3600
QY 3601 TTAAGAGGATGTAATTAATTTAAACAGCATTTCAAGAAATAGCGCAACGCTGCGCT 3660
DB 3601 TTAAGAGGATGTAATTAATTTAAACAGCATTTCAAGAAATAGCGCAACGCTGCGCT 3660
QY 3661 ATAACTGTTAAACATGACGTTTAACTTTTCTGTTTATTTACAGCCATTAATG 3720
DB 3661 ATAACTGTTAAACATGACGTTTAACTTTTCTGTTTATTTACAGCCATTAATG 3720
QY 3721 TACGTCACGTCGATGAAGAACTGTAACCTCACAATTTACAGGAATATCGGTCAAGTCT 3780
DB 3721 TACGTCACGTCGATGAAGAACTGTAACCTCACAATTTACAGGAATATCGGTCAAGTCT 3780
QY 3781 AACACAGAAAGGACTTATATATGTTGAGAGAAACGCTGAATTAATTTGTCGTCGCT 3840

```
|||||
Db 3781 AACACGAAAAGACTTATATAGTGTGGAGAAACAGCTGAATTAATTTGTCCTCGGT 3940
OY 3841 TATGTACAAATACAAAAATATATACACAGATGTTTACAAAATGGTACGTGTACACA 3900
Db 3841 TATGTACAAATACAAAAATATATACACAGATGTTTACAAAATGGTACGTGTACACA 3900
OY 3901 CCAAAATTTCCATGCGACAGAAAAAGATGCCACACCTGTGACTGCTGTAATGAGCC 3960
Db 3901 CCAAAATTTCCATGCGACAGAAAAAGATGCCACACCTGTGACTGCTGTAATGAGCC 3960
OY 3961 GTGCACATTCACGGGGGAGATATATGCTTAAATTTGATGCAATTTTCCTGTGAGTGT 4020
Db 3961 GTGCACATTCACGGGGGAGATATATGCTTAAATTTGATGCAATTTTCCTGTGAGTGT 4020
OY 4021 AATGAAGTTATGATTTAATTTGTTAGTAAATGTTGCTTTTGTATTTTACAGACAGAA 4080
Db 4021 AATGAAGTTATGATTTAATTTGTTAGTAAATGTTGCTTTTGTATTTTACAGACAGAA 4080
OY 4081 AACGTAAATTTGGGATTCAAATGACACAGCTGTGAAATTCAGAAATGTATTAACGACCG 4140
Db 4081 AACGTAAATTTGGGATTCAAATGACACAGCTGTGAAATTCAGAAATGTATTAACGACCG 4140
OY 4141 GCAGTGAACATGGGGGACTACCTACCTAACCAAGATGTTTATTAAGTATGAGATGCAAT 4200
Db 4141 GCAGTGAACATGGGGGACTACCTACCTAACCAAGATGTTTATTAAGTATGAGATGCAAT 4200
OY 4201 ACATTTAAATGTTTCAATTTGCTATACACTGTTGATCAACAACATTAATGATGACAGTCA 4260
Db 4201 ACATTTAAATGTTTCAATTTGCTATACACTGTTGATCAACAACATTAATGATGACAGTCA 4260
OY 4261 AACAAAAATGGTCAAACTCTTTCCCAAGCTGTTTATGCTGTATGTAAGTGAAGTCCACAA 4320
Db 4261 AACAAAAATGGTCAAACTCTTTCCCAAGCTGTTTATGCTGTATGTAAGTGAAGTCCACAA 4320
OY 4321 ATAGACAATGGGATACATACATTTGCTGTCAGAGATACAAACATTAAGTACATCAAT 4380
Db 4321 ATAGACAATGGGATACATACATTTGCTGTCAGAGATACAAACATTAAGTACATCAAT 4380
OY 4381 ACTGTAAAGTGTAGCGAGCGGTACAAACATTTGGGCTGTGAACATTAACGTGACAAAC 4440
Db 4381 ACTGTAAAGTGTAGCGAGCGGTACAAACATTTGGGCTGTGAACATTAACGTGACAAAC 4440
OY 4441 ACAACTTGGGTTCCACATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 4500
Db 4441 ACAACTTGGGTTCCACATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 4500
OY 4501 ATGCCAGAAACACCCATGCGACAGAAACACCCAGATTAATCAAAAAATTAATTTGTCA 4560
Db 4501 ATGCCAGAAACACCCATGCGACAGAAACACCCAGATTAATCAAAAAATTAATTTGTCA 4560
OY 4561 ACCGCTAAATGTGCAACAAACCAAAATGCGTTTGTACAACTGTTGTTCTCCAGAGAAA 4620
Db 4561 ACCGCTAAATGTGCAACAAACCAAAATGCGTTTGTACAACTGTTGTTCTCCAGAGAAA 4620
OY 4621 GAGCAGCTACTTGTGTAAAGCTCAATTTTGAAGCATTATGTTAAAGCTGAAATGAC 4680
Db 4621 GAGCAGCTACTTGTGTAAAGCTCAATTTTGAAGCATTATGTTAAAGCTGAAATGAC 4680
OY 4681 AAGGAAAAATACAGTGTGTGTCGAGCGTGTGAGCTAATATGTGACACAGATTTACTAAA 4740
Db 4681 AAGGAAAAATACAGTGTGTGTCGAGCGTGTGAGCTAATATGTGACACAGATTTACTAAA 4740
OY 4741 ATGCACTTACAGTTTCTGTGAATGTTTGTCCAAAGCAATGACATGCTCCAAATGCC 4800
Db 4741 ATGCACTTACAGTTTCTGTGAATGTTTGTCCAAAGCAATGACATGCTCCAAATGCC 4800
OY 4801 AAGTGTACATGAAAAAATGTCCAAACCCCTCAAGAACTTTTAAACGAGAGATATAGTT 4860
Db 4801 AAGTGTACATGAAAAAATGTCCAAACCCCTCAAGAACTTTTAAACGAGAGATATAGTT 4860
OY 4861 ACAAGCGGAGAGATGCTTTAAGTAGGAGAAATATTAACATTAATTAATTAATGAGT 4920
|||||
5
1
```

```
Db 4861 ACAAGCGGAGAGATGCTTTTAAAGTAGGAGAAATATTAACATTAATTAATGAGT 4920
OY 4921 TATCAACTTTTAGAGATATGTCGCGATTTGTATGCTTAAAGACGATTTAAACAGTT 4980
Db 4921 TATCAACTTTTAGAGATATGTCGCGATTTGTATGCTTAAAGACGATTTAAACAGTT 4980
OY 4981 GACTGGAGCCAAAGCGCTATATGTGATATTTGAAAAATGTAAAGCCACCCACAATTT 5040
Db 4981 GACTGGAGCCAAAGCGCTATATGTGATATTTGAAAAATGTAAAGCCACCCACAATTT 5040
OY 5041 ACAAGCGGAAAAATACCATCGGTAAGAACTTTTATACATTAATTTGACACCCGTAATTT 5100
Db 5041 ACAAGCGGAAAAATACCATCGGTAAGAACTTTTATACATTAATTTGACACCCGTAATTT 5100
OY 5101 TCGTGCATTCGACTTTTCTTATGTTAGTGAAGATGAATGACAAAGTATTAATTAATGAG 5160
Db 5101 TCGTGCATTCGACTTTTCTTATGTTAGTGAAGATGAATGACAAAGTATTAATTAATGAG 5160
OY 5161 TGGATTAACCCGTTTCCAGATGTGAACAAATCATTGCAAGCGCTCTTAATTTGCAAC 5220
Db 5161 TGGATTAACCCGTTTCCAGATGTGAACAAATCATTGCAAGCGCTCTTAATTTGCAAC 5220
OY 5221 GGAAGCTGTACAGGTTCTTCAACGTTTACAAATACGGTCAATCTGTACATTTGGT 5280
Db 5221 GGAAGCTGTACAGGTTCTTCAACGTTTACAAATACGGTCAATCTGTACATTTGGT 5280
OY 5281 TGTGAACGTGATTTACTCTAATTTGGCAGTGAATTTCTACATGCAAGATTCATGCTG 5340
Db 5281 TGTGAACGTGATTTACTCTAATTTGGCAGTGAATTTCTACATGCAAGATTCATGCTG 5340
OY 5341 GATCCACCACTTCTACGTGCGTGCAGAGTGTGTTCAATGCTTCTGACACACTTAACCA 5400
Db 5341 GATCCACCACTTCTACGTGCGTGCAGAGTGTGTTCAATGCTTCTGACACACTTAACCA 5400
OY 5401 GAAACCAAAAAACCAAAACAGCCACAGCCAGCAAGCAACCAACCAACCAACCAAGTT 5460
Db 5401 GAAACCAAAAAACCAAAACAGCCACAGCCAGCAAGCAACCAACCAACCAACCAAGTT 5460
OY 5461 GGAACACATACACCATTAACCAACCAACCAACCAACCAACCAACCAACCAACCAAGT 5520
Db 5461 GGAACACATACACCATTAACCAACCAACCAACCAACCAACCAACCAACCAACCAAGT 5520
OY 5521 AAATGGAAGGAGATGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 5580
Db 5521 AAATGGAAGGAGATGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 5580
OY 5581 CTTGTCGCCCTTATTTGTTTCTAATAATACTGTTTCTTCAAGAGTTGCGC 5640
Db 5581 CTTGTCGCCCTTATTTGTTTCTAATAATACTGTTTCTTCAAGAGTTGCGC 5640
OY 5641 AAGCAAACTGCGACGATTACCAATCTGCAACCGCGCTGTGATTCGGAATTAAGTTTA 5700
Db 5641 AAGCAAACTGCGACGATTACCAATCTGCAACCGCGCTGTGATTCGGAATTAAGTTTA 5700
OY 5701 CATTATTAAGGTTGCAATTAAGGTTTAAATATTTCAATGTTGTTGTTGTTGTTGTTGTT 5760
Db 5701 CATTATTAAGGTTGCAATTAAGGTTTAAATATTTCAATGTTGTTGTTGTTGTTGTTGTT 5760
OY 5761 ATGTTGACCCGTTTATAGTTATGCGCAGCTTGTGCTGATTAATTAAGCAAGATCACT 5820
Db 5761 ATGTTGACCCGTTTATAGTTATGCGCAGCTTGTGCTGATTAATTAAGCAAGATCACT 5820
OY 5821 TTCACGTTATACCTTACGCTATGACTATACGCTTAAAGCTGACGCTGCGTGCAT 5880
Db 5821 TTCACGTTATACCTTACGCTATGACTATACGCTTAAAGCTGACGCTGCGTGCAT 5880
OY 5881 TGTGCGCGGGGCTGAAAAATTAACAAGGGGTACATATCCATTCACAGCGGCAACATTAG 5940
Db 5881 TGTGCGCGGGGCTGAAAAATTAACAAGGGGTACATATCCATTCACAGCGGCAACATTAG 5940
OY 5941 ACACGGTTATTAATATATGATGATGCGCCAAACATCACTGCTGCTAGCAGACAGATGATA 6000
Db 5941 ACACGGTTATTAATATATGATGATGCGCCAAACATCACTGCTGCTAGCAGACAGATGATA 6000
```

QY	6001	GAAAAACATTTTAAAGTTTGTTTAGCGAACTGAAATAAACAATAAATAGGCTTCCAAAGCA	6060
Db	6001	GAAAAACATTTTAAAGTTTGTTTAGCGAACTGAAATAAACAATAAATAGGCTTCCAAAGCA	6060
QY	6061	ACGCGGGAACAACCCCTGGGAAGTAAATCAGAGGGTCTCGTGGCCGATAGGTGGGTGGGAT	6120
Db	6061	ACGCGGGAACAACCCCTGGGAAGTAAATCAGAGGGTCTCGTGGCCGATAGGTGGGTGGGAT	6120
QY	6121	ACGGTACGGGTATTCGAAACAAAGACTTTCCCTTTGGCGAGGCGCTCATCTCGGCACAA	6180
Db	6121	ACGGTACGGGTATTCGAAACAAAGACTTTCCCTTTGGCGAGGCGCTCATCTCGGCACAA	6180
QY	6181	GACCATCTGATCTGGCGTTTTCCTCGCTACCAATCTTTACGCACTTACAGTTGAACAG	6240
Db	6181	GACCATCTGATCTGGCGTTTTCCTCGCTACCAATCTTTACGCACTTACAGTTGAACAG	6240
QY	6241	AATTCCCTCTCACCCTTAAAGCCGCATACAAAAAGTTGACACACAGCGTGGCCCTTA	6300
Db	6241	AATTCCCTCTCACCCTTAAAGCCGCATACAAAAAGTTGACACACAGCGTGGCCCTTA	6300
QY	6301	AGGTGACGTGCTTTCACAGAGAGGTATTTGTTGTTCACAAATGCAAGTTTATTCGAGCCG	6360
Db	6301	AGGTGACGTGCTTTCACAGAGAGGTATTTGTTGTTCACAAATGCAAGTTTATTCGAGCCG	6360
QY	6361	TGTTTGACGGTACCGGCTTAAACGAACATATGCGAGAAAGCCAGGCTCTCTTTGGGTACA	6420
Db	6361	TGTTTGACGGTACCGGCTTAAACGAACATATGCGAGAAAGCCAGGCTCTCTTTGGGTACA	6420
QY	6421	CGCAGTTTATTAAGAACCCGGGTCCACCTCACAAGCATATGGAACCCCTGTGGAATGTCCGAGT	6480
Db	6421	CGCAGTTTATTAAGAACCCGGGTCCACCTCACAAGCATATGGAACCCCTGTGGAATGTCCGAGT	6480
QY	6481	TACCGGACAAGAGATGAGATGTTTCTTGCGCTGTTGTTCAGGAAGGGTTTAAAGAAAGAC	6540
Db	6481	TACCGGACAAGAGATGAGATGTTTCTTGCGCTGTTGTTCAGGAAGGGTTTAAAGAAAGAC	6540
QY	6541	TGTGGAGGGCGTGTCTCGTCCCGCGGTGTTCACAGCCACAGCAGGTCCAGATTGCCGAC	6600
Db	6541	TGTGGAGGGCGTGTCTCGTCCCGCGGTGTTCACAGCCACAGCAGGTCCAGATTGCCGAC	6600
QY	6601	GCCAGCGCTTAAAGTGGCCGTTGTACAGCAGAAAGCCTGTTTGGACCTTCAGGGTATAGAA	6660
Db	6601	GCCAGCGCTTAAAGTGGCCGTTGTACAGCAGAAAGCCTGTTTGGACCTTCAGGGTATAGAA	6660
QY	6661	TGCCAAGGTTTACCATTAAGACGTTAGCGGGTACTCTACAGACTCCCTCTTACACAGCA	6720
Db	6661	TGCCAAGGTTTACCATTAAGACGTTAGCGGGTACTCTCTACAGACTCCCTCTTACACAGCA	6720
QY	6721	TCGGCCAGGGCCCTGAGACTCAAAAGCGTGAAGGGCGGTATCTCACGCCACAGAAAAAGCAAT	6780
Db	6721	TCGGCCAGGGCCCTGAGACTCAAAAGCGTGAAGGGCGGTATCTCACGCCACAGAAAAAGCAAT	6780
QY	6781	TCATGCAAGACCATTAACAAATTTGCCAAGATAGTGCAGGCAAAAAGTTTCAACAGCAGC	6840
Db	6781	TCATGCAAGACCATTAACAAATTTGCCAAGATAGTGCAGGCAAAAAGTTTCAACAGCAGC	6840
QY	6841	TGGCGAAAGACAGAGAGGGGTGTCGCCACATGATTTGGACAGAGGTGGTGGCCGAGCTCG	6900
Db	6841	TGGCGAAAGACAGAGAGGGGTGTCGCCACATGATTTGGACAGAGGTGGTGGCCGAGCTCG	6900
QY	6901	CCCTTAGTACGGCTGTATGTTTCTCGAGTGTCCCAAGAGCGCTGGAGTTGCTGTA	6960
Db	6901	CCCTTAGTACGGCTGTATGTTTCTCGAGTGTCCCAAGAGCGCTGGAGTTGCTGTA	6960
QY	6961	ACGATAGCTGGCCCATATTTGATGTGTGTGACTACACAGAGGCTAAGGTTAAACCGTTAG	7020
Db	6961	ACGATAGCTGGCCCATATTTGATGTGTGTGACTACACAGAGGCTAAGGTTAAACCGTTAG	7020
QY	7021	AGCGCTGGTGGCGGGAACAGGCGCTTACAGTGGGGGGTCAACTGTGTGCTGCCAATTTCG	7080
Db	7021	AGCGCTGGTGGCGGGAACAGGCGCTTACAGTGGGGGGTCAACTGTGTGCTGCCAATTTCG	7080

QY	7081	1GCTGTACTTAACCTAAAGTGCAGAAACAAGGCCGCCAGGAGCAAAAGGAGACCTAAACG	7140
Db	7081	TGCTGTACTTAACCTAAAGTGCAGAAAGAGGCCAGGAGCAAAAGGAGAGCTAAACG	7140
QY	7141	TGTAACAACCTCTTTTCTCTCCACAAACGAGACTGGGGGTTTAAATGAGGCCACGATCAAG	7200
Db	7141	TGTACAACTCTTTTCTCTCCACAAACGAGACTGGGGGTTTAAATGAGGCCACGATCAAG	7200
QY	7201	AAACGGCAGCGAAGCCCTTAAAGGCGTAGACCTTAAACGCCCTGATGCTTCCGTTCA	7260
Db	7201	AAACGGCAGCGAAGCCCTTAAAGGCGTAGACCTTAAACGCCCTGATGCTTCCGTTCA	7260
QY	7261	CGCGGTATACCTTGGCTTACCGCGCGTCTTCTGCCCCATCTCTGGCGAAGTAATGTT	7320
Db	7261	CGCGGTATACCTTGGCTTACCGCGCGTCTTCTGCCCCATCTCTGGCGAAGTAATGTT	7320
QY	7321	ATTACATGCACTTTCTTGACACACCAAAAGCTCCAGAACCAAGCGCTTAACTAGTGACC	7380
Db	7321	ATTACATGCACTTTCTTGACACACCAAAAGCTCCAGAACCAAGCGCTTAACTAGTGACC	7380
QY	7381	ATTATGTGCGACCGCGCCCAACTCAGAGATGTGACAGCTATGTACAGGCAACGCCGG	7440
Db	7381	ATTATGTGCGACCGCGCCCAACTCAGAGATGTGACAGCTATGTACAGGCAACGCCGG	7440
QY	7441	CAAGTGCTTAAACACAGCTGTTCTAATAGACTGAAAGATAGTTTCCCGCGCTAAACACC	7500
Db	7441	CAAGTGCTTAAACACAGCTGTTCTAATAGACTGAAAGATAGTTTCCCGCGCTAAACACC	7500
QY	7501	CTCAGCGCAGGAGACCCCTTACGTGGTGAACCGGAAACAGCCGGAGACCTTAAACGCTGGAGA	7560
Db	7501	CTCAGCGCAGGAGACCCCTTACGTGGTGAACCGGAAACAGCCGGAGACCTTAAACGCTGGAGA	7560
QY	7561	TTCTTGCGCACTTGCGAGCACTTATAGAGACCGCGAAGAGAGGAAACCCGGCCGACGAGC	7620
Db	7561	TTCTTGCGCACTTGCGAGCACTTATAGAGACCGCGAAGAGAGGAAACCCGGCCGACGAGC	7620
QY	7621	ACCCAAAGTACACGACTACTGGCAGCTATGTACAGCCGTGACAGAAAAGCTATCCCGGATTG	7680
Db	7621	ACCCAAAGTACACGACTACTGGCAGCTATGTACAGCCGTGACAGAAAAGCTATCCCGGATTG	7680
QY	7681	GAATCACCAGAGACAGCATTAATACGAGCACTCATTACCAACATCCAAAGTTTTCGA	7740
Db	7681	GAATCACCAGAGACAGCATTAATACGAGCACTCATTACCAACATCCAAAGTTTTCGA	7740
QY	7741	GGGTGTTCMAAGGTATCGACTCAATTTGTGACGAGAGAGTCAAGTTTCCTTAATCGA	7800
Db	7741	GGGTGTTCMAAGGTATCGACTCAATTTGTGACGAGAGAGTCAAGTTTCCTTAATCGA	7800
QY	7801	TGATTTAAATAATTACTTAATTTCCGCGAGCACGTCGTAATTCGGTCCATCATACTCCAGT	7860
Db	7801	TGATTTAAATAATTACTTAATTTCCGCGAGCACGTCGTAATTCGGTCCATCATACTCCAGT	7860
QY	7861	TCTGTGTGAACGTGATGTGAGAGCGCCGTGCGGGTCTCTGAATCTGACTACACAAT	7920
Db	7861	TCTGTGTGAACGTGATGTGAGAGCGCCGTGCGGGTCTCTGAATCTGACTACACAAT	7920
QY	7921	CCCTGCTGTGATCATTTAGGATATATCTGCTGCGGTATCGATGATCTACAGCAACAAGTA	7980
Db	7921	CCCTGCTGTGATCATTTAGGATATATCTGCTGCGGTATCGATGATCTACAGCAACAAGTA	7980
QY	7981	ATCCGGCGATGGGCACTCCCTCCCTCCGAGTGGCTAAAGATGCATTTTTCAGACGTTGTGGA	8040
Db	7981	ATCCGGCGATGGGCACTCCCTCCCTCCGAGTGGCTAAAGATGCATTTTTCAGACGTTGTGGA	8040
QY	8041	CGAAGCTTTAAAGCGCGCGTGTCTCGACCGCGGGGTCTCTACGCGGTGCGCAACTGAAAATCG	8100
Db	8041	CGAAGCTTTAAAGCGCGCGTGTCTCGACCGCGGGGTCTCTACGCGGTGCGCAACTGAAAATCG	8100
QY	8101	TACACCGGAGCATGTTCTGCGACTTCTTCGACACGACGAGCGCGGGGTCCAAACGGCTTAATG	8160
Db	8101	TACACCGGAGCATGTTCTGCGACTTCTTCGACACGACGAGCGCGGGGTCCAAACGGCTTAATG	8160
QY	8161	CCCCCTTTAAATGCGAGTTAGAAATAGCCGAGGCATGATGATGCTTCCGAATTCATTA	8220

Db	8161	CCCCCTTAAATGCAAGGTAGAAATAGCCCGAGCATGATGTTGGTTCCGAATCAATTA	8220
Qy	8221	AAATAAAAATGAAATCAATTTTTCCTCAACACCCGGGGATCCGAGCGGTGCAATCGGGGT	8280
Db	8221	AAATAAAAAATGAAATCAATTTTTCCTCAACACCCGGGGGATCCGAGCGGTGCAATCGGGGT	8280
Qy	8281	TCGTCAAAACCGACGGGAAACCGAGGACACTTACGTGTGGCCGGACCCGACATGAAAGTTTC	8340
Db	8281	TCGTCAAAACCGACGGGAAACCGAGGACACTTACGTGTGGCCGGACCCGACATGAAAGTTTC	8340
Qy	8341	TCACCTGCTGCATGCGCGCTGTCCCGACACCAAGACCCGCCGTGTACCTGTGC	8400
Db	8341	TCACCTGCTGCATGCGCGCTGTCCCGACACCAAGACCCGCCGTGTACCTGTGC	8400
Qy	8401	ACAAATCTCCAGACCAACAAACCCAGTTCTGAAAGACGTCCCGACACGACGCTGG	8460
Db	8401	ACAAATCTCCAGACCAACAAACCCAGTTCTGAAAGACGTCCCGACACGACGCTGG	8460
Qy	8461	CGGAGCTGTGTCTGACGTAAAGACCAACACCTCCGCTTGAGAGAAACGAACCTGTGG	8520
Db	8461	CGGAGCTGTGTCTGACGTAAAGACCAACACCTCCGCTTGAGAGAAACGAACCTGTGG	8520
Qy	8521	ACGTGTGTCCGGATTCACCTCATGTCTACGCGAGGATCAAACTAGCGGGCCATTTCTAA	8580
Db	8521	ACGTGTGTCCGGATTCACCTCATGTCTACGCGAGGATCAAACTAGCGGGCCATTTCTAA	8580
Qy	8581	GGGCACTGTGGCAGATTCAGTTCTACGCGACGACGCTGCTACGCGCGGTGCTAC	8640
Db	8581	GGGCACTGTGGCAGATTCAGTTCTACGCGACGACGCTGCTACGCGCGGTGCTAC	8640
Qy	8641	AGACGATGATGCGGAGGAATACCCCAAGTGTGGGCTCCGGGGCAATGCGCACACGG	8700
Db	8641	AGACGATGATGCGGAGGAATACCCCAAGTGTGGGCTCCGGGGCAATGCGCACACGG	8700
Qy	8701	TGGCTTACCTGGCAAGAAATACGGCGCCGACACGGCTCAGCCTCAGACGACGGCGGCTC	8760
Db	8701	TGGCTTACCTGGCAAGAAATACGGCGCCGACACGGCTCAGCCTCAGACGACGGCGGCTC	8760
Qy	8761	AGCCGGTGCGCCACAGGGCGCCTGCTCCGTGATTAACGTTCCCATGGTACTCAACA	8820
Db	8761	AGCCGGTGCGCCACAGGGCGCCTGCTCCGTGATTAACGTTCCCATGGTACTCAACA	8820
Qy	8821	AATACAGGGGGGTCAACGGGAAACAAACGTTTCCACTCGGAAACCTGGGGTACTTCC	8880
Db	8821	AATACAGGGGGGTCAACGGGAAACAAACGTTTCCACTCGGAAACCTGGGGTACTTCC	8880
Qy	8881	CGGGCGCGGGGTGAGCGCAACCTGTGTGGCGGAAACCTCCCTTAAAGAAAACGGCG	8940
Db	8881	CGGGCGCGGGGTGAGCGCAACCTGTGTGGCGGAAACCTCCCTTAAAGAAAACGGCG	8940
Qy	8941	TCACGGCATCTCTAAGAAAGACACGTCATGATGACCCCATTAATGACCGCTTAATAA	9000
Db	8941	TCACGGCATCTCTAAGAAAGACACGTCATGATGACCCCATTAATGACCGCTTAATAA	9000
Qy	9001	AGCAGCGCGCGGGACAGACATCTAGCAAGTTTCGAGGGGGGAAAGGTTAAAAAGGCGCTG	9060
Db	9001	AGCAGCGCGCGGGACAGACATCTAGCAAGTTTCGAGGGGGGAAAGGCTTAAAAAGGCGCTG	9060
Qy	9061	AGCGCGTGTAGAGGATTAAGGACAACCTTAACCTATTGAAGTCGGTAATCTTGAGCTTA	9120
Db	9061	AGCGCGTGTAGAGGATTAAGGACAACCTTAACCTATTGAAGTCGGTAATCTTGAGCTTA	9120
Qy	9121	TACGACACCTTGGGGAAGGGGTGCCAGGACTTAACCTCCGAGACGTCGATTAATCTCG	9180
Db	9121	TACGACACCTTGGGGAAGGGGTGCCAGGACTTAACCTCCGAGACGTCGATTAATCTCG	9180
Qy	9181	GTCGACTATTGATTTTACGCGACGAGGTTTATTTACGTGTGAATAAATAGCACAGTCAG	9240
Db	9181	GTCGACTATTGATTTTACGCGACGAGGTTTATTTACGTGTGAATAAATAGCACAGTCAG	9240
Qy	9241	GCCTGCCGTGACTATGAGAGACGCGGGGTGCCTAATAGAGATGCCACAGCGCACAGC	9300
Db	9241	GCCTGCCGTGACTATGAGAGACGCGGGGTGCCTAATAGAGATGCCACAGCGCACAGC	9300

Db	9241	GGGTCCCGGAGCATTCGACGAGCGGGGTGGCTTAATATGAGGATCGCAGACGACAGC	9300
QY	9301	ATCTTCAGTTCGTAGACAGCGACGATATGCGCACCGCTTCTGTACGCCCCCGAGAGAC	9360
Db	9301	ATCTTCAGTTCGTATACAGCGACGATATGCGCACCGCTTCTGTACGCCCCCGAGAGAC	9360
QY	9361	AGCTACCCACCCCTATGCGCCGCGGCCCTACTGCGCGGGAAACAGCAAAATTAACCGC	9420
Db	9361	AGCTACCCACCCCTATGCGCGCGGCCCTACTGCGCGGGAAACAGCAAAATTAACCGC	9420
QY	9421	TGCTGAGCATCTAGACCTTTAGAAAAACGTGCGAGCGGGCAACATGCGCAGGAGAC	9480
Db	9421	TGCTGAGGAGATCTAGACCTTTAGAAAAACGTGCGAGCGGGCAACATGCGCAGGAGAC	9480
QY	9481	TGCGAGCATTTATACGCGGAGCTGTGCGGCCCTGCGCGTGCAGTTAGTTCGTTATCTTTG	9540
Db	9481	TGCGAGCATTTATACGCGGAGCTGTGCGGCCCTGCGCGTGCAGTTAGTTCGTTATCTTTG	9540
QY	9541	CGGACCCCGCGAAGTATCGACGCGTGGCCGATCTTCAAAAACAAAAACAGATAGAGAAC	9600
Db	9541	CGGACCCCGCGAAGTATCGAGGCTGGCCGATCTTCAAAAACAAAAACAGATAGAGAAC	9600
QY	9601	TGAACCGGACCTTCTGCGCGTGTGCTAGCGGCAAAAACCTGGTATGAAACGTCCAGCTGT	9660
Db	9601	TGAACCGGACCTTCTGCGCGTGTGCTAGCGGCAAAAACCTGGTATGAAACGTCCAGCTGT	9660
QY	9661	CGCTGGAAGTGGAGACCTTGCGCAAAAAACATCGAGGACAAACTGCGGACTCGAGCGCA	9720
Db	9661	CGCTGGAAGTGGAGACCTTGCGCAAAAAACATCGAGGACAAACTGCGGACTCGAGCGCA	9720
QY	9721	GTCCTCGCGCAGAGATATTGAGCCGAGAGCATTTTGAACACTACACTAGACCCGAAT	9780
Db	9721	GTCCTCGCGCAGAGATATTGAGCCGAGAGCATTTTGAACACTACACTAGACCCGAAT	9780
QY	9781	GTCATATACACTACAGGCTACTTTTACAGTTTACGGGGCGGGTTATATGATGTAACA	9840
Db	9781	GTCATATACACTACAGGCTACTTTTACAGTTTACGGGGCGGGTTATATGATGTAACA	9840
QY	9841	TGTGCTTAATTAACGATGTAGAACCTGCTGTGTAAAAAGCTAGGAGATGTTTTATTGCA	9900
Db	9841	TGTGCTTAATTAACGATGTAGAACCTGCTGTGTAAAAAGCTAGGAGATGTTTTATTGCA	9900
QY	9901	TGCGGCGCAAGAGACTGTGTCGCGATTGGAACCGGGTTGACGTTCTGTCAACACTGC	9960
Db	9901	TGCGGCGCAAGAGACTGTGTCGCGATTGGAACCGGGTTGACGTTCTGTCAACACTGC	9960
QY	9961	GGGGTATCTCCCGCATCCGCGACCCAGACGATATCTGACGTGAGTCCCTTGGGTACAT	10020
Db	9961	GGGGTATCTCCCGCATCCGCGACCCAGACGATATCTGACGTGAGTCCCTTGGGTACAT	10020
QY	10021	GCCTGAGGGAATGGAAGTCTGTACCAATCAAGGGGTCCAGTTTACTGCGGTTTGGCAG	10080
Db	10021	GCCTGAGGGAATGGAAGTCTGTACCAATCAAGGGGTCCAGTTTACTGCGGTTTGGCAG	10080
QY	10081	ACCGACACTGGGATCACCTCTGTAAAGGTTAGGGGGAGCCAAATACAGGGCTGTGTTG	10140
Db	10081	ACCGACACTGGGATCACCTCTGTAAAGGTTAGGGGGAGCCAAATACAGGGCTGTGTTG	10140
QY	10141	AGACAGAACTGAGCAGCTGGGTCTAAAGTAAACAAAAGTTTGGAGCGCCAGCAGCAG	10200
Db	10141	AGACAGAACTGAGCAGCTGGGTCTAAAGTAAACAAAAGTTTGGAGCGCCAGCAGCAG	10200
QY	10201	GGCTGCGGCTCTGCGAGATACGTTAAGGAGAGTGTGCTGGGGGCGCATACAGATACACA	10260
Db	10201	GGCTGCGGCTCTGCGAGATACGTTAAGGAGAGTGTGCTGGGGGCGCATACAGATACACA	10260
QY	10261	ATATATTTCAAAAGGGGTCTCGCGCTCAATTCATGGAACATCAATCTAATTTATTTGGAAG	10320
Db	10261	ATATATTTCAAAAGGGGTCTCGCGCTCAATTCATGGAACATCAATCTAATTTATTTGGAAG	10320
QY	10321	CCGGGCAAAACGGCTCTCAGACCGGGGACGAAAAACAGTGTCTACAAATGGCCAGCTCG	10380
Db	10321	CCGGGCAAAACGGCTCTCAGACCGGGGACGAAAAACAGTGTCTACAAATGGCCAGCTCG	10380

OY	10381	TAACACACGAGGCCGATATGCTACAGAGACCCTGCTCTAATTAACACCAACTAAGCGCGA	10440
Db	10381	TAACACACGAGGCCGATATGCTACAGAGACCCTGCTCTAATTAACACCAACTAAGCGCGA	10440
OY	10441	CTCAGCTCTAGAGATGTTTCCGAGCGGGATGCCATTAATATCCGTTCTCGCGCGGCTTT	10500
Db	10441	CTCAGCTCTAGAGATGTTTCCGAGCGGGATGCCATTAATATCCGTTCTCGCGCGGCTTT	10500
OY	10501	TTAAGCTATAGACGACACCATTAAGACGACTGAGCCGGGATTTGCTCCGAGCTTCTTC	10560
Db	10501	TTAAGCTATAGACGACACCATTAAGACGACTGAGCCGGGATTTGCTCCGAGCTTCTTC	10560
OY	10561	AACAGGCAAACTATACCAACGTTATGCGAAAACAAAACGAGCTTTCACCAACATCAATA	10620
Db	10561	AACAGGCAAACTATACCAACGTTATGCGAAAACAAAACGAGCTTTCACCAACATCAATA	10620
OY	10621	GCAATCTGCGCTCAAGGGAGCGCGGGATCGCAAAAACCGGCCACCCCTCTGAGCCACGGA	10680
Db	10621	GCAATCTGCGCTCAAGGGAGCGCGGGATCGCAAAAACCGGCCACCCCTCTGAGCCACGGA	10680
OY	10681	CCACACCCGTTGCGGCAACCGCGGCAAGGAGCTCATCAAAGCGACAGTATCGCAAG	10740
Db	10681	CCACACCCGTTGCGGCAACCGCGGCAAGGAGCTCATCAAAGCGACAGTATCGCAAG	10740
OY	10741	AACAGTACATGAAAAAGTGTCGCAAGGAGCGGCTTTAAAAACCTAACAGAGTCTGCGAGA	10800
Db	10741	AACAGTACATGAAAAAGTGTCGCAAGGAGCGGCTTTAAAAACCTAACAGAGTCTGCGAGA	10800
OY	10801	CGCAGACCGCGGTGTTGGCAAAACGACTGTGCGCGCTATGCGGGGCGCTCGGCTACG	10860
Db	10801	CGCAGACCGCGGTGTTGGCAAAACGACTGTGCGCGCTATGCGGGGCGCTCGGCTACG	10860
OY	10861	GCGAGGGGCTCGAGGCTGTGAACATTTTCTCTCAAGGGGGGCTTCTGCTGGGCTTCCCT	10920
Db	10861	GCGAGGGGCTCGAGGCTGTGAACATTTTCTCTCAAGGGGGGCTTCTGCTGGGCTTCCCT	10920
OY	10921	GGGAGGGCGCTGCGGCTCGGATCAGATTTTATTCAAAACTCAAAAGTCAATTAANAAT	10980
Db	10921	GGGAGGGCGCTGCGGCTCGGATCAGATTTTATTCAAAACTCAAAAGTCAATTAANAAT	10980
OY	10981	CACATATTTCCCAAGCGCTCAGTTCGGGACACGTAAAGATTTACAGCTGCGAGTTTACG	11040
Db	10981	CACATATTTCCCAAGCGCTCAGTTCGGGACACGTAAAGATTTACAGCTGCGAGTTTACG	11040
OY	11041	GCTGTATTAACCGGGCCCTCAGCGCGCAGGAGCATCTTTCGCCGGCCCGGCACAGCTG	11100
Db	11041	GCTGTATTAACCGGGCCCTCAGCGCGCAGGAGCATCTTTCGCCGGCCCGGCACAGCTG	11100
OY	11101	CGGTGGCCCAAGTGTTCGAGGGCGGCGGAATGCTTCGCGATCAACAAGATGCTGTGTAG	11160
Db	11101	CGGTGGCCCAAGTGTTCGAGGGCGGCGGAATGCTTCGCGATCAACAAGATGCTGTGTAG	11160
OY	11161	AGATGATATGCCCCCAGATTCACCAACCGAAAGACGTGGATACCAAGATTAATTCGTTTT	11220
Db	11161	AGATGATATGCCCCCAGATTCACCAACCGAAAGACGTGGATACCAAGATTAATTCGTTTT	11220
OY	11221	ACCAAACTTCCGGAAGGTGATCTCAACGCGGTACAAAAAGTCCGCTGTCTTATATACGAG	11280
Db	11221	ACCAAACTTCCGGAAGGTGATCTCAACGCGGTACAAAAAGTCCGCTGTCTTATATACGAG	11280
OY	11281	AGCTCGTCTCTCGGTGGCGCTTTATATTCGCACTGCGGAAAAAGACGCTGCGGATATTTT	11340
Db	11281	AGCTCGTCTCTCGGTGGCGCTTTATATTCGCACTGCGGAAAAAGACGCTGCGGATATTTT	11340
OY	11341	CCCTAGGCGCGGAACCTCTCCATCTCCAACTTAAGCGTTAAAGGCTCGAGCTCGGGCC	11400
Db	11341	CCCTAGGCGCGGAACCTCTCCATCTCCAACTTAAGCGTTAAAGGCTCGAGCTCGGGCC	11400
OY	11401	TGTATCTAAGCTACGACCAAGACGCGCGCTGTCTAATTTCTCAAAATACCGGCTGGA	11460
Db	11401	TGTATCTAAGCTACGACCAAGACGCGCGCTGTCTAATTTCTCAAAATACCGGCTGGA	11460

QY	11461	TATTTAAAGACGTGTACGCTCTTCTGTACCATCTGCAACTGTTCGACGGCCATGATG	11520
Db	11461	TATTTAAAGACGTGTACGCTCTTCTGTACCATCTGCAACTGTTCGACGGCCATGATG	11520
QY	11521	ATTAACTAACGGAACGGGTGTCGTGCGGGGGCTGGGTGTGTAATGCGATCGGCACG	11580
Db	11521	ATTAACTAACGGAACGGGTGTCGTCTCTGTGCGGGGGCTGGGTGTGTAATGCGATCGGCACG	11580
QY	11581	GCGGTTTGGCGAAAACGTACACACACCCCCAAGGGGGCGCACACACACGCGAAGCCAAACGGCG	11640
Db	11581	GCGGTTTGGCGAAAACGTACACACACCCCCAAGGGGGCGCACACACACGCGAAGCCAAACGGCG	11640
QY	11641	GGCCCGTGTGACGCCACACTCTCCCGAAGAACCCACTAGGCGCGAGCGTTTAAGTTTGC	11700
Db	11641	GGCCCGTGTGACGGCCACACTCTCCCGAAGAACCCCACTAGGCGCGAGCGTTTAAGTTTGC	11700
QY	11701	GTTGTGACGGGCTGTGGGCGACGGGGGAACCTTCAGGTTTAACCTGGAAAAAACGTTGCG	11760
Db	11701	GTTGTGACGGGCTGTGGGCGACGGGGGAACCTTCAGGTTTAACCTGGAAAAAACGTTGCG	11760
QY	11761	GGCACCGAAGACAAGACGACACAAAGAGCATCTATAGTGTTTTAAAAAAAATATTGTC	11820
Db	11761	GGCACCGAAGACAAGACGACACAAAGAGCATCTGATGTGTTTAAAAAAAATATTGTC	11820
QY	11821	CCGCACATCTTTAAGTGTAGACGGTACCGCAAGGTGGCCACTCGGTGACCTCTATGCA	11880
Db	11821	CCGCACATCTTTTAAAGTGTACAGCCGTACCCGCAAGGTGGCCACTCGGTGACCTCTATGCA	11880
QY	11881	GGGTGACCGCAAGACCGCGGTGACCGGGCAAGCAAGAGTATCGACGCGGTGGCGGAGTAC	11940
Db	11881	GGGTGACCGCAAGACCGCGGTGACCGGGCAAGCAAGAGTATCGACGCGGTGGCGGAGTAC	11940
QY	11941	GAGATTCAACACATGTGACACAGACTACCAAGTGTTTAGCTTCATGCGTGCCTAAACGTCAAC	12000
Db	11941	GAGATTCAACACATGTGACACAGACTACCAAGTGTTTAGCTTCATGCGTGCCTAAACGTCAAC	12000
QY	12001	GGCATAGTAAACACTACACGACAGGAGCTTCACTAACACACGCTGTTTCTCAACCG	12060
Db	12001	GGCATAGTAAACACTACACGACAGGAGCTTCACTAACACACGCTGTTTCTGCAACCG	12060
QY	12061	GTCGAGGGGCTCAACGGATTAACATTCACAGCATACTTCAATGTCAGCGGCTGTATCAACGACA	12120
Db	12061	GTCGAGGGGCTCAACGGATTAACATTCACAGCATACTTCAATGTCAGCGGCTGTATCAACGACA	12120
QY	12121	CCGGGATGTGTTTCCGGGAATTTACAGGGTACAGAACACGGTCAACTGCGAGATCGTGGAC	12180
Db	12121	CCGGGATGTGTTTCCGGGAATTTACAGGGTACAGAACACGGTCAACTGCGAGATCGTGGAC	12180
QY	12181	ATGATTCGCGGTTTCGCGGAACCGTACTGTTTGTCAACGCGCTTGGAGACACGGTA	12240
Db	12181	ATGATTCGCGGTTTCGCGGAACCGTACTGTTTGTCAACGCGCTTGGAGACACGGTA	12240
QY	12241	GAGGTGTCCCGCTTCTGTCCCAACAGACTCAAGCTGCTCGTCCGGAGAAAACCGAAGAC	12300
Db	12241	GAGGTGTCCCGCTTCTGTGTCCCAACAGACTCAAGCTGCTCGTCCGGAGAAAACCGAAGAC	12300
QY	12301	GGGCTTCGGGCGCGCGGCTGTACAAATTTAACACATGTGTGACTTGGCGACCGCGACGGCC	12360
Db	12301	GGGCTTCGGGCGCGCGGCTGTCTCAAAATTTAACACATGTGTGACTTGGCGACCGCGACGGCC	12360
QY	12361	ACCAACCAAAACGGGGGCTTCTGCGCGACTCGGAGGAATTAACGTTATCTGTGAAGGCGGAG	12420
Db	12361	ACCAACCAAAACGGGGGCTTCTGCGCGACTCGGAGGAATTAACACGTTATCTGTGAAGGCGGAG	12420
QY	12421	GACCCCAAGTGTGGGCGTCTGCGCGCTGACGCTCTGTGAAAAACCTTCCCGAGGCGATACAG	12480
Db	12421	GACCCCAAGTGTGGGCGTCTGCGCGCTGACGCTCTGTGAAAAACCTTCCCGAGGCGATACAG	12480
QY	12481	ACGACGACGACGACACTACCACTTCGTGTGGCCAAAGAGTACGACGGCGACCTTCAACGTTC	12540
Db	12481	ACGACGACGACGACGACACTTACCACTTCGTGTGGCCAAAGAGTACGACGGCGACCTTCAACGTTC	12540
QY	12541	CCGGTTCGCCAGGTAACTTACTTACAGGGGACGTACCCCTGACCTCAATATGTTATTACG	12600

```
Db 12541 CGCTCTCCAGGTAATTAATTCACGGGACGTACCCCTGCTCATGATGTTATTCAG 12600
QY 12601 AAAACCTCAACGCCACCATCAAGAAGCTGTCCGATACCCACGCAACAAACGATGCGAG 12660
Db 12601 AAAACCTCAACGCCACCATCAAGAAGCTGTCCGATACCCACGCAACAAACGATGCGAG 12660
QY 12661 CAGTACTACGAACCGAGGGGGGTCTGTTTCTCTCTGTGGAGCGCTTAACGCCGTAGC 12720
Db 12661 CAGTACTACGAACCGAGGGGGGTCTGTTTCTCTCTGTGGAGCGCTTAACGCCGTAGC 12720
QY 12721 CTAGCTGACGAGATGCGGCAATTAACGGGACACGCGACGACCCCGCAACACTCA 12780
Db 12721 CTAGCTGACGAGATGCGGCAATTAACGGGACACGCGACGACCCCGCAACACTCA 12780
QY 12781 ACCGCCAACCGGTTTCGAAGAAGCGTGGTACGACAGCAGGCAAGGCAACGACACTAGG 12840
Db 12781 ACCGCCAACCGGTTTCGAAGAAGCGTGGTACGACAGCAGGCAAGGCAACGACACTAGG 12840
QY 12841 GGGCCCCAGCTGAGTTCCGCTACGACAGCTCCGCGGACATCAACAAAGTGTGAG 12900
Db 12841 GGGCCCCAGCTGAGTTCCGCTACGACAGCTCCGCGGACATCAACAAAGTGTGAG 12900
QY 12901 GAGCTCTCCAGGGCGGTGGCGAGAACAGGTGAGGGACACCTACATGTTGATCAGACAG 12960
Db 12901 GAGCTCTCCAGGGCGGTGGCGAGAACAGGTGAGGGACACCTACATGTTGATCAGACAG 12960
QY 12961 AGCAAGATTAAACCCACACGAGCTAATGACGGGATATACGGGCGCGGCTGTCCGCAAG 13020
Db 12961 AGCAAGATTAAACCCACACGAGCTAATGACGGGATATACGGGCGCGGCTGTCCGCAAG 13020
QY 13021 TTCTGGGGGAGCGCATCTCCGCTACGACAGCTCGTGGCGGTGAGCAGGCTCCGACAG 13080
Db 13021 TTCTGGGGGAGCGCATCTCCGCTACGACAGCTCGTGGCGGTGAGCAGGCTCCGACAG 13080
QY 13081 ATCCACAAAGAGCTCCGACAGCTCCGCGGGGATGTGCTACGCGGCGCCCGCGGTACAG 13140
Db 13081 ATCCACAAAGAGCTCCGACAGCTCCGCGGGGATGTGCTACGCGGCGCCCGCGGTACAG 13140
QY 13141 TTTCAGGTTCTCAACAGCAGCAGCTGTTCAAGGGGCACTGGGACCCAGAAACGAGATC 13200
Db 13141 TTTCAGGTTCTCAACAGCAGCAGCTGTTCAAGGGGCACTGGGACCCAGAAACGAGATC 13200
QY 13201 ATACGAGGAGAACACGAGTGGAGGGGTGCAAAAGAGACGTGCGAATCACTACTCATAGG 13260
Db 13201 ATACGAGGAGAACACGAGTGGAGGGGTGCAAAAGAGACGTGCGAATCACTACTCATAGG 13260
QY 13261 AGCAAGTAACTACTACTACAAAGACTAGTCTTCTGTAATAAATAATTAACACTCCAG 13320
Db 13261 AGCAAGTAACTACTACTACAAAGACTAGTCTTCTGTAATAAATAATTAACACTCCAG 13320
QY 13321 AATATCCACCTCGGTACGTTCAATCGCCCTGAACCTGTCTGTTATAGAAACATAGATTTC 13380
Db 13321 AATATCCACCTCGGTACGTTCAATCGCCCTGAACCTGTCTGTTATAGAAACATAGATTTC 13380
QY 13381 AAGGTCATGAGCTGTACAGCGCGCGGGGAAAAAGCTCTCCGGAGCGCTTTTCATATA 13440
Db 13381 AAGGTCATGAGCTGTACAGCGCGCGGGGAAAAAGCTCTCCGGAGCGCTTTTCATATA 13440
QY 13441 GAAACCATGTTAGGGAAATACAACTACTACAGCAACGCGCTGGCGGAGTCCGGGAGAC 13500
Db 13441 GAAACCATGTTAGGGAAATACAACTACTACAGCAACGCGCTGGCGGAGTCCGGGAGAC 13500
QY 13501 CTGGAACAACAGATGACCTGAACCGCGACCGCTGGCCCGGAGACCTGTCCAGATATGTC 13560
Db 13501 CTGGAACAACAGATGACCTGAACCGCGACCGCTGGCCCGGAGACCTGTCCAGATATGTC 13560
QY 13561 GGGGACCTGGGAGATGCGCGCGACGCTGTTAAAGTGGCCAGTATTAACCCCTG 13620
Db 13561 GGGGACCTGGGAGATGCGCGCGACGCTGTTAAAGTGGCCAGTATTAACCCCTG 13620
QY 13621 TTTCGATCAATGCTGAGCGGGTTCAATTAAAGATGCCCTGCGGGGCAATGCTC 13680
Db 13621 TTTCGATCAATGCTGAGCGGGTTCAATTAAAGATGCCCTGCGGGGCAATGCTC 13680
QY 13681 ATGATCTGGTGAATGTGGCGGTGTCTGATCGTGTGCGTAAACCGGCGCACCAAC 13740
Db 13681 ATGATCTGGTGAATGTGGCGGTGTCTGATCGTGTGCGTAAACCGGCGCACCAAC 13740
QY 13741 GCCATGCCCGAGGCCCATCAGAGTATCTACCCCGACATAGACAAATGCAACCCCTCT 13800
Db 13741 GCCATGCCCGAGGCCCATCAGAGTATCTACCCCGACATAGACAAATGCAACCCCTCT 13800
QY 13801 GGGGCTAAAGTGCACGAGGACGATTAATAACATCTCGCGGCGATGACAGGATCAG 13860
Db 13801 GGGGCTAAAGTGCACGAGGACGATTAATAACATCTCGCGGCGATGACAGGATCAG 13860
QY 13861 CAGGAAGAGCGTATGAGCGGTAGACGAACAGCAGAGGTACGCGCTTTCGCGGC 13920
Db 13861 CAGGAAGAGCGTATGAGCGGTAGACGAACAGCAGAGGTACGCGCTTTCGCGGC 13920
QY 13921 GCGTACAGGACTAAACGCTGCTTACGGGATATAAACCGCTGGAAAAACGAAGGCT 13980
Db 13921 GCGTACAGGACTAAACGCTGCTTACGGGATATAAACCGCTGGAAAAACGAAGGCT 13980
QY 13981 CAAGATTAATGAATGACAAATTAACACACACCGCTGTACTTGGCCGCGCAGAG 14040
Db 13981 CAAGATTAATGAATGACAAATTAACACACACCGCTGTACTTGGCCGCGCAGAG 14040
QY 14041 CCGCGCGGCAATTCATTCAGTCCACCGCGCGGTCCGACACCGCTTACGCGCCCGG 14100
Db 14041 CCGCGCGGCAATTCATTCAGTCCACCGCGCGGTCCGACACCGCTTACGCGCCCGG 14100
QY 14101 CCGCGCGGCAATTCATTCAGTCCACCGCGCGGTCCGACACCGCTTACGCGCCCGG 14160
Db 14101 CCGCGCGGCAATTCATTCAGTCCACCGCGCGGTCCGACACCGCTTACGCGCCCGG 14160
QY 14161 CCGCGCGGCAATTCATTCAGTCCACCGCGCGGTCCGACACCGCTTACGCGCCCGG 14220
Db 14161 CCGCGCGGCAATTCATTCAGTCCACCGCGCGGTCCGACACCGCTTACGCGCCCGG 14220
QY 14221 CCGCGCGGCAATTCATTCAGTCCACCGCGCGGTCCGACACCGCTTACGCGCCCGG 14280
Db 14221 CCGCGCGGCAATTCATTCAGTCCACCGCGCGGTCCGACACCGCTTACGCGCCCGG 14280
QY 14281 ATGATCCGCGTACGATTCGCTCCGCGCAAGGATGGAAGAGGTCTGGGGAGAC 14340
Db 14281 ATGATCCGCGTACGATTCGCTCCGCGCAAGGATGGAAGAGGTCTGGGGAGAC 14340
QY 14341 GTGCTGCTGCCAAGCAAGGTGCATGTGGAGGGGCGGACCGCAAGCGCTCGCGCG 14400
Db 14341 GTGCTGCTGCCAAGCAAGGTGCATGTGGAGGGGCGGACCGCAAGCGCTCGCGCG 14400
QY 14401 GACCCCAAGACCAATTCATCAGCTTACGCGGTACGAGTGTGAAAAACAGTACGG 14460
Db 14401 GACCCCAAGACCAATTCATCAGCTTACGCGGTACGAGTGTGAAAAACAGTACGG 14460
QY 14461 GGGGACAGGTGTGGAGGTACTAGCGCTTCCAAAGGAGCATTAATCCAAAGCGGAAC 14520
Db 14461 GGGGACAGGTGTGGAGGTACTAGCGCTTCCAAAGGAGCATTAATCCAAAGCGGAAC 14520
QY 14521 GTGCTCAAGCTCTGGGGGGAACCGAGGACGCGAGCTGTGGTGAACGTGTTCCGT 14580
Db 14521 GTGCTCAAGCTCTGGGGGGAACCGAGGACGCGAGCTGTGGTGAACGTGTTCCGT 14580
QY 14581 CAACAGTATATTTCTACGGAAGTTCAGCGCGCATTAACGTCACCAATCTCCAG 14640
Db 14581 CAACAGTATATTTCTACGGAAGTTCAGCGCGCATTAACGTCACCAATCTCCAG 14640
QY 14641 CAGGCGCTCAAAACAGACCGCGCGGTGCGGGTCTTCACACGAAGATGAGAC 14700
Db 14641 CAGGCGCTCAAAACAGACCGCGCGGTGCGGGTCTTCACACGAAGATGAGAC 14700
QY 14701 AAAAGATTTCTAAAACGTAAGCTGCGGAGCATCCCGTACAGGAATCAAGCTATG 14760
Db 14701 AAAAGATTTCTAAAACGTAAGCTGCGGAGCATCCCGTACAGGAATCAAGCTATG 14760
```

QY	14761	TCGGGTTTCATGCTCTTCGACCCCTCAGCAGCACCGCTCTCGCTGCGGGGTGGAGGTGTTCC	14820
Db	14761	TCGGGTTTCATGCTCTTCGACCCCTCAGCAGCACCGCTCTCGCTGCGGGGTGGAGGTGTTCC	14820
QY	14821	GAGTCAAAAGCTGGAGACCGCGTTCGCGGGTTCGTTTCGAGTACAGGGGTTTACACAGTTCCGG	14880
Db	14821	GAGTCAAAAGCTGGAGACCGCGTTCGCGGGTTCGTTTCGAGTACAGGGGTTTACACAGTTCCGG	14880
QY	14881	TGGTACTCTGTCGCGCGCGCCAGACCGCCCGCTGGCGGCCAGAGATGCCAGACGGGCGCTG	14940
Db	14881	TGGTACTCTGTCGCGCGCGCCAGACCGCCCGCTGGCGGCCAGAGATGCCAGACGGGCGCTG	14940
QY	14941	GAGTTTGACTGTCAGACTGCGGAGACCTCAGCGTTTCAAGCGGACCGCAGCAGCTGCCCCG	15000
Db	14941	GAGTTTGACTGTCAGACTGCGGAGACCTCAGCGTTTCAAGCGGACCGCAGCAGCTGCCCCG	15000
QY	15001	TACCGCATCTGTGGCGTTTGAATTATCGAGTGCACGTGGAGAGCGGGGATTTCCGTGGCGCACG	15060
Db	15001	TACCGCATCTGTGGCGTTTGAATTATCGAGTGCACGTGGAGAGCGGGGATTTCCGTGGCGCACG	15060
QY	15061	CGGACGCGCGACGCGGTGATCCAGATCTCCTGCGTTTCTACACGACACAGGAAAGCGCG	15120
Db	15061	CGGACGCGCGACGCGGTGATCCAGATCTCCTGCGTTTCTACACGACACAGGAAAGCGCG	15120
QY	15121	CCCAATCCGCCAAACATACTGTTCCAGCGTGGGAGCTGGACCCCATCCCGACACCGAC	15180
Db	15121	CCCAATCCGCCAAACATACTGTTCCAGCGTGGGAGCTGGACCCCATCCCGGACACCGAC	15180
QY	15181	GTTTTGAGTTTCCGTCGCGGAATATGACATGCTGCTGCTGTCGTCGCCATGATCCGCGAC	15240
Db	15181	GTTTTGAGTTTCCGTCGCGGAATATGACATGCTGCTGCTGTCGTCGCCATGATCCGCGAC	15240
QY	15241	TTGCGAGGTGACTTTTAAACGGCGCTTAAACATCTCAACATTCGATTCGCCGACGTAAAC	15300
Db	15241	TTGCGAGGTGACTTTTAAACGGCGCTTAAACATCTCAACATTCGATTCGCCGACGTAAAC	15300
QY	15301	ACGCGACGCTCCCAAGGTGTACAACTTCCTGATTAAACGAATACACAAATAATAAACCGCG	15360
Db	15301	ACGCGACGCTCCCAAGGTGTACAACTTCCTGATTAAACGAATACACAAATAATAAACCGCG	15360
QY	15361	TCGATCTTTTAAAGTTCACGACCGCCGCGGGGGGGAGGGGGGTTCTGAGAGTCCGGCTCA	15420
Db	15361	TCGATCTTTTAAAGTTCACGACCGCCGCGGGGGGGAGGGGGGTTCTGAGAGTCCGGCTCA	15420
QY	15421	AAAAATTAATAGCGGGCATCGTCCCATATGACATGTACAGGTGTGTGCGCAAAAAGCTTC	15480
Db	15421	AAAAATTAATAGCGGGCATCGTCCCATATGACATGTACAGGTGTGTGCGCAAAAAGCTTC	15480
QY	15481	AGCCTCTCCGACATACAAACCTGACACAGGTGGCCAGGCAATGTCGTGGGTGGGAAAAAGAG	15540
Db	15481	AGCCTCTCCGACATACAAACCTGACACAGGTGGCCAGGCAATGTCGTGGGTGGGAAAAAGAG	15540
QY	15541	GACGTATCTGTACAAAGACATTCGCCCTCTGTTTCGCTCAGAGTCCGGGCGGAGGGCTAAG	15600
Db	15541	GACGTATCTGTACAAAGACATTCGCCCTCTGTTTCGCTCAGAGTCCGGGCGGAGGGCTAAG	15600
QY	15601	GTTGGGACAGCTATTGGCGATGAGTACCTGGGCTCTGATGTAGACCTCTTAAAAATGTTTATG	15660
Db	15601	GTTGGGACAGCTATTGGCGATGAGTACCTGGGCTCTGATGTAGACCTCTTAAAAATGTTTATG	15660
QY	15661	ATTACAGCTGGAGATTTTGGGAGATATAGCAACGTCTGGCCCAAGTTTACAGGCGAGGGCGTCCG	15720
Db	15661	ATTACAGCTGGAGATTTTGGGAGATATAGCAACGTCTGGCCCAAGTTTACAGGCGAGGGCGTCCG	15720
QY	15721	ACGCGACGCGCAACAGCTCCGCGTGTTCCTGCTGCTCTGAGAGGCGCCGCGCCAGGGAGAC	15780
Db	15721	ACGCGACGCGCAACAGCTCCGCGTGTTCCTGCTGCTCTGAGAGGCGCCGCGCCAGGGAGAC	15780
QY	15781	TTTTTATCTCCCGGTTCCAAAGCGCCGAGGAGACAGGGGGGCTATCAGGCGCGCAGCGGTATC	15840
Db	15781	TTTTTATCTCCCGGTTCCAAAGCGCCGAGGAGACAGGGGGGCTATCAGGCGCGCAGCGGTATC	15840

QY	1584.1	AACCCCATTCGGGGGTTTACGACGAGCGGGCTGTGTGTGATTTTGGCAGCCTGTAC	15900
Db	1584.1	AACCCCATTCGGGGGTTTACGACGAGCGGGCTGTGTGTGATTTTGGCAGCCTGTAC	15900
QY	1590.1	CCGAGCATTCATCCAGGGGGCAACAACCTGTGTTACTCCACATATATACGCGAGAGACCTGG	15960
Db	1590.1	CCGAGCATTCATCCAGGGGGCAACAACCTGTGTTACTCCACATATATACGCGAGAGACCTGG	15960
QY	1596.1	CACCTGCACCCCAACCTGCAGCGCGGAGACACTACGAGACGTTCGTGTGAGCGCGGACCG	16020
Db	1596.1	CACCTGCACCCCAACCTGCAGCGCGGAGACACTACGAGACGTTCGTGTGAGCGCGGACCG	16020
QY	1602.1	GTACATTTTGTAAAAAAACACAAGCGGAGTCTCTGTGGGAAGACTGCTAACCTGTGG	16080
Db	1602.1	GTACATTTTGTAAAAAAACACAAGCGGAGTCTCTGTGGGAAGACTGCTAACCTGTGG	16080
QY	1608.1	TTAATAAAGGAGAGGGGATTCGGGCGACCCCTGGCGGCTGGCATACCCGTTCGCTAAA	16140
Db	1608.1	TTAATAAAGGAGAGGGGATTCGGGCGACCCCTGGCGGCTGGCATACCCGTTCGCTAAA	16140
QY	1614.1	ACCATTTAGTAAACAACAAGCTGGCCATACAGGTGACATGTAAACGGGTTTACGGGTTTC	16200
Db	1614.1	ACCATTTAGTAAACAACAAGCTGGCCATACAGGTGACATGTAAACGGGTTTACGGGTTTC	16200
QY	1620.1	ACCGGGGTGGCCAGCGGCGCTCTCTCCATGCATTAACATACGGAACCGGTGACGCTCGG	16260
Db	1620.1	ACCGGGGTGGCCAGCGGCGCTCTCTCCATGCATTAACATACGGAACCGGTGACGCTCGG	16260
QY	1626.1	GGGGCGACGATGCTTGAGATGTCAAACTTTACGTGAGGGCCTGACGACGAGAACCTTG	16320
Db	1626.1	GGGGCGACGATGCTTGAGATGTCAAACTTTACGTGAGGGCCTGACGACGAGAACCTTG	16320
QY	1632.1	CGAAGCGGTCCTGGTCCGAGGTGACCCGCCGTCACGGCGGGGGTTTGGCGTCGTAC	16380
Db	1632.1	CGAAGCGGTCCTGGTCCGAGGTGACCCGCCGTCACGGCGGGGGTTTGGCGTCGTAC	16380
QY	1638.1	GGTACACACCGACTCCCTCTTTATCGCTGCGAGCGTTATTTCCGCGGAAGCCGTTTCCGCT	16440
Db	1638.1	GGTACACACCGACTCCCTCTTTATCGCTGCGAGCGTTATTTCCGCGGAAGCCGTTTCCGCT	16440
QY	1644.1	TTTGTGTGACGATCTGGCCGCCAGGATCATCTGCGGACCTGTTCCTCCCAACCATTAAGCTA	16500
Db	1644.1	TTTGTGTGACGATCTGGCCGCCAGGATCATCTGCGGACCTGTTCCTCCCAACCATTAAGCTA	16500
QY	1650.1	GAGCGCGGAAAAGAGTTCAAAGTGTCTCTCTGTGACGAAAAAGGGCTACATCGGGGGTC	16560
Db	1650.1	GAGCGCGGAAAAGAGTTCAAAGTGTCTCTCTGTGACGAAAAAGGGCTACATCGGGGGTC	16560
QY	1656.1	CTATTGAAACGACAAAATGTGTCATGAAAGGGGTGACCTCATTTCTGCAAAAAGGGCTGCAAG	16620
Db	1656.1	CTATTGAAACGACAAAATGTGTCATGAAAGGGGTGACCTCATTTCTGCAAAAAGGGCTGCAAG	16620
QY	1662.1	TTTGTCCAGGAGCATGCGCGGCCCATCTGTGACTGTGTCTCCACATCTCGGAGGTCGAAG	16680
Db	1662.1	TTTGTCCAGGAGCATGCGCGGCCCATCTGTGACTGTGTCTCCACATCTCGGAGGTCGAAG	16680
QY	1668.1	GCTGGGGGGGGGCTGTGTGTGCAACGGCGCGCGCACGGGTATACGAGGAGGGGGCTGGCG	16740
Db	1668.1	GCTGGGGGGGGGCTGTGTGTGCAACGGCGCGCGCACGGGTATACGAGGAGGGGGCTGGCG	16740
QY	1674.1	GCTGGCTTTATTAATAAATCTGAGAAGTCTCAACGCGAGCTATCTGGACCTCCGAAAACAGC	16800
Db	1674.1	GCTGGCTTTATTAATAAATCTGAGAAGTCTCAACGCGAGCTATCTGGACCTCCGAAAACAGC	16800
QY	1680.1	GTCGTGCCCATCGAGCATTAACGTTCTCCACCGAGCTCAGCCGCCCTGTCTGCGATTAC	16860
Db	1680.1	GTCGTGCCCATCGAGCATTAACGTTCTCCACCGAGCTCAGCCGCCCTGTCTGCGATTAC	16860
QY	1686.1	AAGACACACAACTCTGCCCACTCTGGCGGTGTACCAAAAGCTGGCGAGACAGTCCGAGGAG	16920
Db	1686.1	AAGACACACAACTCTGCCCACTCTGGCGGTGTACCAAAAGCTGGCGAGACAGTCCGAGGAG	16920
QY	1692.1	CTGCCCGAGGTGACAGTAAATCTCCCTACGTGTCTTACGCGCGCGGGTCCCTAAG	16980

[illegible]

[illegible]

```
|||||
Db 25681 CCGGAGCTCCCGTCCCGAGAGTCCGGGCTCCCGTCCCGAGGCTCCGGGCTCC 25740
OY 25741 CCGTCCCGAGAGGTCCTCCGGGCTCCCGTCCCGAGAGGTCCTCCGGGCTCCCGG 25800
Db 25741 CCGTCCCGAGAGGTCCTCCGGGCTCCCGTCCCGAGAGGTCCTCCGGGCTCCCGG 25800
OY 25801 AGGTCCTCCGGGCTCCCGTCCCGAGAGGTCCTCCGGGCTCCCGTCCCGAGAGGTC 25860
Db 25801 AGGTCCTCCGGGCTCCCGTCCCGAGAGGTCCTCCGGGCTCCCGTCCCGAGAGGTC 25860
OY 25861 GCTCCCGTCCCGAGAGGTCCTCCGGGCTCCCGTCCCGAGAGGTCCTCCGGGCTCC 25920
Db 25861 GCTCCCGTCCCGAGAGGTCCTCCGGGCTCCCGTCCCGAGAGGTCCTCCGGGCTCC 25920
OY 25921 CCGGAGAGGTCCTCCGGGCTCCCGTCCCGAGAGGTCCTCCGGGCTCCCGGAGGTC 25980
Db 25921 CCGGAGAGGTCCTCCGGGCTCCCGTCCCGAGAGGTCCTCCGGGCTCCCGGAGGTC 25980
OY 25981 CCGGAGGTCCTCCGGGCTCCCGTCCCGAGAGGTCCTCCGGGCTCCCGGAGGTCCT 26040
Db 25981 CCGGAGGTCCTCCGGGCTCCCGTCCCGAGAGGTCCTCCGGGCTCCCGGAGGTCCT 26040
OY 26041 CCGTCCCGAGAGGTCCTCCGGGCTCCCGTCCCGAGAGGTCCTCCGGGCTCCCGG 26100
Db 26041 CCGTCCCGAGAGGTCCTCCGGGCTCCCGTCCCGAGAGGTCCTCCGGGCTCCCGG 26100
OY 26101 AGGTCCTCCGGGCTCCCGTCCCGAGAGGTCCTCCGGGCTCCCGTCCCGAGAGGTC 26160
Db 26101 AGGTCCTCCGGGCTCCCGTCCCGAGAGGTCCTCCGGGCTCCCGTCCCGAGAGGTC 26160
OY 26161 GCTCCCGTCCCGAGAGGTCCTCCGGGCTCCCGTCCCGAGAGGTCCTCCGGGCTCC 26220
Db 26161 GCTCCCGTCCCGAGAGGTCCTCCGGGCTCCCGTCCCGAGAGGTCCTCCGGGCTCC 26220
OY 26221 CCGGAGAGGTCCTCCGGGCTCCCGTCCCGAGAGGTCCTCCGGGCTCCCGGAGGTC 26280
Db 26221 CCGGAGAGGTCCTCCGGGCTCCCGTCCCGAGAGGTCCTCCGGGCTCCCGGAGGTC 26280
OY 26281 CCGGAGGTCCTCCGGGCTCCCGTCCCGAGAGGTCCTCCGGGCTCCCGGAGGTCCT 26340
Db 26281 CCGGAGGTCCTCCGGGCTCCCGTCCCGAGAGGTCCTCCGGGCTCCCGGAGGTCCT 26340
OY 26341 CCGTCCCGAGAGGTCCTCCGGGCTCCCGTCCCGAGAGGTCCTCCGGGCTCCCGG 26400
Db 26341 CCGTCCCGAGAGGTCCTCCGGGCTCCCGTCCCGAGAGGTCCTCCGGGCTCCCGG 26400
OY 26401 AGGTCCTCCGGGCTCCCGTCCCGAGAGGTCCTCCGGGCTCCCGGAGGTCCTCCGG 26460
Db 26401 AGGTCCTCCGGGCTCCCGTCCCGAGAGGTCCTCCGGGCTCCCGGAGGTCCTCCGG 26460
OY 26461 GCTCCCGTCCCGAGAGGTCCTCCGGGCTCCCGTCCCGAGAGGTCCTCCGGGCTCC 26520
Db 26461 GCTCCCGTCCCGAGAGGTCCTCCGGGCTCCCGTCCCGAGAGGTCCTCCGGGCTCC 26520
OY 26521 CCGGAGTTCACAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAG 26580
Db 26521 CCGGAGTTCACAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAG 26580
OY 26581 TTGTACATACACAGCGGTCGCGATTCGCGCCGCGCATGCAAAAATAACGTTGGGTTCC 26640
Db 26581 TTGTACATACACAGCGGTCGCGATTCGCGCCGCGCATGCAAAAATAACGTTGGGTTCC 26640
OY 26641 GAAACGCGTACGTCGTTAGTTCATAGCACGTTTCGTCACGTCAGAGTGGTTA 26700
Db 26641 GAAACGCGTACGTCGTTAGTTCATAGCACGTTTCGTCACGTCAGAGTGGTTA 26700
OY 26701 GTTTTGTGTAGCGAATGCAACAGAGTACGTCGCTGACACGGGAAAGGAGTGTAA 26760
Db 26701 GTTTTGTGTAGCGAATGCAACAGAGTACGTCGCTGACACGGGAAAGGAGTGTAA 26760
OY 26761 CCGCAGTGTACCGGTCGCGCATACGTTTAACTGCAACTGCGGTCGCGCGG 26820
|||||
Db 26761 CCGCAGTGTACCGGTCGCGCATACGTTTAACTGCAACTGCGGTCGCGCGG 26820
OY 26821 TACCTTAAGTTACGTTAGTGAATTAATGAGGCTGTTACGAGGCTCCGCGCCCTGA 26880
Db 26821 TACCTTAAGTTACGTTAGTGAATTAATGAGGCTGTTACGAGGCTCCGCGCCCTGA 26880
OY 26881 GGAAGAAATGAATTTCTTTCGCACTTACGTTTATGCTATAGAGGCTATCTTCTTA 26940
Db 26881 GGAAGAAATGAATTTCTTTCGCACTTACGTTTATGCTATAGAGGCTATCTTCTTA 26940
OY 26941 CTGTGGGCTCGGAGGAGGAGGAGTACCTGACATCCGCTGTTAGCCCTATTAAGAAT 27000
Db 26941 CTGTGGGCTCGGAGGAGGAGGAGTACCTGACATCCGCTGTTAGCCCTATTAAGAAT 27000
OY 27001 TATCAGCGCTTCTCAGAGAGAGGCTCCGCTGTAACGAGAGGCTTTCGCGCACCGA 27060
Db 27001 TATCAGCGCTTCTCAGAGAGAGGCTCCGCTGTAACGAGAGGCTTTCGCGCACCGA 27060
OY 27061 TTACGCTCTCTGCGGAGCTAAAGCCATAGGCCAAGGATGCTGCAATTAACACGGA 27120
Db 27061 TTACGCTCTCTGCGGAGCTAAAGCCATAGGCCAAGGATGCTGCAATTAACACGGA 27120
OY 27121 CCGAGCGCACACTGAGGTCGCGCTTTGGCGCTTTGGGCTTTGGGCTATGTCGTA 27180
Db 27121 CCGAGCGCACACTGAGGTCGCGCTTTGGCGCTTTGGGCTTTGGGCTATGTCGTA 27180
OY 27181 TAAAGTTAAAGACGAGACGCTCTTTTAACTGTCGCTATAGCCGTCGTACGC 27240
Db 27181 TAAAGTTAAAGACGAGACGCTCTTTTAACTGTCGCTATAGCCGTCGTACGC 27240
OY 27241 GTACAGAGGCTGAGAGTCTCAGTGTTCGTTTCACACGCGCAATGGAGGACTACGGA 27300
Db 27241 GTACAGAGGCTGAGAGTCTCAGTGTTCGTTTCACACGCGCAATGGAGGACTACGGA 27300
OY 27301 TTACTGCGAGCAATCTAGAGCATCGCGCAACCGAGAGACATGCTGTAAGCAT 27360
Db 27301 TTACTGCGAGCAATCTAGAGCATCGCGCAACCGAGAGACATGCTGTAAGCAT 27360
OY 27361 TCGGCTGCTCTTCTGCGGCTAGTGGCGCTGTTTCCATACAGGCTATAGTGTGCTT 27420
Db 27361 TCGGCTGCTCTTCTGCGGCTAGTGGCGCTGTTTCCATACAGGCTATAGTGTGCTT 27420
OY 27421 ACCGCTATTCCTCCCACTGACCTTAAGTGAAGCGGATGTAAGACCAATAACA 27480
Db 27421 ACCGCTATTCCTCCCACTGACCTTAAGTGAAGCGGATGTAAGACCAATAACA 27480
OY 27481 AAACAGCTAACGTCGTAATTCGTTGGAACATTTTATTTAGACAGTTCCTGCAACA 27540
Db 27481 AAACAGCTAACGTCGTAATTCGTTGGAACATTTTATTTAGACAGTTCCTGCAACA 27540
OY 27541 TTTTGTATCTGTACACAGGAGGCGGCTGTGCGCTGACCTCCACCGGCGCCGCGG 27600
Db 27541 TTTTGTATCTGTACACAGGAGGCGGCTGTGCGCTGACCTCCACCGGCGCCGCGG 27600
OY 27601 ACTGTCGATCTGTGATCGAGAGGCGGAGCAAGCGGAGGAGGAGAGAGTGAAG 27660
Db 27601 ACTGTCGATCTGTGATCGAGAGGCGGAGCAAGCGGAGGAGGAGAGTGAAG 27660
OY 27661 GAATGCGCTTACATTAACAGATTCCTTGAGCGCGCGGAGCTGAGATTCGCGCTG 27720
Db 27661 GAATGCGCTTACATTAACAGATTCCTTGAGCGCGCGGAGCTGAGATTCGCGCTG 27720
OY 27721 CGAGACCGGCTGTGTGCGCTCGCGGCTCGGAGGAGGAGGAGGAGGAGGAGGAGG 27780
Db 27721 CGAGACCGGCTGTGTGCGCTCGCGGCTCGGAGGAGGAGGAGGAGGAGGAGGAGG 27780
OY 27781 GCGGCTCTGTGATGAGGCTGTGAGGAGTGGAGTGGCTGCGGATTAACACTGCG 27840
Db 27781 GCGGCTCTGTGATGAGGCTGTGAGGAGTGGAGTGGCTGCGGATTAACACTGCG 27840
OY 27841 GCTGTACGCTAGTACGAGCGGAGAGCGGTAGGCTGTGAGGAGTGAAGTGAAGGCG 27900
Db 27841 GCTGTACGCTAGTACGAGCGGAGAGCGGTAGGCTGTGAGGAGTGAAGTGAAGGCG 27900
```

QY 27901 GTGGTTGCGGTCTGTGGTCCGCTCTGTGCGCGAGGTCGTGCAGACGGGCTCGTTTAA 27960
D 27901 GTGGTTGCGGTCTGTGGTCCGCTCTGTGCGCGAGGTCGTGCAGACGGGCTCGTTTAA 27960
QY 27961 GGTCCCTCAGATCCGCTGTAATGTCCAAATATGTTTTTGGACAGCGCATACGTCCTTGT 28020
D 27961 GGTCCCTCAGATCCGCTGTAATGTCCAAATATGTTTTTGGACAGCGCATACGTCCTTGT 28020
QY 28021 GTATGCGGACCTCTCGCTGGAACCGGGGCTGTCGGAAGTCCACGTCCTGTTTG 28080
D 28021 GTATGCGGACCTCTCGCTGGAACCGGGGCTGTCGGAAGTCCACGTCCTGTTTG 28080
QY 28081 GCTTCTGTGGCGAGAGGTCGCGGAGACGTAGCCGTACGTGCGAAGTAATAGCTGCGG 28140
D 28081 GCTTCTGTGGCGAGAGGTCGCGGAGACGTAGCCGTACGTGCGAAGTAATAGCTGCGG 28140
QY 28141 CATACGAGAGGTTGGGGGCGAAACCGCACTGGAAAGGAAACGCTGGCGCGACGGCG 28200
D 28141 CATACGAGAGGTTGGGGGCGAAACCGCACTGGAAAGGAAACGCTGGCGCGACGGCG 28200
QY 28201 GTGCGTACGATGGGAGGTCAGGTCAGGGGGGTATCCAGATGATAGCGCGCGCTTG 28260
D 28201 GTGCGTACGATGGGAGGTCAGGTCAGGGGGGTATCCAGATGATAGCGCGCGCTTG 28260
QY 28261 CCGGCAATCGAGGGTGGCGGCAAGAAACGTACGTCGGGTGGCCCTGGTTCGCATGTTATCGA 28320
D 28261 CCGGCAATCGAGGGTGGCGGCAAGAAACGTACGTCGGGTGGCCCTGGTTCGCATGTTATCGA 28320
QY 28321 GACTGCTCTCACCATTGCTAGAAAGGTCCTTTGGGAATGTGATGTTGCTCCGGGA 28380
D 28321 GACTGCTCTCACCATTGCTAGAAAGGTCCTTTGGGAATGTGATGTTGCTCCGGGA 28380
QY 28381 GGGGCGTCATGTTGGGTGGGTGCGGGTTACGCGAGTGTGAGCGCAAGGAAACGTGGCTG 28440
D 28381 GGGGCGTCATGTTGGGTGGGTGCGGGTTACGCGAGTGTGAGCGCAAGGAAACGTGGCTG 28440
QY 28441 CTTTAAATACGTAATCTGCGCACTGCGCAAGCCCTTATCTGTTTTGAGCAGGTCG 28500
D 28441 CTTTAAATACGTAATCTGCGCACTGCGCAAGCCCTTATCTGTTTTGAGCAGGTCG 28500
QY 28501 TCGCATCTCGGATTAATCCGCGCTGATCGCCTTTGGGCAATGATGTCCTCAAGAGGGCG 28560
D 28501 TCGCATCTCGGATTAATCCGCGCTGATCGCCTTTGGGCAATGATGTCCTCAAGAGGGCG 28560
QY 28561 -CGAATCTGGCGGTGATCGTGAAGTCTGCAAGAAATCTAAACATTAACGCTTATTTAC 28620
D 28561 CGAATCTGGCGGTGATCGTGAAGTCTGCAAGAAATCTAAACATTAACGCTTATTTAC 28620
QY 28621 CCGCTTCCTCTCGGCTAAGGAATCAAACTTGGAGACGACCATGTAAGGTCGTGTCGT 28680
D 28621 CCGCTTCCTCTCGGCTAAGGAATCAAACTTGGAGACGACCATGTAAGGTCGTGTCGT 28680
QY 28681 AAACGCGGATTAAGACCCCTACGCTCCCAAGTGGCGACAGAGAGAGCTGCTGAACGCG 28740
D 28681 AAACGCGGATTAAGACCCCTACGCTCCCAAGTGGCGACAGAGAGAGCTGCTGAACGCG 28740
QY 28741 GTGGGTATGGGTCTTGAAGTCTTCTGAGTGGAGGAGCAAGGAGAGCTCCGGA 28800
D 28741 GTGGGTATGGGTCTTGAAGTCTTCTGAGTGGAGGAGCAAGGAGAGCTCCGGA 28800
QY 28801 GCCATGTGTAACTATCCAAACAGGGGTCGCGAGGATGAGGTTAGTGAATCTAGG 28860
D 28801 GCCATGTGTAACTATCCAAACAGGGGTCGCGAGGATGAGGTTAGTGAATCTAGG 28860
QY 28861 CCGCTCGGAGTCCCGCGAGCCGCTGACGCGCAGGCGCAAGAAATCTGCTGTAGCT 28920
D 28861 CCGCTCGGAGTCCCGCGAGCCGCTGACGCGCAGGCGCAAGAAATCTGCTGTAGCT 28920
QY 28921 TGGCCAGGCAAAATATCCGCTGATGTTACTTGGAAAGACGATGTTGACCTGAGGG 28980
D 28921 TGGCCAGGCAAAATATCCGCTGATGTTACTTGGAAAGACGATGTTGACCTGAGGG 28980
D 28981 TGGCCAGGCAAAATATCCGCTGATGTTACTTGGAAAGACGATGTTGACCTGAGGG 28980

QY 28981 CTTGCGGAGACGTCTATGTTTATGCTAGAGGTCCTGTAACGAGAGAGGTCGCCA 29040
D 28981 CTTGCGGAGACGTCTATGTTTATGCTAGAGGTCCTGTAACGAGAGAGGTCGCCA 29040
QY 29041 CGATTGAGGCTCTAAATACAGTCCCTTTCTATCTTTGGTAGGCTACACAGTCCAGT 29100
D 29041 CGATTGAGGCTCTAAATACAGTCCCTTTCTATCTTTGGTAGGCTACACAGTCCAGT 29100
QY 29101 ATCCCCAACGTACAGGAGATCAATGTTGGGTGCTGTCGCGGAGCCGAGAGATGA 29160
D 29101 ATCCCCAACGTACAGGAGATCAATGTTGGGTGCTGTCGCGGAGCCGAGAGATGA 29160
QY 29161 GCGCGGCTCTTGGGGGCTGATGTCGCGCTTATCCGTTGAGAAATTTAAATACGTTTC 29220
D 29161 GCGCGGCTCTTGGGGGCTGATGTCGCGCTTATCCGTTGAGAAATTTAAATACGTTTC 29220
QY 29221 TCCCTGGCAGCTCAGTCTTCTTACCTGTCGTGCGAAATGTACAACTACGCTTTA 29280
D 29221 TCCCTGGCAGCTCAGTCTTCTTACCTGTCGTGCGAAATGTACAACTACGCTTTA 29280
QY 29281 ACGGTACCTTGAAGAGGCAATGCAATACCGGAGAGGAGATATTGCTCCG 29340
D 29281 ACGGTACCTTGAAGAGGCAATGCAATACCGGAGAGGAGATATTGCTCCG 29340
QY 29341 GCGCTAAGTTCGCTGGAAGTTCGAAAAATCGTTTACGATGGGTTAAAGAGATGGGG 29400
D 29341 GCGCTAAGTTCGCTGGAAGTTCGAAAAATCGTTTACGATGGGTTAAAGAGATGGGG 29400
QY 29401 TTTCTGACGCAAGTTCCTCTCAGAAACCAAAAGGGGGCTCTGGCTTTACTTCAAG 29460
D 29401 TTTCTGACGCAAGTTCCTCTCAGAAACCAAAAGGGGGCTCTGGCTTTACTTCAAG 29460
QY 29461 GGGCTCGGCTCTTAAAGGTTAGGCGCATGCTTTTTTGGCACTGGGGTTAAGCC 29520
D 29461 GGGCTCGGCTCTTAAAGGTTAGGCGCATGCTTTTTTGGCACTGGGGTTAAGCC 29520
QY 29521 ACAGCGTACGCGGTTCGGAACCTAAGCATGGAATATCTATTAACCTAGGCA 29580
D 29521 ACAGCGTACGCGGTTCGGAACCTAAGCATGGAATATCTATTAACCTAGGCA 29580
QY 29581 GCGCATACCATGTCGCTGCTGTCAGAAACCAAAAGGGGGCTCTGGCTTTACTTCAAG 29640
D 29581 GCGCATACCATGTCGCTGCTGTCAGAAACCAAAAGGGGGCTCTGGCTTTACTTCAAG 29640
QY 29641 CTGACACGAGCCCTGGGTGAGTGTGTCGCGGCAAGATTTTATCTGACTTAATTA 29700
D 29641 CTGACACGAGCCCTGGGTGAGTGTGTCGCGGCAAGATTTTATCTGACTTAATTA 29700
QY 29701 TTTCCGGCCACATTAATGCAAGCAAGTCAATCTTGAACAAGTGGGAACGTCGCGGTACG 29760
D 29701 TTTCCGGCCACATTAATGCAAGCAAGTCAATCTTGAACAAGTGGGAACGTCGCGGTACG 29760
QY 29761 GTGGCTTCGTGAGGCAAGTGTGTCGATGTTCCGCGGTTACACGGGATTCGCGCTGG 29820
D 29761 GTGGCTTCGTGAGGCAAGTGTGTCGATGTTCCGCGGTTACACGGGATTCGCGCTGG 29820
QY 29821 ATTTGCTCGCGGCTCCGCGCTTAAAGTCTCAACAGAGGAGATACGTTGTTGCTTCA 29880
D 29821 ATTTGCTCGCGGCTCCGCGCTTAAAGTCTCAACAGAGGAGATACGTTGTTGCTTCA 29880
QY 29881 ATTAACAGCTAGTGTAGGTCGCTCAACACTACGAGTGGCGACCGGACAGTATCCAG 29940
D 29881 ATTAACAGCTAGTGTAGGTCGCTCAACACTACGAGTGGCGACCGGACAGTATCCAG 29940
QY 29941 GACCAAAAATTAACCTGTCGTAGTGTGTTAACTCCGAATTTGGCTTTTCAATATCTC 30000
D 29941 GACCAAAAATTAACCTGTCGTAGTGTGTTAACTCCGAATTTGGCTTTTCAATATCTC 30000
QY 30001 GTGTGCGAGACCGGGGGGCGAGTGGTGGAAGAGATGGGCGCACGGCTTCTGCGCGCT 30060
D 30001 GTGTGCGAGACCGGGGGGCGAGTGGTGGAAGAGATGGGCGCACGGCTTCTGCGCGCT 30060
QY 30061 TAAACGTAGCGAGCTTTGAGCTGAATACAGGCTGCGAGCTCCCTGAACGTGACCTTTTG 30120

```
|||||
Db 30061 TAAAGCTAGCGAGCTTTGAGCTGATACAGGCTGCGAGGCTCCCTGAACTGATGCTTTG 30120
Oy 30121 GTTCAGATGTCAAAGATTTCGTTAAATCTGGAACCGGTACAGTTGACGAGAGAGAT 30180
Db 30121 GTTCAGAGATGTCAAAGATTTCGTTAAATCTGGAACCGGTACAGTTGACGAGAGAT 30180
Oy 30181 GTGTTTATGATGGATATGAGCTTTGCTCCAGCGCCGTAGATACGACCCGGAGACAA 30240
Db 30181 GTGTTTATGATGGATATGAGCTTTGCTCCAGCGCCGTAGATACGACCCGGAGACAA 30240
Oy 30241 AAACGAGTGGGGGGCTGGGGCGCGGAAAGATTGGGGAGTATTTCTGTCAG 30300
Db 30241 AAACGAGTGGGGGGCTGGGGCGCGGAAAGATTGGGGAGTATTTCTGTCAG 30300
Oy 30301 GAAATCAAAAAGTTGCTCCCTTTTAAAGTATTTGTTGACCCGAGGGTCTTCTACCT 30360
Db 30301 GAAATCAAAAAGTTGCTCCCTTTTAAAGTATTTGTTGACCCGAGGGTCTTCTACCT 30360
Oy 30361 GGAATAATCTCCACCCAGAGAGAGCCAGGTTGAGGGCGCGTGGGCGATCTGGTCT 30420
Db 30361 GGAATAATCTCCACCCAGAGAGAGCCAGGTTGAGGGCGCGTGGGCGATCTGGTCT 30420
Oy 30421 GATTGGGCGACGTCCTCAATAGCAGCTAAACCAAACCTAAGCCTAGTGGCGAGAGCC 30480
Db 30421 GATTGGGCGACGTCCTCAATAGCAGCTAAACCAAACCTAAGCCTAGTGGCGAGAGCC 30480
Oy 30481 GGCTCGAGAGTTCATTGTGACGTTGAAAAGGAGGAGCGTTCGCTGTAACAAAGTGT 30540
Db 30481 GGCTCGAGAGTTCATTGTGACGTTGAAAAGGAGGAGCGTTCGCTGTAACAAAGTGT 30540
Oy 30541 GCGAAGAGTATAGAGATCTGCTCCAGTGGCTGACCGGTACCGGGGTCTTGGAGAC 30600
Db 30541 GCGAAGAGTATAGAGATCTGCTCCAGTGGCTGACCGGTACCGGGGTCTTGGAGAC 30600
Oy 30601 GGGTAGCAGTCCGCTCTGTCGCAACGTCGCGTATATCAAGTGTGTTAAAGATCCGC 30660
Db 30601 GGGTAGCAGTCCGCTCTGTCGCAACGTCGCGTATATCAAGTGTGTTAAAGATCCGC 30660
Oy 30661 GTTGTACTTTGTTCTTTGTTTAAAGGCGCTAGAGAGGCGGCTTCGCTGATTCGAATA 30720
Db 30661 GTTGTACTTTGTTCTTTGTTTAAAGGCGCTAGAGAGGCGGCTTCGCTGATTCGAATA 30720
Oy 30721 TGTAACTCGAAACCCAGGCGCTTCGTTTGTGTTAGTGAGACAAAGCTGCGCAG 30780
Db 30721 TGTAACTCGAAACCCAGGCGCTTCGTTTGTGTTAGTGAGACAAAGCTGCGCAG 30780
Oy 30781 CTTTGTGCCAGGTTATCCAGAGGCGCTTCGAGTGGCGCAACGGGTCCTGTCG 30840
Db 30781 CTTTGTGCCAGGTTATCCAGAGGCGCTTCGAGTGGCGCAACGGGTCCTGTCG 30840
Oy 30841 GTGACAGTATACCCGTTGAGAGGAGCAGCGGCGCTGCTGTCGATACGTTGCGGAC 30900
Db 30841 GTGACAGTATACCCGTTGAGAGGAGCAGCGGCGCTGCTGTCGATACGTTGCGGAC 30900
Oy 30901 ATCCGCTGAAAGTCTTGATGATGAGAGGCGCTTGAAGTATAGGCGAGACATTAAGCT 30960
Db 30901 ATCCGCTGAAAGTCTTGATGATGAGAGGCGCTTGAAGTATAGGCGAGACATTAAGCT 30960
Oy 30961 TAGAGACGTGAGTTTAAAGTTGTTGCTGCTGCAAAATCTGCGGGAACACCCCTCG 31020
Db 30961 TAGAGACGTGAGTTTAAAGTTGTTGCTGCTGCAAAATCTGCGGGAACACCCCTCG 31020
Oy 31021 TTGCAATGCGTTATCTGTGAGGCTACTGTACACAGGCGCGATTTGCGAGACATTTGTT 31080
Db 31021 TTGCAATGCGTTATCTGTGAGGCTACTGTACACAGGCGCGATTTGCGAGACATTTGTT 31080
Oy 31081 TTGCTATCATGACAGGCTTGGCAGAGCTCCAGACGGAGATCTGTTACCGTGAATCC 31140
Db 31081 TTGCTATCATGACAGGCTTGGCAGAGCTCCAGACGGAGATCTGTTACCGTGAATCC 31140
Oy 31141 CGGCTCTCGGGGGCTATTGGACAAGACGCGTCTCATGTGCTCGGGCGCATTTT 31200
Db 31141 CGGCTCTCGGGGGCTATTGGACAAGACGCGTCTCATGTGCTCGGGCGCATTTT 31200

|||||
Db 31141 CGGCTCTCGGGGGCTATTGTACACAAGACGCTCTCATGTGCTCGGGGGCATTTT 31200
Oy 31201 GGGTTGCGGGTTTATGATGTTTGGCATTTGGCGATTTGCCGTTCCCTGCCCCGGAGCAGATC 31260
Db 31201 GGGTTGCGGGTTTATGATGTTTGGCATTTGGCGATTTGGCGATTTGCCGTTCCCTGCCCCGGAGCAGATC 31260
Oy 31261 CCCGACATGTTTGAATTTGTTTCTAGTTCGGGCGATGACCATCTCTGTTTCCCGTTGGTG 31320
Db 31261 CCCGACATGTTTGAATTTGTTTCTAGTTCGGGCGATGACCATCTCTGTTTCCCGTTGGTG 31320
Oy 31321 CTTTGCAGCAGCTTGTCTAGTTCAGCGAGAGAGGTTTTCACAGCTGTGAACCT 31380
Db 31321 CTTTGCAGCAGCTTGTCTAGTTCAGCGAGAGAGGTTTTCACAGCTGTGAACCT 31380
Oy 31381 TAGCGCCAGCTGTTGATTTGCGATCAACAAACGCTTCTCTTCTCTATCAGAGATG 31440
Db 31381 TAGCGCCAGCTGTTGATTTGCGATCAACAAACGCTTCTCTCTCTATCAGAGATG 31440
Oy 31441 TTTGTGAATTAACCAAGCTTTGATGAGTGGGGGGCCCAAAAAGTTGGGTATTTGGCG 31500
Db 31441 TTTGTGAATTAACCAAGCTTTGATGAGTGGGGGGCCCAAAAAGTTGGGTATTTGGCG 31500
Oy 31501 CGCTGTTTCTGGGTATCTCATACAGATTTTCTGACGTCGCGATCTTCCATTTGGC 31560
Db 31501 CGCTGTTTCTGGGTATCTCATACAGATTTTCTGACGTCGCGATCTTCCATTTGGC 31560
Oy 31561 TAAAAAACCCTTAAGCCGCGCGAGCTGTGTATTAATGATAGCGGAAACGCTGATG 31620
Db 31561 TAAAAAACCCTTAAGCCGCGCGAGCTGTGTATTAATGATAGCGGAAACGCTGATG 31620
Oy 31621 ACTCAGTATGATTTTAAATGATTTTCTGTTCTGTTTAAATGAGCCAGGGCCTTACCG 31680
Db 31621 ACTCAGTATGATTTTAAATGATTTTCTGTTCTGTTTAAATGAGCCAGGGCCTTACCG 31680
Oy 31681 ACCAGTTTCTGTCCTCTTGGCGCGGCTGCTCCATATATATCCAGGAATCTGCAGT 31740
Db 31681 ACCAGTTTCTGTCCTCTTGGCGCGGCTGCTCCATATATATCCAGGAATCTGCAGT 31740
Oy 31741 GGTGAAGCCCTGCATGCTGTATTTTATTTGCGTTGCGGGGAAATACAGCCGCG 31800
Db 31741 GGTGAAGCCCTGCATGCTGTATTTTATTTGCGTTGCGGGGAAATACAGCCGCG 31800
Oy 31801 TTAGGACAGTCTGATCAATTAAGTACGACGTTTGTGATGATGATTTGATTTACGGTAA 31860
Db 31801 TTAGGACAGTCTGATCAATTAAGTACGACGTTTGTGATGATGATTTGATTTACGGTAA 31860
Oy 31861 GCACACAATCTGCTATTCGCTTACCTAGGAAACCTCGAAAAAATCTTAATTTAAGCT 31920
Db 31861 GCACACAATCTGCTATTCGCTTACCTAGGAAACCTCGAAAAAATCTTAATTTAAGCT 31920
Oy 31921 TTTTGTGCTCCCTGAGTGTGGGCGAATTTGAAAGAACTTTTAAATATCATCAAGCAGC 31980
Db 31921 TTTTGTGCTCCCTGAGTGTGGGCGAATTTGAAAGAACTTTTAAATATCATCAAGCAGC 31980
Oy 31981 GGTGTTGATTAACCGTGGATTAAGTGAAGTGGGCGGAGTTCCAGCCGCTTTGGCGTG 32040
Db 31981 GGTGTTGATTAACCGTGGATTAAGTGAAGTGGGCGGAGTTCCAGCCGCTTTGGCGTG 32040
Oy 32041 AGCCCGAAGGGCTTCGAGGCTGCGAGAGCTGCTTCAATTTGATTTCAAAACGCGCATGGCG 32100
Db 32041 AGCCCGAAGGGCTTCGAGGCTGCGAGAGCTGCTTCAATTTGATTTCAAAACGCGCATGGCG 32100
Oy 32101 AAGAGGCTGTGGCTTTGGCGAGCGCTTTCGCTCAATGATGCGGAGTGGAGGCTTAAT 32160
Db 32101 AAGAGGCTGTGGCTTTGGCGAGCGCTTTCGCTCAATGATGCGGAGTGGAGGCTTAAT 32160
Oy 32161 GGGAGAGTCTTCCAGCATCTGATGAGCTTTGAGACGCGGAAAGCAGCATCTTGAGTATG 32220
Db 32161 GGGAGAGTCTTCCAGCATCTGATGAGCTTTGAGACGCGGAAAGCAGCATCTTGAGTATG 32220
Oy 32221 ATGATGTCTCCCGTGTGATAGCAGCGGCTTATATGAGCCCTGGAAGTCAAAACTATG 32280
Db 32221 ATGATGTCTCCCGTGTGATAGCAGCGGCTTATATGAGCCCTGGAAGTCAAAACTATG 32280
```

Oy	32281	ACGTACCCACGCTCCGTCGCGGAACCGCGTGGGAATTACTGCACCCGCAAGCCCTGTATG	32340
Db	32281	ACGTACCCACGCTCCGTCGCGGAACCGCGTGGGAATTACTGCACCCGCAAGCCCTGTATG	32340
Oy	32341	CACATCCGAGGTGCCCCCTAAAGAGGCGGTGGTGGCGGCGGTGGCGGCGCTCCCAAGG	32400
Db	32341	CACATCCGAGGTGCCCCCTAAAGAGGCGGTGGTGGCGGCGGTGGCGGCGCTCCCAAGG	32400
Oy	32401	TGTCGCGGCTCTCGGCGTAGACTTCATATGTGTTGACAGACAGATTTGGCGATAGAGAGA	32460
Db	32401	TGTCGCGGCTCTCGGCGTAGACTTCATATGTGTTGACAGACAGATTTGGCGATAGAGAGA	32460
Oy	32461	CGCGGCGAGCTTACCGGGGGCTCAAGTTTCTTCCGAGAGCGAGCGAATATGGGGAATATC	32520
Db	32521	CGGAGCGTACTACTACACGCGCGGGTTGAAACGCGTGAACAAGAAATTTACCTCCGGGC	32580
Oy	32581	GTAGGGGTGCATCTCGGAGCCCTCGTCGACAAACCTAGTCACGGTGGCGGGTTAACAC	32640
Db	32581	GTAGGGGTGCATCTCGGAGCCCTCGTCGACAAACCTAGTCACGGTGGCGGGTTAACAC	32640
Oy	32641	GTAAAGACTAAACGTCGCGCTGAGTGTATAGTTTAAAACTTGCCTGGCGGATTAAGAGACATG	32700
Db	32641	GTAAAGACTAAACGTCGCGCTGAGTGTATAGTTTAAAACTTGCCTGGCGGATTAAGAGAGATG	32700
Oy	32701	ATGCTAAGGTTGATGTACCCAGGCGGGTATCCGCTGGCGGTTACTTCATGTACAGCCGATC	32760
Db	32701	ATGCTAAGGTTGATGTACCCAGGCGGGTATCCGCTGGCGGTTACTTCATGTACAGCCGATC	32760
Oy	32761	CTATGACGGATATAGAAATGCCCTTTTAACTCATCTAGAGGGGTATAGGTTGGAA	32820
Db	32761	CTATGACGGATATAGAAATGCCCTTTTAACTCATCTAGAGGGGTATAGGTTGGAA	32820
Oy	32821	AAACAAGCGTATTGAATTCAATGACGTGGCATGGTGGCCGACAGAAACGCTTAAAGCTATC	32880
Db	32821	AAACAAGCGTATTGAATTCAATGACGTGGCATGGTGGCCGACAGAAACGCTTAAAGCTATC	32880
Oy	32881	CCGAGCCCATGAATTTTGGACGAGTGTAAATTCAATTGCAATTCGCTTAAAGAAACAGCGAGGA	32940
Db	32881	CCGAGCCCATGAATTTTGGACGAGTGTAAATTCAATTGCAATTCGCTTAAAGAAACAGCGAGGA	32940
Oy	32941	TAGTTAAGCAAGGACCCAGGGAATTTGATCACTTCTGCTCGCTATACGCGTGTGAGA	33000
Db	32941	TAGTTAAGCAAGGACCCAGGGAATTTGATCACTTCTGCTCGCTATACGCGTGTGAGA	33000
Oy	33001	GCAAGTTGGCGTACCGCTTCTGTGCGACACCGCCGCGCATCGGTCCGAACCTTGCAACCGT	33060
Db	33001	GCAAGTTGGCGTACCGCTTCTGTGCGACACCGCCGCGCATCGGTCCGAACCTTGCAACCGT	33060
Oy	33061	GGCTGTGTGGGAAACGCTAGACAAAGCGCACGGAATTGGATTGTTTGGACAGACACTATC	33120
Db	33061	GGCTGTGTGGGAAACGCTAGACAAAGCGCACGGAATTGGATTGTTTGGACAGACACTATC	33120
Oy	33121	TGTCGCGAAGCGTGTGTTTCCGCTGGTTCACGTAAGTAAGTACAGAGGCTAACCGCGGATC	33180
Db	33121	TGTCGCGAAGCGTGTGTTTCCGCTGGTTCACGTAAGTAAGTACAGAGGCTAACCGCGGATC	33180
Oy	33181	ATCTGTTTCAAAATCTTCTCTTTTCTCGGACACAGACGGCGGATGTGTGCTTTTCTATA	33240
Db	33181	ATCTGTTTCAAAATCTTCTCTTTTCTCGGACACAGACGGCGGATGTGTGCTTTTCTATA	33240
Oy	33241	CGCTCAACAGTTCGGAGGCGCACAGGGGCAATTCAAAATCGAAGGCCGTTAAGAAAGAAAG	33300
Db	33241	CGCTCAACAGTTCGGAGGCGCACAGGGGCAATTCAAAATCGAAGGCCGTTAAGAAAGAAAG	33300
Oy	33301	GAATCAGCAAAACTTACTTGCAGACAGGTAGCGTGGCGTACCATGCCGTTCTGTACGT	33360
Db	33301	GAATCAGCAAAACTTACTTGCAGACAGGTAGCGTGGCGTACCATGCCGTTCTGTACGT	33360

QY	33361	GGGATGATGATGCAATATCTCCACCGGAGCAAAATGGTTAGCTGGTGACAAACTGGT	33420
Db	33361	GGGGATGATGATGCAATATCTCCACCGGAGCAAAATGGTTAGCTGGTGACAAACTGGT	33420
QY	33421	CCATAGAGGACATATGCAATATATAATCCAGATTGACTCATGGGTTCTTAACCCTAACAA	33480
Db	33421	CCATAGAGGACATATGCAATATATAATCCAGATTGACTCATGGGTTCTTAACCCTAACAA	33480
QY	33481	AACATCATGAACAGAGTATGATACCCATGGTGGCAGAAATGTTAGTATCGTTAAAGAAC	33540
Db	33481	AACATCATGAACAGAGTATGATACCCATGGTGGCAGAAATGTTAGTATCGTTAAAGAAC	33540
QY	33541	ACGTGACCTTAATGAGAGGTCTGTTGGGACTCTTTAAGACGTACGAAAGCTTCAAAATTT	33600
Db	33541	ACGTGACCTTAATGAGAGGTCTGTTGGGACTCTTTAAGACGTACGAAAGCTTCAAAATTT	33600
QY	33601	TAATTGTTGACGACGAGAACATCTAGATGATCGGTGGCCGTGGGGAAATATTTATG	33660
Db	33601	TAATTGTTGACGACGAGAACATCTAGATGATCGGTGGCCGTGGGGAAATATTTATG	33660
QY	33661	GGCAGGATGATGTCAAATGAGAGCTATTAAACACAGACAGTGAACGTGGCAGCTCTTGAAA	33720
Db	33661	GGCAGGATGATGTCAAATGAGAGCTATTAAACACAGACAGTGAACGTGGCAGCTCTTGAAA	33720
QY	33721	GCTACATTTCAAAGCCTAACCAATTTGGAAGGCAATGGCGGATATAGTTTATATTTT	33780
Db	33721	GCTACATTTCAAAGCCTAACCAATTTGGAAGGCAATGGCGGATATAGTTTATATTTT	33780
QY	33781	TTTACTATTAATAGGTCTCTGTACAGGACAAATAGCTGATGATGATAAAATCAAAATGTA	33840
Db	33781	TTTACTATTAATAGGTCTCTGTACAGGACAAATAGCTGATGATGATAAAATCAAAATGTA	33840
QY	33841	GAGTTGGAAATTTAATGAGAACATTTACCAATTTAATTTGAGAAACGTAAAGCAAGATTA	33900
Db	33841	GAGTTGGAAATTTAATGAGAACATTTACCAATTTAATTTGAGAAACGTAAAGCAAGATTA	33900
QY	33901	ACATCTATTTGATATGAGAAATGCGTGATACGATTTCTTACTGCTGGAACCATTTGCTGTG	33960
Db	33901	ACATCTATTTGATATGAGAAATGCGTGATACGATTTCTTACTGCTGGAACCATTTGCTGTG	33960
QY	33961	ACTTTGGAAAAACAAAAGATTTGCTGCTCGATCAAGATATAGTTAATGTCATATATATGAC	34020
Db	33961	ACTTTGGAAAAACAAAAGATTTGCTGCTCGATCAAGATATAGTTAATGTCATATATATGAC	34020
QY	34021	TATACATTTTGTAAATCTTCAAGTACACATGATTAATTAACCTTACGGGTGATTTTAATAC	34080
Db	34021	TATACATTTTGTAAATCTTCAAGTACACATGATTAATTAACCTTACGGGTGATTTTAATAC	34080
QY	34081	AGTTCCTTGGCAGGTTTTACTGGGAATTTTAATGTAATGACACATGCTTTAAACACAGGC	34140
Db	34081	AGTTCCTTGGCAGGTTTTACTGGGAATTTTAATGTAATGACACATGCTTTAAACACAGGC	34140
QY	34141	GTTTATTTAACGAAAGCTGAAATTAATTACCAACTCAACAAACCTTAAGATCTTTTATAC	34200
Db	34141	GTTTATTTAACGAAAGCTGAAATTAATTACCAACTCAACAAACCTTAAGATCTTTTATAC	34200
QY	34201	GGCGAAAAAATAAATGACGAAATGTTCCAAATTAATCTTGAATTAATCCATGTAAATAT	34260
Db	34201	GGCGAAAAAATAAATGACGAAATGTTCCAAATTAATCTTGAATTAATCCATGTAAATAT	34260
QY	34261	TCCGGCATTAATACAGAAAAATTTGGATATTAATGTAATCAAGTTCAAAATTTCAAGTGAATGA	34320
Db	34261	TCCGGCATTAATACAGAAAAATTTGGATATTAATGTAATCAAGTTCAAAATTTCAAGTGAATGA	34320
QY	34321	AATATGCAATGTTGACGATGTTGGTGGTTCGATGCAACATTTCCACGCTTAAAGGC	34380
Db	34321	AATATGCAATGTTGACGATGTTGGTGGTTCGATGCAACATTTCCACGCTTAAAGGC	34380
QY	34381	TATATATCTTAATCGTGAATTAATTTGATGCTTAAATAATCAAACTATGCTCTGGGTGTAAT	34440
Db	34381	TATATATCTTAATCGTGAATTAATTTGATGCTTAAATAATCAAACTATGCTCTGGGTGTAAT	34440
QY	34441	GGCGGAAATCTTAATTAATCTTGTGATTTGGCAATTTTAACAAAAAATTTTACAGAAATG	34500

```

DB      34441 GGGCGAAATCTTATTAATCTCTGATTTGGCATTTTACCAAAAATTTTACAGAAATG 34500
OY      34501 TTTGTTTCAGTTATAGATAGTCCGCTTAATGCCATTGATATCTCAAGAAACTTTTG 34560
DB      34501 TTTGTTTCAGTTATAGATAGTCCGCTTAATGCCATTGATATCTCAAGAAACTTTTG 34560
OY      34561 GGTATTGGAAGCAAGAGGTCCTGTCAAAATCCTTCAAAATGAAATGATATCTTATCTTTC 34620
DB      34561 GGTATTGGAAGCAAGAGGTCCTGTCAAAATCCTTCAAAATGAAATGATATCTTATCTTTC 34620
OY      34621 TTTTGTGAAGTACTGACGATAATTTTATTTATATAAAATCTTCAAAAGCAGCAATTA 34680
DB      34621 TTTTGTGAAGTACTGACGATAATTTTATTTATATAAAATCTTCAAAAGCAGCAATTA 34680
OY      34681 GTTAAAGTTGGGTGTTGTTGACGAGCATGTTGCAGCGTTAGAAAGTTTAATGCATTTATTA 34740
DB      34681 GTTAAAGTTGGGTGTTGTTGACGAGCATGTTGCAGCGTTAGAAAGTTTAATGCATTTATTA 34740
OY      34741 AGGCTCTGCTACCCCAACGTTTAAGTTATATGACGTAAATTTGGAACGTTGCGCATATT 34800
DB      34741 AGGCTCTGCTACCCCAACGTTTAAGTTATATGACGTAAATTTGGAACGTTGCGCATATT 34800
OY      34801 GCAGAGTCCAGCTTTTAACTTTCGCGCAATATGATATGCTTATCAGTAATATGAT 34860
DB      34801 GCAGAGTCCAGCTTTTAACTTTCGCGCAATATGATATGCTTATCAGTAATATGAT 34860
OY      34861 CAAGAGTCTGATTTTCAATGTTTAAATTTGTAATTAATACACCTAAGGTTGGTGTA 34920
DB      34861 CAAGAGTCTGATTTTCAATGTTTAAATTTGTAATTAATACACCTAAGGTTGGTGTA 34920
OY      34921 ATTCAAAAGAAATGTATATTTACTAATTTACATGATACCAATATACGTAATAATTT 34980
DB      34921 ATTCAAAAGAAATGTATATTTACTAATTTACATGATACCAATATACGTAATAATTT 34980
OY      34981 CAGCTAACCAACACATTTAG 35000
DB      34981 CAGCTAACCAACACATTTAG 35000

RESULT 2
AAI64291
ID      AAI64291 standard; DNA; 128139 BP.
XX
XX      AAI64291;
AC
XX      22-APR-2002 (first entry)
DT
XX
XX      RRV genome nucleotide sequence.
DE
XX
XX      RRV; rhesus rhadinovirus; Japanese macaque virus; multiple sclerosis;
KM      JMHV; cytosstatic; antilastmatic; antiallergic; dermatological;
KM      vulnery; gene therapy; leucopenia; thrombocytopenia;
KM      inflammatory disease; asthma; allergy; dermatitis; virus; ds.
XX
OS      Macaca mulatta rhadinovirus 17577.
XX
FH      Key
FH      Location/Qualifiers
FT      1353..2674
FT      /tag= a
FT      /product= "RV R1"
FT      /complement= (2692..3258)
FT      CDS
FT      /tag= b
FT      /product= "dihydrofolate reductase"
FT      /label= RV_ORF2
FT      /note= "has similarity to Kaposi's sarcoma-associated
FT      virus (KSHV) open reading frame (ORF) 2"
FT      3676..5613
FT      CDS
FT      /tag= c
FT      /product= "complement binding protein"
FT      /label= RV_ORF4
FT      /note= "has similarity to KSHV ORF4"
FT      6045..9443
FT      CDS

```

```

FT      /tag= d
FT      /product= "ssDNA binding protein"
FT      /label= RV_ORF6
FT      /note= "has similarity to KSHV ORF6"
FT      9468..11528
FT      CDS
FT      /tag= e
FT      /product= "transport protein"
FT      /label= RV_ORF7
FT      /note= "has similarity to KSHV ORF7"
FT      11515..14004
FT      CDS
FT      /tag= f
FT      /product= "glycoprotein B"
FT      /label= RV_ORF8
FT      /note= "has similarity to KSHV ORF8"
FT      14122..17166
FT      CDS
FT      /tag= g
FT      /product= "DNA polymerase protein"
FT      /label= RV_ORF9
FT      /note= "has similarity to KSHV ORF9"
FT      17261..18511
FT      CDS
FT      /tag= h
FT      /label= RV_ORF10
FT      /note= "has similarity to KSHV ORF10"
FT      18520..19749
FT      CDS
FT      /tag= i
FT      /label= RV_ORF11
FT      /note= "has similarity to KSHV ORF11"
FT      complement (19921..20544)
FT      CDS
FT      /tag= j
FT      /product= "RV R2"
FT      /label= RV_ORF
FT      /note= "has similarity to KSHV interleukin (IL)-6 gene"
FT      complement (20777..2178)
FT      CDS
FT      /tag= k
FT      /product= "thymidylate synthase"
FT      /label= RV_ORF70
FT      /note= "has similarity to KSHV ORF70"
FT      complement (22245..22592)
FT      CDS
FT      /tag= l
FT      /product= "RV R3"
FT      /note= "has similarity to KSHV K4. viral MIP gene"
FT      26846..27409
FT      CDS
FT      /tag= m
FT      /product= "Bcl2-homologue"
FT      /label= RV_ORF16
FT      /note= "has similarity to KSHV ORF16"
FT      complement (27515..29125)
FT      CDS
FT      /tag= n
FT      /label= RV_ORF17
FT      /note= "has similarity to KSHV ORF17"
FT      28998..29897
FT      CDS
FT      /tag= o
FT      /label= RV_ORF18
FT      /note= "has similarity to KSHV ORF18"
FT      complement (29905..31548)
FT      CDS
FT      /tag= p
FT      /product= "tegument protein"
FT      /label= RV_ORF19
FT      /note= "has similarity to KSHV ORF19"
FT      complement (31043..32095)
FT      CDS
FT      /tag= q
FT      /label= RV_ORF20
FT      /note= "has similarity to KSHV ORF20"
FT      32094..33767
FT      CDS
FT      /tag= r
FT      /product= "thymidine kinase"
FT      /label= RV_ORF21
FT      /note= "has similarity to KSHV ORF21"
FT      33754..35868
FT      CDS
FT      /tag= s
FT      /product= "glycoprotein H"
FT      /label= RV_ORF22
FT      /note= "has similarity to KSHV ORF22"

```


FT CDS complement (35865..37073)
 FT /tag- t
 FT /label- RRV_ORF23
 FT /note- "has similarity to KSHV ORF23"
 FT complement (37123..39321)
 FT /tag- u
 FT /label- RRV_ORF24
 FT /note- "has similarity to KSHV ORF24"
 FT 39323..43459
 FT /tag- v
 FT /product- "major capsid protein"
 FT /label- RRV_ORF25
 FT /note- "has similarity to KSHV ORF25"
 FT 43491..44408
 FT /tag- w
 FT /product- "capsid protein"
 FT /label- RRV_ORF26
 FT /note- "has similarity to KSHV ORF26"
 FT 44433..45242
 FT /tag- x
 FT /label- RRV_ORF27
 FT /note- "has similarity to KSHV ORF27"
 FT 45408..45683
 FT /tag- y
 FT /label- RRV_ORF28
 FT /note- "has similarity to KSHV ORF28"
 FT complement (45733..46779)
 FT /tag- z
 FT /label- RRV_ORF29b
 FT /note- "has similarity to KSHV ORF29b"
 FT 46905..47135
 FT /tag- aa
 FT /label- RRV_ORF30
 FT /note- "has similarity to KSHV ORF30"
 FT 47093..47746
 FT /tag- ab
 FT /label- RRV_ORF31
 FT /note- "has similarity to KSHV ORF31"
 FT 47683..49077
 FT /tag- ac
 FT /label- RRV_ORF32
 FT /note- "has similarity to KSHV ORF32"
 FT 49049..50059
 FT /tag- ad
 FT /label- RRV_ORF33
 FT /note- "has similarity to KSHV ORF33"
 FT complement (49977..50960)
 FT /tag- ae
 FT /label- RRV_ORF29a
 FT /note- "has similarity to KSHV ORF29a"
 FT 50959..51942
 FT /tag- af
 FT /label- RRV_ORF34
 FT /note- "has similarity to KSHV ORF34"
 FT 51923..52372
 FT /tag- ag
 FT /label- RRV_ORF35
 FT /note- "has similarity to KSHV ORF35"
 FT 52278..53585
 FT /tag- ah
 FT /product- "kinase"
 FT /label- RRV_ORF36
 FT /note- "has similarity to KSHV ORF36"
 FT 53566..55008
 FT /tag- ai
 FT /product- "alkaline exonuclease"
 FT /label- RRV_ORF37
 FT /note- "has similarity to KSHV ORF37"
 FT 54963..55172
 FT /tag- aj
 FT /label- RRV_ORF38
 FT /note- "has similarity to KSHV ORF38"
 FT complement (55255..56391)
 FT CDS

FT /tag- ak
 FT /product- "glycoprotein M"
 FT /label- RRV_ORF39
 FT /note- "has similarity to KSHV ORF39"
 FT 56526..57932
 FT /tag- al
 FT /product- "helicase/prinase"
 FT /label- RRV_ORF40
 FT /note- "has similarity to KSHV ORF40"
 FT 57917..58528
 FT /tag- am
 FT /product- "helicase/prinase"
 FT /label- RRV_ORF41
 FT /note- "has similarity to KSHV ORF41"
 FT complement (58525..59343)
 FT /tag- an
 FT /label- RRV_ORF42
 FT /note- "has similarity to KSHV ORF42"
 FT complement (59297..61027)
 FT /tag- ao
 FT /product- "capsid protein"
 FT /label- RRV_ORF43
 FT /note- "has similarity to KSHV ORF43"
 FT

Query Match 84.1%; Score 29420; DB 24; Length 128139;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 29420; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5581 CTGCTGCCCTTTATGTTGTTTCTAAATTAACGTTTTCCTTACGACGTTGCC 5640
 DB 1 CTGCTGCCCTTTATGTTGTTTCTAAATTAACGTTTTCCTTACGACGTTGCC 60
 QY 5641 AGGCAACTGCAGCATTAACCAATCGCAACCGCGTGAATTCGGAAATTAAGTTA 5700
 DB 61 AGGCAACTGCAGCATTAACCAATCGCAACCGCGTGAATTCGGAAATTAAGTTA 120
 QY 5701 CATTATTCAGGTGCCAATAAAGGTGTTTAAATATTCATATGTTGTTTCATGTTT 5760
 DB 121 CATTATTCAGGTGCCAATAAAGGTGTTTAAATATTCATATGTTGTTTCATGTTT 180
 QY 5761 ATGTTGACCCGTTTATGTTATTCGCGCCACCTTGTTGCTATATATAGACATCT 5820
 DB 181 ATGTTGACCCGTTTATGTTATTCGCGCCACCTTGTTGCTATATATAGACATCT 240
 QY 5821 TTCACGTTATCTTACGTTACGTTATGATGATGATGATGATGATGATGATGAT 5880
 DB 241 TTCACGTTATCTTACGTTACGTTATGATGATGATGATGATGATGATGATGAT 300
 QY 5881 TGTGGCCGGGCTGAAATTAACACAGGGGTATCATATCATCCAGGGGACACATTAG 5940
 DB 301 TGTGGCCGGGCTGAAATTAACACAGGGGTATCATATCATCCAGGGGACACATTAG 360
 QY 5941 ACACGTTTATTAACATATATCGGATGCGCCACCAATACGTGCTAGCGACATGTA 6000
 DB 361 ACACGTTTATTAACATATATCGGATGCGCCACCAATACGTGCTAGCGACATGTA 420
 QY 6001 GAAAAACATTTTAACGTTTGTGTTAGCAACTGGAATTAACATATATGCTTCCAAAGCA 6060
 DB 421 GAAAAACATTTTAACGTTTGTGTTAGCAACTGGAATTAACATATATGCTTCCAAAGCA 480
 QY 6061 ACAGCGGACAAACCCCTGGAAGATATCAAGGGGTCTGTCGCCGATAGGCTGCGGAT 6120
 DB 481 ACAGCGGACAAACCCCTGGAAGATATCAAGGGGTCTGTCGCCGATAGGCTGCGGAT 540
 QY 6121 ACAGTTACGCTATTCGAACAAAGACTTCCCTTTCGCGAGGCGTCCATCTCGGCAACA 6180
 DB 541 ACAGTTACGCTATTCGAACAAAGACTTCCCTTTCGCGAGGCGTCCATCTCGGCAACA 600
 QY 6181 GACCATCTGATCTGGGCTTTCGCTACCAATCCCTTACGAGCTTACAGTTGAAACG 6240
 DB 601 GACCATCTGATCTGGGCTTTCGCTACCAATCCCTTACGAGCTTACAGTTGAAACG 660
 QY 6241 AATTCCCTCTACCGTAAGCCGCAATACAAAAAGTTGACACGACGAGCTCGCCGTTA 6300

|||||
Db 661 AATTCCCTCACCGTAAAGCGCATACAAAAAGTTGACACCGACGCTCGCGTTA 720
QY 6301 AGGTGACGTCTTTCACAGAGAGTATTTGTTTCAATGCAAGTTTATTCAGCGCG 6360
Db 721 AGGTGACGTCTTTCACAGAGAGTATTTGTTTCAATGCAAGTTTATTCAGCGCG 780
QY 6361 TGTTTGACGTACCGGCTTTAACCAACTATGCGAGGAAGCGGCTCTCTTTGGGTACA 6420
Db 781 TGTTTGACGTACCGGCTTTAACCAACTATGCGAGGAAGCGGCTCTCTTTGGGTACA 840
QY 6421 CGAGTTTATAGAACCGGCTCCACGCTACAGCATATGGAACCCCTGCGAATGTCGAGT 6480
Db 841 CGAGTTTATAGAACCGGCTCCACGCTACAGCATATGGAACCCCTGCGAATGTCGAGT 900
QY 6481 TACCGGACAAGATGATGATTTCTTGGCGTTTGTGTTAGGAAGGTTTAAAGAAAGAC 6540
Db 901 TACCGGACAAGATGATGATTTCTTGGCGTTTGTGTTAGGAAGGTTTAAAGAAAGAC 960
QY 6541 TGTGAGAGGGGCTGCTGCTCCGCGGTGTTCCAGACCAGAGGTGCAAGATTGCGGAC 6600
Db 961 TGTGAGAGGGGCTGCTGCTCCGCGGTGTTCCAGACCAGAGGTGCAAGATTGCGGAC 1020
QY 6601 GCCAGGCGTTTAAAGTGGCGTGTGAGAGCAACCTGTTGCACTCAGCGGTATAGAA 6660
Db 1021 GCCAGGCGTTTAAAGTGGCGTGTGAGAGCAACCTGTTGCACTCAGCGGTATAGAA 1080
QY 6661 TGCAGAGTTTACCAATAAAGAGCTTACGCGTACCTCTACGATCCCTCTTTACAGCA 6720
Db 1081 TGCAGAGTTTACCAATAAAGAGCTTACGCGTACCTCTACGATCCCTCTTTACAGCA 1140
QY 6721 TGCAGAGCGCTGAGACTCAAAAGAGTGAAGCGGCTCATCAAGCAAGAAAGCAAT 6780
Db 1141 TGCAGAGCGCTGAGACTCAAAAGAGTGAAGCGGCTCATCAAGCAAGAAAGCAAT 1200
QY 6781 TCAATGAGGACCTTACCAATAAAGTGAAGTGAAGCAAGAAAGCTTTTCAACGACGC 6840
Db 1201 TCAATGAGGACCTTACCAATAAAGTGAAGTGAAGCAAGAAAGCTTTTCAACGACGC 1260
QY 6841 TGCAGAAAGAGCAGAGAGGCTGCTCCACATGATTTGAGACAGCGTCTGCGAGAGTGC 6900
Db 1261 TGCAGAAAGAGCAGAGAGGCTGCTCCACATGATTTGAGACAGCGTCTGCGAGAGTGC 1320
QY 6901 CCTTATGTAAGCGCTGATGTTTCTGAGTGTCCCAAGAGCGGTGCGAGTTGCTGAAT 6960
Db 1321 CCTTATGTAAGCGCTGATGTTTCTGAGTGTCCCAAGAGCGGTGCGAGTTGCTGAAT 1380
QY 6961 AGCATAGCTGGCCATATTTGATGTTGTCACCTCACCAGAGGCTAGGGTTAAAGCGTTAG 7020
Db 1381 AGCATAGCTGGCCATATTTGATGTTGTCACCTCACCAGAGGCTAGGGTTAAAGCGTTAG 1440
QY 7021 AGCGTGTGTCGCGGCAAGAGCGGTTACGTCGCGGGTCAACTGTTCTGCTGCAATTCG 7080
Db 1441 AGCGTGTGTCGCGGCAAGAGCGGTTACGTCGCGGGTCAACTGTTCTGCTGCAATTCG 1500
QY 7081 TGTGTACTACTAATAAAGTGCAGAGCAAGCGCCAGGGGCAAAAAGGAGAGCTAAACG 7140
Db 1501 TGTGTACTACTAATAAAGTGCAGAGCAAGCGCCAGGGGCAAAAAGGAGAGCTAAACG 1560
QY 7141 TGTACAACTCTCTTTTCTCCCAACAGGAGTGGGGTTTAAATGAGGCCACATCAAG 7200
Db 1561 TGTACAACTCTCTTTTCTCCCAACAGGAGTGGGGTTTAAATGAGGCCACATCAAG 1620
QY 7201 AAAAGGCAAGCAAGCTTTAAAGGGGTAACCTCAAAAGCGCTCGATGTTCTTCGTTCA 7260
Db 1621 AAAAGGCAAGCAAGCTTTAAAGGGGTAACCTCAAAAGCGCTCGATGTTCTTCGTTCA 1680
QY 7261 CGCGGTATACACTGCGGCTACGCGCGCTTCTTCCGCCCATCTGCTGGGCAAGTTATGTT 7320
Db 1681 CGCGGTATACACTGCGGCTACGCGCGCTTCTTCCGCCCATCTGCTGGGCAAGTTATGTT 1740
QY 7321 ATTACATGCAAGTTCTTTCAGAACACCAAAAAGCTTCAGGAACGAGCGTTTAAATGCTC 7380
|||||

Db 1741 ATTACATGCAAGTTCTTTCAGAACACCAAAAAGCTTCAGGAACGAGCGTTTAAATGCTC 1800
QY 7381 ATTATGTGCGACACCGCGCCCACTCAGAGATGTGACAGCTATATGCAAGGCAACGCGG 7440
Db 1801 ATTATGTGCGACACCGCGCCCACTCAGAGATGTGACAGCTATATGCAAGGCAACGCGG 1860
QY 7441 CAACGTGCTCAACACGCTGTTCTATAGACTGAAGATAGGTTTCCCGCGTAAACACC 7500
Db 1861 CAACGTGCTCAACACGCTGTTCTATAGACTGAAGATAGGTTTCCCGCGTAAACACC 1920
QY 7501 CTCAGCGAGGAGCCCTTACGTTGTCGCGGAACGCGGAGCTTTAAACGACTTGAGA 7560
Db 1921 CTCAGCGAGGAGCCCTTACGTTGTCGCGGAACGCGGAGCTTTAAACGACTTGAGA 1980
QY 7561 TTCTGGGCAACTTCGCGAGCTTTAGAGACCGCGAAGAGAGCAAGAACCCGCGCAGAGC 7620
Db 1981 TTCTGGGCAACTTCGCGAGCTTTAGAGACCGCGAAGAGAGCAAGAACCCGCGCAGAGC 2040
QY 7621 ACCCAAGTACAGTACTGCGAGCTATGTCAGACCGTACAGAAAGCTATCCGCGATTG 7680
Db 2041 ACCCAAGTACAGTACTGCGAGCTATGTCAGACCGTACAGAAAGCTATCCGCGATTG 2100
QY 7681 GAATCACCGGAAGCAAGATATCAGTGAACCTCATCCACATCCAAAGTTTCTCA 7740
Db 2101 GAATCACCGGAAGCAAGATATCAGTGAACCTCATCCACATCCAAAGTTTCTCA 2160
QY 7741 GGGTGTTCAGAGGCTATGCACTCAATGTGAGCGAGAGAGTCAATGAAGTTCTGTAATGCA 7800
Db 2161 GGGTGTTCAGAGGCTATGCACTCAATGTGAGCGAGAGAGTCAATGAAGTTCTGTAATGCA 2220
QY 7801 TGAATTAATAATTAATTAATTTCCGCGAGAGCTCAATGCTGCTCATCATCTCAGT 7860
Db 2221 TGAATTAATAATTAATTAATTTCCGCGAGAGCTCAATGCTGCTCATCATCTCAGT 2280
QY 7861 TGTGTCGCAAGCTGTATGTCAGAGCGCGCGCGGCTGCTGCTGAATCTGCTACAAAT 7920
Db 2281 TGTGTCGCAAGCTGTATGTCAGAGCGCGCGCGGCTGCTGCTGAATCTGCTACAAAT 2340
QY 7921 CCTGCTGTGATCATTCAGAGATATCTGCTGCGGCTACTGATGATCTACGAACAAGATA 7980
Db 2341 CCTGCTGTGATCATTCAGAGATATCTGCTGCGGCTACTGATGATCTACGAACAAGATA 2400
QY 7981 ATCCGCGATGGGATCTCTCCCTCCGAGTGGCTAAAGATGCAATTTTCAGAGCTTGTGA 8040
Db 2401 ATCCGCGATGGGATCTCTCCCTCCGAGTGGCTAAAGATGCAATTTTCAGAGCTTGTGA 2460
QY 8041 CGAAGTTTAAAGGGGCTGCTGAGCGCGGGTCTCAAGGGGTGCGAACTGAATATG 8100
Db 2461 CGAAGTTTAAAGGGGCTGCTGAGCGCGGGTCTCAAGGGGTGCGAACTGAATATG 2520
QY 8101 TACACGGGACATGTTCTGCGACTTCTGACACCGACGAGCGGGGTCCAAAGGCTTAATG 8160
Db 2521 TACACGGGACATGTTCTGCGACTTCTGACACCGACGAGCGGGGTCCAAAGGCTTAATG 2580
QY 8161 CCCCCTTTAAATGCAAGTTAGATAGCCCGAGCATGATGTCGTTCCGAATTCATTA 8220
Db 2581 CCCCCTTTAAATGCAAGTTAGATAGCCCGAGCATGATGTCGTTCCGAATTCATTA 2640
QY 8221 AAATTAATAATTAATTAATTTTTCACACCGCGGGATCCGAGGGGTCAGTCGAGG 8280
Db 2641 AAATTAATAATTAATTAATTTTTCACACCGCGGGATCCGAGGGGTCAGTCGAGG 2700
QY 8281 TGTCTAACCGAGGAGGAGACGAGGACTTACGTGTGCGCGGACGCTACATGAAGTTTC 8340
Db 2701 TGTCTAACCGAGGAGGAGACGAGGACTTACGTGTGCGCGGACGCTACATGAAGTTTC 2760
QY 8341 TCAATCGCTGATTCGCGGCTGTTCCCGACACCAAGACCGCGGCTGTACTGTGGC 8400
Db 2761 TCAATCGCTGATTCGCGGCTGTTCCCGACACCAAGACCGCGGCTGTACTGTGGC 2820
QY 8401 ACAAGATCTCCGACGACCAACAAACCGCGGTTCTGAAAGACGTCGCGGACGAGACTGG 8460
Db 2821 ACAAGATCTCCGACGACCAACAAACCGCGGTTCTGAAAGACGTCGCGGACGAGACTGG 2880

QY	8461	CGAGACTGCTGCTACGTAAGAACAACACCTTCGGCTTGAGAAACGACGTGCTGG	8520
Db	2881	CGGAGCTGCTGCTGACGTAAAGAACCAACCTCGCGTTGAGGAAACGAACTGCTGG	2940
QY	8521	ACGAGCTCGGGAATTCACATGTCGTAACGCGAGAGATCAAACTGAAGGGCCATTCTAA	8580
Db	2941	ACGAGGTTCCGGATTCACATGTCGTAACGCGAGAGATCAAACTGAAGGGCCATTCTAA	3000
QY	8581	GGGCGATGCGCAGATTCTAGTTCTTACGCGCAAGACGTGCACTGCTCAGCGCGGTGCTAC	8640
Db	3001	GGGCGATGCGCAGATTCTAGTTCTTACGCGCAAGACGTGCACTGCTCAGCGCGGTGCTAC	3060
QY	8641	AGACGATGATGCCGAGGAATACCCCAACGTCTGGGCTCCGGCGCAATGCCACACCGG	8700
Db	3061	AGACGATGATGCCGAGGAATACCCCAACGTCTGGGCTCCGGCGCAATGCCACACCGG	3120
QY	8701	TGGCTTACCTGGCAAGAAATTAACGGCGCCACCGCCCTACCGTCAGACGACGGCGGTC	8760
Db	3121	TGGCTTACCTGGCAAGAAATTAACGGCGCCACCGCCCTACCGTCAGACGACGGCGGTC	3180
QY	8761	AGCCGCTGCCGCAACAGGCGCCTGCGTCCGTTGATTAACGTTCCATGGTAGTCAACA	8820
Db	3181	AGCCGCTGCCGCAACAGGCGCCTGCGTCCGTTGATTAACGTTCCCATGGTAGTCAACA	3240
QY	8821	AATACACGGGGGTCAACGGGAACAACAACGTTTTCACCTGGGGAACCTGGGGTACTTCG	8880
Db	3241	AATACACGGGGGTCAACGGGAACAACAACGTTTTCACCTGGGGAACCTGGGGTACTTCG	3300
QY	8881	CGGGCGCGGGGTGGACCGCAACTGTGTGGCGGAAGCTCCCGCTTTAAGAAACGGGCG	8940
Db	3301	CGGGCGCGGGGTGGACCGCAACTGTGTGGCGGAAGCTCCCGCTTTAAGAAACGGGCG	3360
QY	8941	TCAGCGCCATGCTAAGAAAGACACGTGATGATGACCCCAATTATCGACCGCTAATAA	9000
Db	3361	TCAGCGCCATGCTAAGAAAGACACGTGATGATGACCCCAATTATCGACCGCTAATAA	3420
QY	9001	AGCAGCGCGGGGACAGACATTCAGACGTCGAGGCGGGAAGGCTTAAAGAGACGTGC	9060
Db	3421	AGCAGCGCGGGGACAGACATTCAGACGTCGAGGCGGGAAGGCTTAAAGAGACGTGC	3480
QY	9061	AGCGGCTGTTAGAGATTAAGACAAACCTTAACATTAAGTAAGTCGGTAATCTTGAAGCTTA	9120
Db	3481	AGCGGCTGTTAGAGATTAAGACAAACCTTAACATTAAGTAAGTCGGTAATCTTGAAGCTTA	3540
QY	9121	TACGACACCTGGGGAAGGGCTGCCAGCACTTAAGCTCCGAGAGCGTGCATAATTACCTCG	9180
Db	3541	TACGACACCTGGGGAAGGGCTGCCAGCACTTAAGCTCCGAGAGCGTGCATAATTACCTCG	3600
QY	9181	GTCGACTATTGATGTGACGGACGAGGGTTATTACCTGTTGGATTAATTAACACAGTCAG	9240
Db	3601	GTCGACTATTGATGTGACGGACGAGGGTTATTATTACCTGTTGGATTAATTAACACAGTCAG	3660
QY	9241	GCGTGCCCTGGACTATCGAGGACCGGGGTGCCCTTAATAGAGATCGCCAGACGCAGACG	9300
Db	3661	GCGTGCCCTGGACTATCGAGGACCGGGGTGCCCTTAATAGAGATCGCCAGACGCAGACG	3720
QY	9301	ATCTTCAGTTGCTGAGACAGCGATATCGCACCGCTTCTGTACAGCCCCCGAGGAAC	9360
Db	3721	ATCTTCAGTTGCTGAGACAGCGATATCGCACCGCTTCTGTACAGCCCCCGAGGAAC	3780
QY	9361	AGCTACCGACCCCTAAGCCCGGGCCCTCACTGCGCGGGGAAMAACGAAAAATTAAACGGC	9420
Db	3781	AGCTACCGACCCCTAAGCCCGGGCCCTCACTGCGCGGGGAAMAACGAAAAATTAAACGGC	3840
QY	9421	TGCTGAGGAGATCTAGACCTTTAGAAAAACCTGTGCAGGCGGGCAACAATGGCCAGGGAC	9480
Db	3841	TGCTGAGGAGATCTAGACCTTTAGAAAAACCTGTGCAGGCGGGCAACAATGGCCAGGGAC	3900
QY	9481	TCGCAGCAATTATACGCGCAGCTGTGCGCCCTGCGCTGCAGCTGATGCTGTGTTATCTTTG	9540
Db	3901	TCGCAGCAATTATACGCGCAGCTGTGCGCCCTGCGCTGCAGCTGATGCTGTGTTATCTTTG	3960

QY	9541	CGGACCCGCCAAGTATGACGGGTGCCGCAATTTAAAAACAAAACACAGATGAGAAC	9600
Db	3961	CGGACCCGCCAAGTATGACGGGTGCCGCAATTTAAAAACAAAACACAGATGAGAAC	4020
QY	9601	TGAACCGGACCTTCTCCGCTGTACGCAAGAAAACCTGGTAGACGTCCAGCTGT	9660
Db	4021	TGAACCGGACCTTCTCCGCTGTACGCAAGAAAACCTGGTAGACGTCCAGCTGT	4080
QY	9661	CGCTCGAAGTGGACACCTGGCCAAAACATCGAGGCAACAACTCGACGAGCTGGAGCGCA	9720
Db	4081	CGCTCGAAGTGGACACCTGGCCAAAACATCGAGGCAACAACTCGACGAGCTGGAGCGCA	4140
QY	9721	GTCCTGGCGCAGAGATATTGCAGCCGAGACATTTTGAACACTACCTGAGACCCGAAT	9780
Db	4141	GTCCTGGCGCAGAGATATTGCAGCCGAGAGCATTTTGAACACTACCTGAGACCCGAAT	4200
QY	9781	GTCACCTACACTACAGGTACTACTTTACGTTTACGGGGCGGGTTAATAGATGTAAACA	9840
Db	4201	GTCACCTACACTACAGGTACTACTTTACGTTTACGGGGCGGGTTAATAGATGTAAACA	4260
QY	9841	TGTGCTTAATTAAMCGATGTAGAACTGCTGTGTAAAAAGACTAGGAGGTGTGTATATGCA	9900
Db	4261	TGTGCTTAATTAAMCGATGTAGAACTGCTGTGTAAAAAGACTAGGAGGTGTGTATATGCA	4320
QY	9901	TCGGTGCAAAAGAAAGCTCTCTCCGGATTGAACCGGGTTCTGACGTTTCTGTCAACACTCC	9960
Db	4321	TCGGTGCAAAAGAAAGCTCTCTCCGGATTGAACCGGGTTCTGACGTTTCTGTCAACACTCC	4380
QY	9961	GGGGTATCTCCCGCATCCGCGACCCGACACCTTAACGTCACGTAGTGCCTGTGTAACAT	10020
Db	4381	GGGGTATCTCCCGCATCCGCGACCCGACACCTTAACGTCACGTAGTGCCTGTGTAACAT	4440
QY	10021	GCTGTAGGGAAMTGAAGCTGTACCAAAATCAGGGGTCACGATTACTCGCGGTGTGGCAG	10080
Db	4441	GCTGTAGGGAAMTGAAGCTGTACCAAAATCAGGGGTCACGATTACTCGCGGTGTGGCAG	4500
QY	10081	ACCGCACACTGCGATCACCTCTGTATAGAAGSTTATGGGCGGACCAATACAGCGCTTTTGG	10140
Db	4501	ACCGCACACTGCGATCACCTCTGTATAGAAGSTTATGGGCGGACCAATACAGCGCTTTTGG	4560
QY	10141	AGACAGAACTGAGCCACTGGGTGCTAAATTAACAAAAGCTTGTGGAGCGGACGACACAG	10200
Db	4561	AGACAGAACTGAGCCACTGGGTGCTAAATTAACAAAAGCTTGTGGAGCGGACGACACAG	4620
QY	10201	GCGTCCGGTCTCTGCGAGATCAGTTAAGGAGTGTGCTGCGTGGCGGCATACAAAGTACAA	10260
Db	4621	GCGTCCGGTCTCTGCGAGATCAGTTAAGGAGTGTGCTGCGTGGCGGCATACAAAGTACAA	4680
QY	10261	ATATATTTCAACCGGGTGTCCGCGTCAATCATGTGAACATATCAATCTAATTTATTTGAGACG	10320
Db	4681	ATATATTTCAACCGGGTGTCCGCGTCAATCATGTGAACATATCAATCTAATTTATTTGAGACG	4740
QY	10321	CCGGGCAAAACCGGCTCCGACACCGGGGACGAAAACGATGCTACAAAATGGCCAGCTCC	10380
Db	4741	CCGGGCAAAACCGGCTCCGACACCGGGGACGAAAACGATGCTACAAAATGGCCAGCTCC	4800
QY	10381	TAAACACAGAGGCGGATATGACAGAGACCGTGCGCTAATTAACACCAAACTPAAGGCGCA	10440
Db	4801	TAAACACAGAGGCGGATATGACAGAGACCGTGCGCTAATTAACACCAAACTPAAGGCGCA	4860
QY	10441	CTCACCTTCTACGACTGTTTCCGACCGGATCCCATAGAAATCCCTGTTCTCGGGCGCTTCT	10500
Db	4861	CTCACCTTCTACGACTGTTTCCGACCGGATCCCATAGAAATCCCTGTTCTCGGGCGCTTCT	4920
QY	10501	TTAACTCTATAGACGACACCATTAAGGCACTGAGCCGGGATTTCTCCGTGACGTTCTTTC	10560
Db	4921	TTAACTCTATAGACGACACCATTAAGGCACTGAGCCGGGATTTCTCCGTGACGTTCTTTC	4980
QY	10561	AACAGGCAAACTATACCAAGCTTATGGGAAAACAAAACGAGCTGTACACAGACTCAATA	10620
Db	4981	AACAGGCAAACTATACCAAGCTTATGGGAAAACAAAACGAGCTGTACACAGACTCAATA	5040
QY	10621	GCAATCTGTGCTCAAGGAGGCGGGGATTCGCAAAAACCGGCACTCCCTCGAGGCAACGTA	10680

|||||
Db 5041 GCATCTGCTCAGGGAGCGGGGATCGCAAAACCGGCCACCCCTCGAGCCACGGGA 5100
QY 10681 CCACCAACCGTGGCGGCAACCGCGGCAAGCAGCTCATCAAAAGACGACATATGCAAAAG 10740
Db 5101 CCACCAACCGTGGCGGCAACCGCGGCAAGCAGCTCATCAAAAGACGACATATGCAAAAG 5160
QY 10741 AACAGTACATGAAAAAGGTGGCCAGGAGCGGCTTTAAAAAACTAACAGAGTGTCTGCAGA 10800
Db 5161 AACAGTACATGAAAAAGGTGGCCAGGAGCGGCTTTAAAAAACTAACAGAGTGTCTGCAGA 5220
QY 10801 CGCAGAGCGGGGCTTTGGCAAAACGCACTCGCATGGCGGATGGGGGGGGGCTGCGCTACG 10860
Db 5221 CGCAGAGCGGGGCTTTGGCAAAACGCACTCGCATGGCGGATGGGGGGGGGCTGCGCTACG 5280
QY 10861 GCGAGGCGTCCGAGCTGTGTGAACATTTTCTCCTCAGGGCGGCGCTTGTGTGCGCTCCCT 10920
Db 5281 GCGAGGCGTCCGAGCTGTGTGAACATTTTCTCCTCAGGGCGGCGCTTGTGTGCGCTCCCT 5340
QY 10921 GCGAGGCGGCTGCGCGCTCGGATCAGATTTTATTCGAAAACTCAAAAGTACATTAAAACT 10980
Db 5341 GCGAGGCGGCTGCGCGCTCGGATCAGATTTTATTCGAAAACTCAAAAGTACATTAAAACT 5400
QY 10981 CACTATATTCGAGCGGCTCAGTGGGAGACGTAAGATATACAGATTAACGAGCTTTACG 11040
Db 5401 CACTATATTCGAGCGGCTCAGTGGGAGACGTAAGATATTAACGAGCTTTACGAGCTTTACG 5460
QY 11041 GCGTGTATTAACCGGCGCCCTGACGCGCCAGAGGAGTCTTTCCCGGCGCCGCGCAACGTG 11100
Db 5461 GCGTGTATTAACCGGCGCCCTGACGCGCCAGAGGAGTCTTTCCCGGCGCCGCGCAACGTG 5520
QY 11101 GCGTGGCCGAGTCTTCGAGGGGGCGGGAATGTTCCGATCACAAGATGTGTGTGAG 11160
Db 5521 GCGTGGCCGAGTCTTCGAGGGGGCGGGAATGTTCCGATCACAAGATGTGTGTGAG 5580
QY 11161 AGATGATATGGCCCGAGATTCAACGGAAGACGTGATAGACGACATTTAATCGTTTTT 11220
Db 5581 AGATGATATGGCCCGAGATTCAACGGAAGACGTGATAGACGACATTTAATCGTTTTT 5640
QY 11221 ACCAACTTCGCGAAGGTGATCTCAACGCGGTACAAAAAGTCCGCTGTGCTTTATACGAG 11280
Db 5641 ACCAACTTCGCGAAGGTGATCTCAACGCGGTACAAAAAGTCCGCTGTGCTTTATACGAG 5700
QY 11281 AGCTGTCTCTCGGCGGCGCTTTAATACGCAAGTGGGAAAAAGCGTGGCGATATTTT 11340
Db 5701 AGCTGTCTCTCGGCGGCGCTTTAATACGCAAGTGGGAAAAAGCGTGGCGATATTTT 5760
QY 11341 CCTAGCGCGGAGAAACTCTCATCTCCAACTAGAGTTAAAGGCTGAGGTCGCGCC 11400
Db 5761 CCTAGCGCGGAGAAACTCTCATCTCCAACTAGAGTTAAAGGCTGAGGTCGCGCC 5820
QY 11401 TGTATCTTAACGTAACGACAGACGCGCGCTCGTCTAATTTCTCAAAATACCGGTGA 11460
Db 5821 TGTATCTTAACGTAACGACAGACGCGCGCTCGTCTAATTTCTCAAAATACCGGTGA 5880
QY 11461 TATTTAAAGAACCTGTACGCTCTGTGTACATCAGCTGCAATGTGCCAGCGCATGAG 11520
Db 5881 TATTTAAAGAACCTGTACGCTCTGTGTACATCAGCTGCAATGTGCCAGCGCATGAG 5940
QY 11521 ATAATAACCGAAGCGTGTCTCTGCGGGGCGTGGTGTATATCGCATGGGACG 11580
Db 5941 ATAATAACCGAAGCGTGTCTCTGCGGGGCGTGGTGTATATCGCATGGGACG 6000
QY 11581 GCGGTTGGGAAAACGTCAACACCCCAAGGGCGGACACGACGCGGAAGCAAGCGCG 11640
Db 6001 GCGGTTGGGAAAACGTCAACACCCCAAGGGCGGACACGACGCGGAAGCAAGCGCG 6060
QY 11641 GCGCGGTGAGCGCCCAACACCTCCGAGAACCCACTAGGGCGGAGGCTTTAAGTTGCG 11700
Db 6061 GCGCGGTGAGCGCCCAACACCTCCGAGAACCCACTAGGGCGGAGGCTTTAAGTTGCG 6120
QY 11701 GTGTGACGCGCTTCGGCAACGCGGACATCTTCAGGTTTAACTGAAAAAAGCGTGTGCG 11760
|||||

Db 6121 GTGTGACGCGCTTCGGCCACCGCGCAACTCTTCAGGTTTAACTGAAAAAAGCGTGTGCG 6180
QY 11761 GGCACCGAGAGACAAGACGACCAAGAAGCATCTGATGGTGTATTTAAAAAATATTTGTC 11820
Db 6181 GGCACCGAGAGACAAGACGACCAAGAAGCATCTGATGGTGTATTTAAAAAATATTTGTC 6240
QY 11821 CCGCACATCTTTAAGGTACAGCGGTACCCGAAGTGGCCACTCGGTGACCGTCTATCGA 11880
Db 6241 CCGCACATCTTTAAGGTACAGCGGTACCCGAAGTGGCCACTCGGTGACCGTCTATCGA 6300
QY 11881 GGGTGGACGAGACCGCCGCTGACCGGCAAGCAAGAGTATCTCGACCGGCGCGCATG 11940
Db 6301 GGGTGGACGAGACCGCCGCTGACCGGCAAGCAAGAGTATCTCGACCGGCGCGCATG 6360
QY 11941 GAGATCAACACATGAGACAGACGACCTCAAGTGTTCATGCTCATGTGGCGTTAAACGTAAC 12000
Db 6361 GAGATCAACACATGAGACAGACGACCTCAAGTGTTCATGCTCATGTGGCGTTAAACGTAAC 6420
QY 12001 GGCATAGTAAACACTTACAGCGGACGAGGACCTTCAACCAAGACCGTGTTCGAAACCG 12060
Db 6421 GGCATAGTAAACACTTACAGCGGACGAGGACCTTCAACCAAGACCGTGTTCGAAACCG 6480
QY 12061 GTGAGGGGCTACGGGATTAACATCCAGCATCTTCAAGTCAAGCGGCTGTGTAACAGACA 12120
Db 6481 GTGAGGGGCTACGGGATTAACATCCAGCATCTTCAAGTCAAGCGGCTGTGTAACAGACA 6540
QY 12121 CCGGAGATGGTTTCCGGGAATTTACAGGGTCAGAACACCGGTCAACTGCGAGATCGTGGAC 12180
Db 6541 CCGGAGATGGTTTCCGGGAATTTACAGGGTCAGAACACCGGTCAACTGCGAGATCGTGGAC 6600
QY 12181 ATGATGCGCGCTTCGGCGGACCGGTACTGTATTTTGTACCGGCTTGGGAGACGGTA 12240
Db 6601 ATGATGCGCGCTTCGGCGGACCGGTACTGTATTTTGTACCGGCTTGGGAGACGGTA 6660
QY 12241 GAGGTGTCCCGCTTCGACACAAGCACTCAAGCTGCTGCGCGGAGAAAAACCGAAAAAC 12300
Db 6661 GAGGTGTCCCGCTTCGACACAAGCACTCAAGCTGCTGCGCGGAGAAAAACCGAAAAAC 6720
QY 12301 GGCCTTGGCGCGCGCTGTCTCAAAATTAACACATGTGTGACTTGGCGCGCGCACGCC 12360
Db 6721 GGCCTTGGCGCGCGCTGTCTCAAAATTAACACATGTGTGACTTGGCGCGCGCACGCC 6780
QY 12361 ACCACCGAAACCGGGTCTTCGCGGACCTGGGGAATTAACCGGTATCTGTGAAAGCGGAG 12420
Db 6781 ACCACCGAAACCGGGTCTTCGCGGACCTGGGGAATTAACCGGTATCTGTGAAAGCGGAG 6840
QY 12421 GACCCCAAGTGGCGGCTTGCAGGCTGTGGAAGAACTCCGCCAGGGCGATATACG 12480
Db 6841 GACCCCAAGTGGCGGCTTGCAGGCTGTGGAAGAACTCCGCCAGGGCGATATACG 6900
QY 12481 ACGAGCGACGAGGCGCACTACACTTGTGTGCAACGAGCGTACGCGCATCTTCAAGTCC 12540
Db 6901 ACGAGCGACGAGGCGCACTACACTTGTGTGCAACGAGCGTACGCGCATCTTCAAGTCC 6960
QY 12541 CCGCTCTCCAGGTAACATACTTCAAGGCGGACGTAACCTGTGCTCAATGATTTATTCAG 12600
Db 6961 CCGCTCTCCAGGTAACATACTTCAAGGCGGACGTAACCTGTGCTCAATGATTTATTCAG 7020
QY 12601 AAAACCCITCAAGCGCACATCAAGAAGCTGTCCGATACCAAGCAAAACGATTCGAG 12660
Db 7021 AAAACCCITCAAGCGCACATCAAGAAGCTGTCCGATACCAAGCAAAACGATTCGAG 7080
QY 12661 CAGTACTACGAACCGAGGGGGGTGTGTTTCTCTGTGTGACCGCTTAAACGCGCGTAAGC 12720
Db 7081 CAGTACTACGAACCGAGGGGGGTGTGTTTCTCTGTGTGACCGCTTAAACGCGCGTAAGC 7140
QY 12721 CTAGCTGACGAGATCGCGGAATTTAAAGGCAACGACGACACCCCGACCAACCTCA 12780
Db 7141 CTAGCTGACGAGATCGCGGAATTTAAAGGCAACGACGACACCCCGACCAACCTCA 7200
QY 12781 ACCGCAACCGGCTTCGAAGAAGCGTGGTACGAGACGAGCAAGGACGACCTATAGC 12840
Db 7201 ACCGCAACCGGCTTCGAAGAAGCGTGGTACGAGACGAGCAAGGACGACCTATAGC 7260
|||||

OY	12841	GCGCCCAAGTCGATGTTGGCTTACGACAAAGCTCCGCGCAGCATCAACAGSTGCTGGAG	12900
Db	7261	GCGCCCAAGCTGCGATGTTCCGCTTACGACAAAGCTCCGCGCAGCATCAACAGSTGCTGGAG	7320
OY	12901	GAGCTCTCCAGGGGCGTGGTGGCGAGAAACAGTGTAGGGACACCTTACATGTGGTATGCAACCTG	12960
Db	7321	GAGCTCTCCAGGGGCGTGGTGGCGAGAAACAGTGTAGGGACACCTTACATGTGGTATGCAACCTG	7380
OY	12961	AGCAAGATTAAACCCACACAGCTTAAAGACGGCGATTTACGGGCGCGCGGTGTGGCCAAAG	13020
Db	7381	AGCAAGATTAAACCCACACAGCTTAAAGACGGCGATTTACGGGCGCGCGGTGTGGCCAAAG	7440
OY	13021	TTGCTGGGCGACGCCATCTCTCGTGAAGGACTGCGTGGCGGTGACCAGCGTTCGTCAAC	13080
Db	7441	TTTCTGGGCGACGCCATCTCTCGTGAAGGACTGCGTGGCGGTGACCAGCGTTCGTCAAC	7500
OY	13081	ATCCACAAGAGCCTCCGCGACAGTCCACCCCGGGGATGTGTACTCGGGAGCCCGCGGTCAAG	13140
Db	7501	ATCCACAAGAGCCTCCGCGACAGTCCACCCCGGGGATGTGTACTCGGGAGCCCGCGGTCAAG	7560
OY	13141	TTTCAGTTCCTCAACACAGCACACGCTGTTCAAGGGCCAGCTGGGACCCAGAAACAGATTC	13200
Db	7561	TTTCAGTTCCTCAACACAGCACACGCTGTTCAAGGGCCAGCTGGGACCCAGAAACAGATTC	7620
OY	13201	ATACTGACGGAACAACCAAGGTGGAGGGGCTGCMAAGAGACTGCGAACACTTCTTACAGC	13260
Db	7621	ATACTGACGGAACAACCAAGGTGGAGGGGCTGCMAAGAGACTGCGAACACTTCTTACAGC	7680
OY	13261	AGCAACGATTAACCTACTACTCAAAAGACTACGTTCTGTGTAAAAAATTAAACACTTCCGAG	13320
Db	7681	AGCAACGATTAACCTACTACTCAAAAGACTACGTTCTGTGTAAAAAATTAAACACTTCCGAG	7740
OY	13321	ATATCCACCCCTCGGTACGTTCAATGCGCCGTGAACCTTCGTTATAGAGAACTAGATTTC	13380
Db	7741	ATATCCACCCCTCGGTACGTTCAATGCGCCGTGAACCTTCGTTATAGAGAACTAGATTTC	7800
OY	13381	AGGCTCATTCGACGCTGTACAGCCCGCGGGAGAAAAACCTCTCCGGGAGGCTTTTGCATATA	13440
Db	7801	AGGCTCATTCGACGCTGTACAGCCCGCGGGAGAAAAACCTCTCCGGGAGGCTTTTGCATATA	7860
OY	13441	GAAACCATGTTTCAGAGGAATTCACACTACTACAGCAACGCGCTGAGCGGAGTCCGGAGAGAC	13500
Db	7861	GAAACCATGTTTCAGAGGAATTCACACTACTACAGCAACGCGCTGAGCGGAGTCCGGAGAGAC	7920
OY	13501	CTGGACAACACGATTCGACCTGAAACCGCGACCGCTGCGCGACCTGTCCGATATAGTC	13560
Db	7921	CTGGACAACACGATTCGACCTGAAACCGCGACCGCTGCGCGACCTGTCCGATATAGTC	7980
OY	13561	GCGGACCTGGGGCGATGTCGGCGCGCACAGGTCGTTAACTGGGCCAGTATGCGTATTAACCTTG	13620
Db	7981	GCGGACCTGGGGCGATGTCGGCGCGCACAGGTCGTTAACTGGGCCAGTATGCGTATTAACCTTG	8040
OY	13621	TTTCGATCAATTCGTGAGCGGGTTCATTAACTTTATAAAGTCCGTTCCGGGGCATGCTC	13680
Db	8041	TTTCGATCAATTCGTGAGCGGGTTCATTAACTTTATAAAGTCCGTTCCGGGGCATGCTC	8100
OY	13681	ATGATCTCTGATTTGTTGGCGGTCTGTATCGTCTGTTTGGCGTTAAACCGCGCGCACCAAC	13740
Db	8101	ATGATCTCTGATTTGTTGGCGGTCTGTATCGTCTGTTTGGCGTTAAACCGCGCGCACCAAC	8160
OY	13741	GCCATTCGCCAGCGCCCATCAGAGTATGATTAACCCGACATATAGACAAAATGACGCCCTCT	13800
Db	8161	GCCATTCGCCAGCGCCCATCAGAGTATGATTAACCCGACATATAGACAAAATGACGCCCTCT	8220
OY	13801	GGCGGTAAAGTTCGACCGAGAGAGATTTAAAAACATTCTCGCGCGCATTCGACCAAGCTACAG	13860
Db	8221	GGCGGTAAAGTTCGACCGAGAGAGATTTAAAAACATTCTCGCGCGCATTCGACCAAGCTACAG	8280
OY	13861	CAGGAAGAGCTGAGCGGCTTATAGACGAACAGCAGAGCTCAGCGCCTCTGCTTTTCCGGCGC	13920
Db	8281	CAGGAAGAGCTGAGCGGCTTATAGACGAACAGCAGAGCTCAGCGCCTCTGCTTTTCCGGCGC	8340

QY	13921	GCCTCACAAGGACTAAAAAGCTCGCTTTAGGGGATATAAACCGCTGGAAAACGAAGAGCT	13980
Db	8341	GCCTCAACAGGACTAAAAAGCTCGCTTTAGGGGATATAAACCGCTGGAAAACGAAGAGCT	8400
QY	13981	CAAGAATATGAATGACCAATTAACCAACACCCACAGCCGTGTACTGTGGCCGGCAGAG	14040
Db	8401	CAAGAATATGAATGACCAATTAACCAACACCCACAGCCGTGTACTGTGGCCGGCAGAG	8460
QY	14041	CCGGCGGCGCAATCGATTCCGCGACCCGGCCGATCCCGACACACCTCTAGCCGCCCCGGG	14100
Db	8461	CCGGCGGCGCAATCGATTCCGCGACCCGGCCGATCCCGACACACCTCTAGCCGCCCCGGG	8520
QY	14101	CGTCCGGCGTCTGTATCATCATATGATTTCTTTAAACCGTACTGGGCCCTTCGGAGCCA	14160
Db	8521	CGTCCGGCGTCTGTATCATCATATGATTTCTTTAAACCGTACTGGGCCCTTCGGAGCCA	8580
QY	14161	CGCCCGCACTCACAGAGGACCGAGTGCCTCCGGCCCTTGCGCGGCCCGGAGACCGTTCCAG	14220
Db	8581	CGCCCGCACTCACAGAGGACCGAGTGCCTCCGGCCCTTGCGCGGCCCGGAGACCGTTCCAG	8640
QY	14221	CCGCCACACAGACGTTTTGCAGAGCTCATCCCGCCCTGCCTCGAAGCGACAGGGGACAGCGG	14280
Db	8641	CCGCCACACAGACGTTTTGCAGAGCTCATCCCGCCCTGCCTCGAAGCGACAGGGGACAGCGG	8700
QY	14281	ATGATCCCGGTCACGATCCCGTTCCGCGCAACGTACTTGGAGAACGGTCTCGCGAGAC	14340
Db	8701	ATGATCCCGGTCACGATCCCGTTCCGCGCAACGTACTTGGAGAACGGTCTCGCGAGAC	8760
QY	14341	GTGCTGCTCCGCCAACGAAGCGTCCATGTGGACGGCCGGGACCGCAAGCCCTCGCCCG	14400
Db	8761	GTGCTGCTCCGCCAACGAAGCGTCCATGTGGACGGCCGGGACCGCAAGCCCTCGCCCG	8820
QY	14401	GACCCCAAGACCAATCATCATACGTTTACAGCGCTACAGAGCTGTTTAAACAACGTACGG	14460
Db	8821	GACCCCAAGACCAATCATCATACGTTTACAGCGCTACAGAGCTGTTTAAACAACGTACGG	8880
QY	14461	GCGGACAGGTGTGCGGAGTACCTAGCCGCTTCCAAACGAGACATTATCCCAAGCGGAAC	14520
Db	8881	GCGGACAGGTGTGCGGAGTACCTAGCCGCTTCCAAACGAGACATTATCCCAAGCGGAAC	8940
QY	14521	GTGCTCAAAGCTCTCGGGGGCCAAACCGAGAGCGACACAGGCTGTGCTGAACTGTTCCGT	14580
Db	8941	GTGCTCAAAGCTCTCGGGGGCCAAACCGAGAGCGGACACAGGCTGTGCTGAACTGTTCCGT	9000
QY	14581	CAACAGGATATTTCTACGCGGAAGTTCACAGCCGGCATTTAAGCTCACCCATCTCTCCAG	14640
Db	9001	CAACAGGATATTTCTACGCGGAAGTTCACAGCCGGCATTTAAGCTCACCCATCTCTCCAG	9060
QY	14641	CAGGCCCTCAAGAACACAGCCGCGCGTGCCTGTGCGCTTCTCGACCAAGAGATGAAC	14700
Db	9061	CAGGCCCTCAAGAACACAGCCGCGCGTGCCTGTGCGCTTCTCGACCAAGAGATGAAC	9120
QY	14701	AAAGAATTTCTCAAAACGTCACAGCTGCGCGAGCATCCGTCACGGAAATCACGCTATCG	14760
Db	9121	AAAGAATTTCTCAAAACGTCACAGCTGCGCGAGCATCCGTCACGGAAATCACGCTATCG	9180
QY	14761	TTCGGTTCCATGCTCTGACGCCCTCAGAGACCGCGCTGTGCGCGGGGGGAGAGGTTC	14820
Db	9181	TTCGGTTCCATGCTCTGACGCCCTCAGAGACCGCGCTGTGCGCGGGGGGAGAGGTTC	9240
QY	14821	GAGTCAAAACGCGAGCGCGTTCGCGCGGTTGTTCTGTGATCACGGGTTTACCAAGTTCCGG	14880
Db	9241	GAGTCAAAACGCGAGCGCGTTCGCGCGGTTGTTCTGTGATCACGGGTTTACCAAGTTCCGG	9300
QY	14881	TGTTACTCTGTCGCGCGCGCCACGCCCCCGCTGCGGCGCAGAGATGCCAGAGCGCCCTG	14940
Db	9301	TGTTACTCTGTCGCGCGCGCCACGCCCCCGCTGCGGCGCAGAGATGCCAGAGCGCCCTG	9360
QY	14941	GAGTTTACGTCACACTGGGAGGACCTCAGGTTTCAAGCGGACCGCACACTGTGCCCCCG	15000
Db	9361	GAGTTTACGTCACACTGGGAGGACCTCAGGTTTCAAGCGGACCGCACACTGTGCCCCCG	9420
QY	15001	TACCGCATCTGCGGCTTTGATTATCGAGTGTCACTGGAAGGCGGGAATTTCCGTGCGCCACG	15060

```
|||||
Db 9421 TACGATCGTGCGCTTTGATGATGAGTGCAGTGGAGGCGGGATTTCCGTGCGACG 9480
QY 15061 CCGGACGGGACGCGGTGATCCAGATCTCCGCTTTCTACACGACCAAGGAGCGG 15120
Db 9481 CCGGACGGGACGCGGTGATCCAGATCTCCGCTTTCTACACGACCAAGGAGCGG 9540
QY 15121 CCCATCCGCAAACTACTGTTACGCTGGGAGCGAGTCCGACCCATCCCGACCGAC 15180
Db 9541 CCCAAATCCGCAAACTACTGTTACGCTGGGAGCGAGTCCGACCCATCCCGACCGAC 9600
QY 15181 GTTTGGAGTTCCGCGGAATATGACATGCTGCTGCTTCCCATGATCCGCGAC 15240
Db 9601 GTTTGGAGTTCCGCGGAATATGACATGCTGCTGCTTCCCATGATCCGCGAC 9660
QY 15241 TTGAGGTGAGCTTTTAAACCGGCTATAACATCTCAACTTCGATCTCCGTAATAC 15300
Db 9661 TTGAGGTGAGCTTTTAAACCGGCTATAACATCTCAACTTCGATCTCCGTAATAC 9720
QY 15301 ACCGAGCGTCCGAGGTGATCAACCTTCGATTAAACGAATACAAAAATAAACCGG 15360
Db 9721 ACCGAGCGTCCGAGGTGATCAACCTTCGATTAAACGAATACAAAAATAAACCGG 9780
QY 15361 TCCATCTTGAAGTTACAGACGCCGCTGGCGGGGAGGGGGTTATGAGTGGTCTCA 15420
Db 9781 TCCATCTTGAAGTTACAGACGCCGCTGGCGGGGAGGGGGTTATGAGTGGTCTCA 9840
QY 15421 AAAATTTAAATAGCGGGCATCGTCCCATAGACATGTACAGGTGTGTGCGAAAACTC 15480
Db 9841 AAAATTTAAATAGCGGGCATCGTCCCATAGACATGTACAGGTGTGTGCGAAAACTC 9900
QY 15481 AACCTCTCGGACATCAAACTGACACAGGGGCGCAGGACATGCTGGGTGGAAAAAGAG 15540
Db 9901 AACCTCTCGGACATCAAACTGACACAGGGGCGCAGGACATGCTGGGTGGAAAAAGAG 9960
QY 15541 GACGTATCTACAGGACATTCCTCCCTCTGTTTCGCTCAGTCCGGGCGGACAGGCTAAG 15600
Db 9961 GACGTATCTACAGGACATTCCTCCCTCTGTTTCGCTCAGTCCGGGCGGACAGGCTAAG 10020
QY 15601 GTGGGACGTATTCGCTGATGACATCGCTGCTGATGAGACCTTTAAATGTTATG 15660
Db 10021 GTGGGACGTATTCGCTGATGACATCGCTGCTGATGAGACCTTTAAATGTTATG 10080
QY 15661 ATACACGTGAGATTTCCGAGATAGCCAGCTGCGCCAAATATCAGGCCAGGCGCTCAG 15720
Db 10081 ATACACGTGAGATTTCCGAGATAGCCAGCTGCGCCAAATATCAGGCCAGGCGCTCAG 10140
QY 15721 ACGGACGGCCAAACAGTCCGCTGTTCTCTGCTGCTGAGAGCCGCGGACAGGAGAC 15780
Db 10141 ACGGACGGCCAAACAGTCCGCTGTTCTCTGCTGCTGAGAGCCGCGGACAGGAGAC 10200
QY 15781 TTTATCTCCGCTTCCAAACGCCCGAGGACAGGGGGCTATCAGGGCGCGACGTGATC 15840
Db 10201 TTTATCTCCGCTTCCAAACGCCCGAGGACAGGGGGCTATCAGGGCGCGACGTGATC 10260
QY 15841 AACCCCATTCGCGGGTTTACAGACAGCGGCTGCTGCTGATTTTCCAGCCCTGATC 15900
Db 10261 AACCCCATTCGCGGGTTTACAGACAGCGGCTGCTGCTGATTTTCCAGCCCTGATC 10320
QY 15901 CCGAGCATATCCAGGCGCACAACTGTCTACTCCACATGATACAGGAGAGACGTG 15960
Db 10321 CCGAGCATATCCAGGCGCACAACTGTCTACTCCACATGATACAGGAGAGACGTG 10380
QY 15961 CACCTGACACCCCAACCTGAAGCGGACAGACTAGAGACGTTGCTGAGAGCGGACCG 16020
Db 10381 CACCTGACACCCCAACCTGAAGCGGACAGACTAGAGACGTTGCTGAGAGCGGACCG 10440
QY 16021 GTACATTTTGTAAAAAACAACAAGGGAGTCTGTCTGGAGAACTGCTAACCGTGTG 16080
Db 10441 GTACATTTTGTAAAAAACAACAAGGGAGTCTGTCTGGAGAACTGCTAACCGTGTG 10500
QY 16081 TTAGAAAAAGCAAGGGCATTCGGGCGACACCTGGGGGCTGGGATGACCCGTGCTAAA 16140
|||||

Db 10501 TTAGAAAAAGCAAGGGCATTCGGGCGACACCTGGGGGCTGGGATGACCCGTGCTAAA 10560
QY 16141 ACCATCTAGATTAACACAGCTGGCCATCAAGTACATGTAACCGGGTTAACGGGTTTC 16200
Db 10561 ACCATCTAGATTAACACAGCTGGCCATCAAGTACATGTAACCGGGTTAACGGGTTTC 10620
QY 16201 ACCGGGGTGGCCAGCGGCTCCTCCATGATGATTAACATAGCGGAAACCGTGCCTCG 16260
Db 10621 ACCGGGGTGGCCAGCGGCTCCTCCATGATGATTAACATAGCGGAAACCGTGCCTCG 10680
QY 16261 GGGCGCACGATGCTGAGATGTCAAAGTCTTACGTTACGTTACGTTACGTTACGTTAC 16320
Db 10681 GGGCGCACGATGCTGAGATGTCAAAGTCTTACGTTACGTTACGTTACGTTACGTTAC 10740
QY 16321 CGAAGCGTCTCGGTGCGAGGTGACCGCCGCTCAGAGCGCGCGGTTTGGCGTCTAC 16380
Db 10741 CGAAGCGTCTCGGTGCGAGGTGACCGCCGCTCAGAGCGCGCGGTTTGGCGTCTAC 10800
QY 16381 GGTGACACGAGTCTCCTCTTTATCGGTGCGAGGTATTTCCGGGGAACCGTTTCGCT 16440
Db 10801 GGTGACACGAGTCTCCTCTTTATCGGTGCGAGGTATTTCCGGGGAACCGTTTCGCT 10860
QY 16441 TTCTGTGAGATCTGGCGCGCAGAGTACATGCGGACCTGTTCCCGCACCTTAAGCTA 16500
Db 10861 TTCTGTGAGATCTGGCGCGCAGAGTACATGCGGACCTGTTCCCGCACCTTAAGCTA 10920
QY 16501 GAGGCGGAAAAGACGTTCAAGTGTCTGTCTGCTGACGAAAAAGCGCTATCGGGGTC 16560
Db 10921 GAGGCGGAAAAGACGTTCAAGTGTCTGTCTGCTGACGAAAAAGCGCTATCGGGGTC 10980
QY 16561 CTATTGACGACAAATGCTCATGAAAGGGGTGACGCTCATTCGCAAAAGCGCTGCAAG 16620
Db 10981 CTATTGACGACAAATGCTCATGAAAGGGGTGACGCTCATTCGCAAAAGCGCTGCAAG 11040
QY 16621 TTTGTCCAGAGAGATGCGCGCATCTGAGACCTGCTGCTCCACAGATCCGAGGTCAAG 16680
Db 11041 TTTGTCCAGAGAGATGCGCGCATCTGAGACCTGCTGCTCCACAGATCCGAGGTCAAG 11100
QY 16681 GCTGCGCGCGGCTGTTGTGCAAGCGGCGCGGACGCGGTATACGAGGAGGCGTCCG 16740
Db 11101 GCTGCGCGCGGCTGTTGTGCAAGCGGCGCGGACGCGGTATACGAGGAGGCGTCCG 11160
QY 16741 GCTGCGCGCGGCTGTTGTGCAAGCGGCGCGGACGCGGTATACGAGGAGGCGTCCG 16800
Db 11161 GCTGCGCGCGGCTGTTGTGCAAGCGGCGCGGACGCGGTATACGAGGAGGCGTCCG 11220
QY 16801 GTCTGCGCCATGAGAGCTTAACTGCTTCCACGAGCTCAGCGCCGCTGTCGATTAAC 16860
Db 11221 GTCTGCGCCATGAGAGCTTAACTGCTTCCACGAGCTCAGCGCCGCTGTCGATTAAC 11280
QY 16861 AAGACACCAACCTGCGCCACCTGCGGTGTGACAAAGCTGCGAGACAGGTGCGAGAG 16920
Db 11281 AAGACACCAACCTGCGCCACCTGCGGTGTGACAAAGCTGCGAGACAGGTGCGAGAG 11340
QY 16921 CTGCGCCAGGTGACAGATGAATCCCTGCTGCTGTTGAGAGCGCGCGGCTCCGTAAG 16980
Db 11341 CTGCGCCAGGTGACAGATGAATCCCTGCTGCTGTTGAGAGCGCGCGGCTCCGTAAG 11400
QY 16981 TCGGACCTGCGCAACACCGGATTAAGTCAGACAGACACAGATTCCGTCGCGGTGAC 17040
Db 11401 TCGGACCTGCGCAACACCGGATTAAGTCAGACAGACACAGATTCCGTCGCGGTGAC 11460
QY 17041 CTATATTTGACAAACTGTTGACAGGGCGGCGCAACATCTCAAGTGTGTTGGCAAC 17100
Db 11461 CTATATTTGACAAACTGTTGACAGGGCGGCGCAACATCTCAAGTGTGTTGGCAAC 11520
QY 17101 AACGGGACACAGGTGCGCATCTCTTAATTTTCTAACAGTCCGATTAAGCTGTT 17160
Db 11521 AACGGGACACAGGTGCGCATCTCTTAATTTTCTAACAGTCCGATTAAGCTGTT 11580
QY 17161 TCGTGAAGCCCAATTGGAAGAGCCAACTAAGACGCGCGGACGAGGTCCGACGGGA 17220
Db 11581 TCGTGAAGCCCAATTGGAAGAGCCAACTAAGACGCGCGGACGAGGTCCGACGGGA 11640
```


QY 17221 GACCTGAGCGGAGAGAGCGACCAACGAGACCGCCACCATGCTGCTTAACGAACGTGC 17280
|||||
Db 11641 GACCTGAGGCGGAGAGAGCGACCAACGAGACCGCCACCATGCTGCTTAACGAACGTGC 11700
QY 17281 GGTGGTCTTGCGGAGCTGGGAGAGTGAATTTTACCGGGGTAGATTAAGCTTCTCAACT 17340
|||||
Db 11701 GGTGGTCTTGCGGAGCTGGGAGAGTGAATTTTACCGGGGTAGATTAAGCTTCTCAACT 11760
QY 17341 CACCGCGCTCAACAGCTTCAAGGGCCACGGGGGTACGCCAGGGTCCGACTCCGCTTCTC 17400
|||||
Db 11761 CACCGCGCTCAACAGCTTCAAGGGCCACGGGGGTACGCCAGGGTCCGACTCCGCTTCTC 11820
QY 17401 GCTGACACAGTACTCCACCAACAGATTTTCGGTTTCGAGCTGTGACGGCTCTCAAGAACT 17460
|||||
Db 11821 GCTGACACAGTACTCCACCAACAGATTTTCGGTTTCGAGCTGTGACGGCTCTCAAGAACT 11880
QY 17461 GCCCCCCCTTCCGAGCTGGCTGGCCCTTATCGCCCCGTTGGATTTCCGGCGCGACGCGGA 17520
|||||
Db 11881 GCCCCCCCTTCCGAGCTGGCTGGCCCTTATCGCCCCGTTGGATTTCCGGCGCGACGCGGA 11940
QY 17521 CGGCGGCGGCTGGGCCCCGGGGTTCTGCTGGAAGCTCTGCGCCCGGTGACCGGTTGGGT 17580
|||||
Db 11941 CGGCGGCGGCTGGGCCCCGGGGTTCTGCTGGAAGCTCTGCGCCCGGTGACCGGTTGGGT 12000
QY 17581 AAACGCGAGCGGCGGCGACAGATCCGGTTCTGCTCTCTCTTTCTAAGCCGATCGACT 17640
|||||
Db 12001 AAACGCGAGCGGCGGCGACAGATCCGGTTCTGCTCTCTCTTTCTAAGCCGATCGACT 12060
QY 17641 GGAAGCGCGGCTCAGCTACTCTTTCGGCGAAGAACGGCGCGCGCTCGAGAGGCGACCCC 17700
|||||
Db 12061 GGAAGCGCGGCTCAGCTACTCTTTCGGCGAAGAACGGCGCGCGCTCGAGAGGCGACCCC 12120
QY 17701 AAAGCCACCTGGGCGGCGAAGAACCTGCCGGGAGACCCCTGGCGGCTCTCCGGCGAGGC 17760
|||||
Db 12121 AAAGCCACCTGGGCGGCGAAGAACCTGCCGGGAGACCCCTGGCGGCTCTCCGGCGAGGC 12180
QY 17761 GTCTCAGACGTGCCCCCATTTCTTTCGTTGCGTATTTTCCACGGCCAACTCGGTGGCTG 17820
|||||
Db 12181 GTCTCAGACGTGCCCCCATTTCTTTCGTTGCGTATTTTCCACGGCCAACTCGGTGGCTG 12240
QY 17821 CCTAAGCCTTGTGGGTTACAGGTGAGAGCCGTTTTCGGATGACGGCGCGACAGAGGACG 17880
|||||
Db 12241 CCTAAGCCTTGTGGGTTACAGGTGAGAGCCGTTTTCGGATGACGGCGCGACAGAGGACG 12300
QY 17881 GCGGATCTCCCGAAATACGTCAAGTTAGTAACTCCGGGGGTAAAGCTGTGCAAGGAGCTC 17940
|||||
Db 12301 GCGGATCTCCCGAAATACGTCAAGTTAGTAACTCCGGGGGTAAAGCTGTGCAAGGAGCTC 12360
QY 17941 CGTTTCAACGCTGTCCCGGTGCGGGGTAAAGCGGCGCAATGGAATCATCTACGCTCC 18000
|||||
Db 12361 CGTTTCAACGCTGTCCCGGTGCGGGGTAAAGCGGCGCAATGGAATCATCTACGCTCC 12420
QY 18001 CCGGAGACCCCAACGCGAGATAGTCTTGCGGCACTCCGAGCCGCTCTGCCACCCACAC 18060
|||||
Db 12421 CCGGAGACCCCAACGCGAGATAGTCTTGCGGCACTCCGAGCCGCTCTGCCACCCACAC 12480
QY 18061 CCGGCGGCGCGGTATTTGGGGGTCTAAGCGGAGCGCGAAGAAACCATCCAACTGGAACCTC 18120
|||||
Db 12481 CCGGCGGCGCGGTATTTGGGGGTCTAAGCGGAGCGCGAAGAAACCATCCAACTGGAACCTC 12540
QY 18121 CCGGGAAGTCCGGGTTCAAGTTAACTCTTCAACAGGAGCGCGCTTGCGGGCGATCTGCG 18180
|||||
Db 12541 CCGGGAAGTCCGGGTTCAAGTTAACTCTTCAACAGGAGCGCGCTTGCGGGCGATCTGCG 12600
QY 18181 GTTTTCTGTACGGGCGGTGGCAGCGAGCCCTATTGTGTGACCCCGGCACTTGTGCT 18240
|||||
Db 12601 GTTTTCTGTACGGGCGGTGGCAGCGAGCCCTATTGTGTGACCCCGGCACTTGTGCT 12660
QY 18241 TTCCGGTTGGACAACCCACCTGGCGCTATTCAACCCCAAGGTTACCCCGACGACTATAAA 18300
|||||
Db 12661 TTCCGGTTGGACAACCCACCTGGCGCTATTCAACCCCAAGGTTACCCCGACGACTATAAA 12720

QY 18301 AAGAGACACCCCTTGTGGCGCGCGCGCCCTGCTCCCGCTGCTGATTAAGTCTCCGCGA 18360
|||||
Db 12721 AAGAGACACCCCTTGTGGCGCGCGCGCCCTGCTCCCGCTGCTGATTAAGTCTCCGCGA 12780
QY 18361 CGACGGCGCGGAGACTCTGCTCCGCTTACCAAGACCCGGGGCGCTCTCCATTAAAGCGGT 18420
|||||
Db 12781 CGACGGCGCGGAGACTCTGCTCCGCTTACCAAGACCCGGGGCGCTCTCCATTAAAGCGGT 12840
QY 18421 CACAAATCCCGGTGCTTCCAGGGGTGCTCGGGGAGTGTACAGTGTCCCTACGCGA 18480
|||||
Db 12841 CACAAATCCCGGTGCTTCCAGGGGTGCTCGGGGAGTGTACAGTGTCCCTACGCGA 12900
QY 18481 CAACGGGGTCCAGAAAGCATGAACCATTAAGCGCAACGATGGGAACACCGGCTTTC 18540
|||||
Db 12901 CAACGGGGTCCAGAAAGCATGAACCATTAAGCGCAACGATGGGAACACCGGCTTTC 12960
QY 18541 TTTCGGCGGAGTGGCAGAGCTCGAGCTAGTGGACAAAGCGGACGCCAGGTTACAGCTCC 18600
|||||
Db 12961 TTTCGGCGGAGTGGCAGAGCTCGAGCTAGTGGACAAAGCGGACGCCAGGTTACAGCTCC 13020
QY 18601 CTGGTGTGGCGCGCACTATTCAAGAGCGGTACAGTGTGAGAGGATGAGAGCTG 18660
|||||
Db 13021 CTGGTGTGGCGCGCACTATTCAAGAGCGGTACAGTGTGAGAGGATGAGAGCTG 13080
QY 18661 TGGGTCAAGAGAGTCTCCGTGCTGCGCGCATGCCCCAGCATCGGAGAGACTGTGCGG 18720
|||||
Db 13081 TGGGTCAAGAGAGTCTCCGTGCTGCGCGCATGCCCCAGCATCGGAGAGACTGTGCGG 13140
QY 18721 AAGAGTTTCCCGGCTTCCGCTTTCGCGAGGCGCACTTGGGCGATCGGGGAACGCGACC 18780
|||||
Db 13141 AAGAGTTTCCCGGCTTCCGCTTTCGCGAGGCGCACTTGGGCGATCGGGGAACGCGACC 13200
QY 18781 GTGTTTACGCTTCCGCTTTCGCGAGGCGCACTTGAACATAGAACCCGCGGTGTGAG 18840
|||||
Db 13201 GTGTTTACGCTTCCGCTTTCGCGAGGCGCACTTGAACATAGAACCCGCGGTGTGAG 13260
QY 18841 CCGCGGATCGGAGCTGTGCTGCGGGTTACGCTCCGCAAAACAGCGGGGTGCGGA 18900
|||||
Db 13261 CCGCGGATCGGAGCTGTGCTGCGGGTTACGCTCCGCAAAACAGCGGGGTGCGGA 13320
QY 18901 TACGGAATTAAGGATTCGTGGCGATCGTTAAGGTGGTGGCCCGCGGGGTGTTGCTTA 18960
|||||
Db 13321 TACGGAATTAAGGATTCGTGGCGATCGTTAAGGTGGTGGCCCGCGGGGTGTTGCTTA 13380
QY 18961 CACTTTCACAAGACCGCGTTCGATGCGCTGACAAGCGGTGACGACGAGAGGCTCC 19020
|||||
Db 13381 CACTTTCACAAGACCGCGTTCGATGCGCTGACAAGCGGTGACGACGAGAGGCTCC 13440
QY 19021 AGGCTTAACCTGTGAAGAGCCGTGGATAAAAATTCAGGCTTTCGCTTATGTGAGAG 19080
|||||
Db 13441 AGGCTTAACCTGTGAAGAGCCGTGGATAAAAATTCAGGCTTTCGCTTATGTGAGAG 13500
QY 19081 ACCGCGACCCATTTCTTCTTAACCCAGAACCAAGCCCTTTTACCGAGCGAAAGTTTGC 19140
|||||
Db 13501 ACCGCGACCCATTTCTTCTTAACCCAGAACCAAGCCCTTTTACCGAGCGAAAGTTTGC 13560
QY 19141 CGCCTGATCATGGAACAAGACGAGCGGCGCTTCAACACCGCTACTGTGGAAGACAG 19200
|||||
Db 13561 CGCCTGATCATGGAACAAGACGAGCGGCGCTTCAACACCGCTACTGTGGAAGACAG 13620
QY 19201 CAGGTGAGGTGACCGGTGACCCCGCCGGAACAATCTGTACGAGCGGCCCGGTAGC 19260
|||||
Db 13621 CAGGTGAGGTGACCGGTGACCCCGCCGGAACAATCTGTACGAGCGGCCCGGTAGC 13680
QY 19261 GCGAACCTGTGCTTCCACCGGTTAATGCGCAATGCGCTTTCGCAACAACCATATTGAA 19320
|||||
Db 13681 GCGAACCTGTGCTTCCACCGGTTAATGCGCAATGCGCTTTCGCAACAACCATATTGAA 13740
QY 19321 CTCGCCGTGCTGTACACAAGGCGGATTTATACGCCCGCTGTGTACGTGAGGCGTACGCTG 19380
|||||
Db 13741 CTCGCCGTGCTGTACACAAGGCGGATTTATACGCCCGCTGTGTACGTGAGGCGTACGCTG 13800
QY 19381 TGCATCCCAACCAACTGTAGCAAAATTCGTAAAGGTACGTTAAACACTTACGCTCTGCGCATTT 19440

|||||
Db 13801 TGCATCCACCCAACTGTAGCAATTCGTAAAGTACAGGTAAACACTACCTACGCTTCGCGATTT 13860
QY 19441 AACCGCAAGCTGACGGGCGATTATTAGCAATCAAGCCACACGCGGGTTCCGGATTACG 19500
|||||
Db 13861 AACCGCAAGCTGACGGGCGATTATTAGCAATCAAGCCACACGCGGGTTCCGGATTACG 13920
QY 19501 GACTGGAGTGGCCACCGCAACCGGGGAGATAGAGATTTTGGTAACCAAGCTGTCCGAGGC 19560
|||||
Db 13921 GACTGGAGTGGCCACCGCAACCGGGGAGATAGAGATTTTGGTAACCAAGCTGTCCGAGGC 13980
QY 19561 CCGGTGTACATACAGCACCGGGAGACGCTGGGGCAAGCCATCTCGTGTTCGGCGCGCG 19620
|||||
Db 13981 CCGGTGTACATACAGCACCGGGAGACGCTGGGGCAAGCCATCTCGTGTTCGGCGCGCG 14040
QY 19621 TTGCGTGGCCCGGCGAACTGGGGAGCTCTCGGCGACCGATCGCGCGCTCGAGCTG 19680
|||||
Db 14041 TTGCGTGGCCCGGCGAACTGGGGAGCTCTCGGCGACCGATCGCGCGCTCGAGCTG 14100
QY 19681 CCGGGGGGGGTGACAGTGGACAGCCAAAGCTGTAGGTTTGAAGCACTGTACCTGTTT 19740
|||||
Db 14101 CCGGGGGGGGTGACAGTGGACAGCCAAAGCTGTAGGTTTGAAGCACTGTACCTGTTT 14160
QY 19741 TCCACGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 19800
|||||
Db 14161 TCCACGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 14220
QY 19801 TCATTTCTCGGGGTCCGCGCGCTCGGAGACACACAGGTGGCTCAAAACACCCCTCCGC 19860
|||||
Db 14221 TCATTTCTCGGGGTCCGCGCGCTCGGAGACACACAGGTGGCTCAAAACACCCCTCCGC 14280
QY 19861 ACCCTCGGACCAAAACAGTTAACGCTTCGTTAGATGACGTTATTTATTTATTTA 19920
Db 14281 ACCCTCGGACCAAAACAGTTAACGCTTCGTTAGATGACGTTATTTATTTATTTA 14340
QY 19921 TTACATCATAGCTATTGTGCGGGCGCCGTCGCCGCAAAACATCTGTAGATTTTCCAGTAT 19980
|||||
Db 14341 TTACATCATAGCTATTGTGCGGGCGCCGTCGCCGCAAAACATCTGTAGATTTTCCAGTAT 14400
QY 19981 GCGAAACGCGTGTAGACAAAGTCCCGGGGGCTCTGCTCCCAACGACGACGAGTTT 20040
|||||
Db 14401 GCGAAACGCGTGTAGACAAAGTCCCGGGGGCTCTGCTCCCAACGACGACGAGTTT 14460
QY 20041 TTCATTAAGCTCCGGGCGCCACATCTGTATTTCAGGAGCTCTCTCAATTAAGAGATC 20100
|||||
Db 14461 TTCATTAAGCTCCGGGCGCCACATCTGTATTTCAGGAGAGCTCTCTCAATTAAGAGATC 14520
QY 20101 GAGGGGGGACACACACGAGTACCGCGGAGCCAAATGGCGGGGCTCCGCGTCCCGCG 20160
|||||
Db 14521 GAGGGGGGACACACACGAGTACCGCGGAGCCAAATGGCGGGGCTCCGCGTCCCGCG 14580
QY 20161 CCGGTGTGTACAGACATCTCTAAGTGGCTCAAGTAACTCTGTAGAGCCCGGAGCCGCG 20220
|||||
Db 14581 CCGGTGTGTACAGACATCTCTAAGTGGCTCAAGTAACTCTGTAGAGCCCGGAGCCGCG 14640
QY 20221 AACCATGGGCTCATACACTGGGCGCCGGAAGCTGGGGGCTGGCACTCAAGCTTAA 20280
|||||
Db 14641 AACCATGGGCTCATACACTGGGCGCCGGAAGCTGGGGGCTGGCACTCAAGCTTAA 14700
QY 20281 CATCATATATAGGAATGAACAAACGACATGTATGGCGGGGTACTACGCGACCGAGAG 20340
|||||
Db 14701 CATCATATATAGGAATGAACAAACGACATGTATGGCGGGGTACTACGCGACCGAGAG 14760
QY 20341 AATGGAGTGTGGCACAGGTAAACGACAGCGCTGTATGTTAAACCCACTTCAGACAG 20400
|||||
Db 14761 AATGGAGTGTGGCACAGGTAAACGACAGCGCTGTATGTTAAACCCACTTCAGACAG 14820
QY 20401 GCGGGGGGGGTGTCTGAAGAGAGCGGTTGGCGCGCCACTGGGGGAGAAAGCTTAT 20460
|||||
Db 14821 GCGGGGGGGGTGTCTGAAGAGAGCGGTTGGCGCGCCACTGGGGGAGAAAGCTTAT 14880
QY 20461 TCCACGCGGACGTGGGGGAGCGGCTAGAGGCTGGCGCCCAACAGAGAGTTAA 20520
|||||

Db 14881 TCCAGCGGACGTGGGGGAGGGCGCAGCGTATAGGCTGGCGGCCCAACACGACAGGTAA 14940
QY 20521 CAAGACGAACCAAGACAGGAGACATGACCGGTTAAATTAATTAATTAATTAATTAATTA 20580
|||||
Db 14941 CAAGACGAACCAAGACAGGAGAAATGACCGTTAAATTAATTAATTAATTAATTAATTA 15000
QY 20581 GCGCGGTCAAGCCAGGTCATTTAAACACACCGCGCGCCCAACCGCGGGGCGG 20640
|||||
Db 15001 GCGCGGTCAAGCCAGGTCATTTAAACACACCGCGCGCCCAACCGCGGGGCGG 15060
QY 20641 CCGCCTTGGAACCGGTTCTCTTCCAAATGCAAAAGAACCGCGTCACAAAAAGGCGCTGTTT 20700
|||||
Db 15061 CCGCCTTGGAACCGGTTCTCTTCCAAATGCAAAAGAACCGCGTCACAAAAAGGCGCTGTTT 15120
QY 20701 GAACCCATTTTGTGCTATCGGCTGCTTTTCAAGTACGAAACCGGCTGTCCAAAACA 20760
|||||
Db 15121 GAACCCATTTTGTGCTATCGGCTGCTTTTCAAGTACGAAACCGGCTGTCCAAAACA 15180
QY 20761 CCCAACGGGGGTGTCTCAAAAGGCGCATTCATCTGTATGGGGATGGGGGTGTAGC 20820
|||||
Db 15181 CCCAACGGGGGTGTGTCTCAAAAGGCGCATTCATCTGTATGGGGATGGGGGTGTAGC 15240
QY 20821 CCTGAGACTCAGATCCGCGCGCATTAAGTCTCTCCAGACGCGCACCTTTCTCAAAATCT 20880
|||||
Db 15241 CCTGAGACTCAGATCCGCGCGCATTAAGTCTCTCCAGACGCGCGCACCTTTCTCAAAATCT 15300
QY 20881 TCAAGCGCGGAAACGACGCGGGGCTCTCCGACGCTGAAGACGACGAGGATCAAGTGT 20940
|||||
Db 15301 TCAAGCGCGGAAACGACGCGGGGCTCTCCGACGCTGAAGACGACGAGGATCAAGTGT 15360
QY 20941 TGTGTAAAGCTGGGGGTACCCAAAGGTGTGCAAAAGCTCCCGGGGTCAAGCCGCTGA 21000
|||||
Db 15361 TGTGTAAAGCTGGGGGTACCCAAAGGTGTGCAAAAGCTCCCGGGGTCAAGCCGCTGA 15420
QY 21001 CGTGACGATCAGATACGTACAGAGAGGCGTACGTGGCGGTGTTAAAGGGAGCCGAGGC 21060
|||||
Db 15421 CGTGACGATCAGATACGTACAGAGAGGCGTACGTGGCGGTGTTAAAGGGAGCCGAGGC 15480
QY 21061 CCATGTGCGGAGCTCTGTGTACAGTGTGACAGGACGCTCCCGGAGCACAGTAAACT 21120
|||||
Db 15481 CCATGTGCGGAGCTCTGTGTACAGTGTGACAGGACGCTCCCGGAGCACAGTAAACT 15540
QY 21121 GACACAAACGTAAGACAGAGGAGAGCCATCGCGCGAGGTCCGCGGGGTTCCAGCGGC 21180
|||||
Db 15541 GACACAAACGTAAGACAGAGGAGAGCCATCGCGCGAGGTCCGCGGGGTTCCAGCGGC 15600
QY 21181 ACATTAACGATGGCGCGATGTGGGGCGCGCTGTATTATGATTCACACAGTAAACGAGCT 21240
|||||
Db 15601 ACATTAACGATGGCGCGATGTGGGGCGCGCTGTATTATGATTCACACAGTAAACGAGCT 15660
QY 21241 GGTCCACCCCTGACCCCTGTGTAGTGTGGGCTCGGGCCCCCTGTATCTCCGCCCAAAATGTC 21300
|||||
Db 15661 GGTCCACCCCTGACCCCTGTGTAGTGTGGGCTCGGGCCCCCTGTATCTCCGCCCAAAATGTC 15720
QY 21301 TCCACTGGAACCCGTAACAGCGGCCCAAGTGTGCGCTCGGGGGGTCCCGAAGCCCTGGG 21360
|||||
Db 15721 TCCACTGGAACCCGTAACAGCGGCCCAAGTGTGCGCTCGGGGGGTCCCGAAGCCCTGGG 15780
QY 21361 CCGCAAAAAGGCGCGGACCCGCTGCGCTCCCAATTTTACGCGCGCGCGACGATTT 21420
|||||
Db 15781 CCGCAAAAAGGCGCGGAGCCGCTGCGCTCCCAATTTTACGCGCGCGCGACGATTT 15840
QY 21421 CCGTGGAGTGGTGGAGCCCTGTATTAACACAGCAACCTCTCCACAGAGCCCTCCAAA 21480
|||||
Db 15841 CCGTGGAGTGGTGGAGCCCTGTATTAACACAGCAACCTCTCCACAGAGCCCTCCAAA 15900
QY 21481 ACACCTTTTGTGTGTTAACAAGGAACCTGCTCCCTGAGTTATATGGGGCTCAAGGC 21540
|||||
Db 15901 ACACCTTTTGTGTGTTAACAAGGAACCTGCTCCCTGAGTTATATGGGGCTCAAGGC 15960
QY 21541 CGAACACGACCTGTGTGCCACAGCGCTGTCTCTCCCTGACAGCGGTTTAAATA 21600
|||||
Db 15961 CGAACACGACCTGTGTGCCACAGCGCTGTCTCTCCCTGACAGCGGTTTAAATA 16020
|||||

Qy 21601 TTAATTCAGATGCGCCAAAGTACTGACGTGCGCGTGGTCGCCGGCAGCGCAGCGGA 21660
D 16021 TTTAAATCCAGGTGGCCCAAGACTGACGTGCGCGTGGTCGCCGGCAGCGCAGCGGA 16080
Qy 21661 CGGCGCGGACACTTTCGGGTGGGAAAAAAACCCGGAAGTGTGCGCGCGCATTTCCAGCA 21720
D 16081 CGGCGCGGACACTTTCGGGTGGGAAAAAAACCCGGAAGTGTGCGCGCGCATTTCCAGCA 16140
Qy 21721 CGCAAAAGGGTAAATTTTTTTTAACTAGACGATACCGAGATGTGACAGGACATCATTA 21780
D 16141 CGCAAAAGGGTAAATTTTTTTTAACTAGACGATACCGAGATGTGACAGGACATCATTA 16200
Qy 21781 TTAACACGAGGTCTTTACACTATTAACGCTAAACGCTGAAGACAACTATTTTAA 21840
D 16201 TTAACACGAGGTCTTTACACTATTAACGCTAAACGCTGAAGACAACTATTTTAA 16260
Qy 21841 AGCGAGTGGGGCGGGCGGACACAGGCGCGCGCGGTGTTAGCAGTAAATTAACCA 21900
D 16261 AGCGAGCTGGGGCGGGCGGACACAGGCGCGCGCGGTGTTAGCAGTAAATTAACCA 16320
Qy 21901 CGTGGTCTCCCAAGCGCTCTCCCGAGGTGAGCGTCTCCCAAGCGCAAAACACAC 21960
D 16321 CGTGGTCTCCCAAGCGCTCTCCCGAGGTGAGCGTCTCCCAAGCGCAAAACACAC 16380
Qy 21961 AGATAATAATAATAATACATGTTATTTTATTAACCTTAACGCGGATATGCTT 22020
D 16381 AGATAATAATAATAATACATGTTATTTTATTAACCTTAACGCGGATATGCTT 16440
Qy 22021 AACAGGGGCCAATAGAACAAAGTGCAGGCGCGCATTCGCGCTCAAAAGCAACCGCA 22080
D 16441 AACAGGGGCCAATAGAACAAAGTGCAGGCGCGCATTCGCGCTCAAAAGCAACCGCA 16500
Qy 22081 CACCGGGGCTGTAAAGCGGTAACAAACAACTATTAGCAATGTGTAACGCTAAATCCA 22140
D 16501 CACCGGGGCTGTAAAGCGGTAACAAACAACTATTAGCAATGTGTAACGCTAAATCCA 16560
Qy 22141 ACCCTGCGCTGCCGAGCCATTCGCGCCAGCTGCGCTACGTCGAGGGTGTTCCTAAGTCG 22200
D 16561 ACCCTGCGCTGCCGAGCCATTCGCGCCAGCTGCGCTACGTCGAGGGTGTTCCTAAGTCG 16620
Qy 22201 CATTTTACGCCCTTGGCAGCGCGCGCTGTGCGTTAATGTGTTCCTAATCCCGTCGA 22260
D 16621 CATTTTACGCCCTTGGCAGCGCGCGCTGTGCGTTAATGTGTTCCTAATCCCGTCGA 16680
Qy 22261 AGGCGCTCTTGGGAATGTCGAATGAGGCTGGCGGGTCTTTCGCCCTTTTGGGAGCG 22320
D 16681 AGGCGCTCTTGGGAATGTCGAATGAGGCTGGCGGGTCTTTCGCCCTTTTGGGAGCG 16740
Qy 22321 TTGTCCACCGCTGGAAGCAGTTTCTTCACTGCGTGTCCCGGGATTGGCAGACAGCTTT 22380
D 16741 TTGTCCACCGCTGGAAGCAGTTTCTTCACTGCGTGTCCCGGGATTGGCAGACAGCTTT 16800
Qy 22381 TTAACGGGGGAGTGTAAATATACAGCGCTGCACCGAGCACTGCAGAGAGTGTGGAG 22440
D 16801 TTAACGGGGGAGTGTAAATATACAGCGCTGCACCGAGCACTGCAGAGAGTGTGGAG 16860
Qy 22441 TTAAGAGACACTAAACCGGGGAGGAGATGATTAATCAATCCCAACAGCAGAGTTG 22500
D 16861 TTAAGAGACACTAAACCGGGGAGGAGATGATTAATCAATCCCAACAGCAGAGTTG 16920
Qy 22501 GGGCGGGGTCCGCTCATGAGACCCATAGAAAGCATAATCACTACACAGCGCAACCC 22560
D 16921 GGGCGGGGTCCGCTCATGAGACCCATAGAAAGCATAATCACTACACAGCGCAACCC 16980
Qy 22561 GCAGAAAAAGCAGCAGAAAAAGSCCTCATGTGACAAAAACAAACAAAGAGCGG 22620
D 16981 GCAGAAAAAGCAGCAGAAAAAGSCCTCATGTGACAAAAACAAACAAAGAGCGG 17040
Qy 22621 GTGCGTGTGGCTTGGCAGCAGCGCTGCGCGTGTGGCAGCGGTTGAGCGGCTC 22680
D 17041 GTGCGTGTGGCTTGGCAGCAGCGCTGCGCGTGTGGCAGCGGTTGAGCGGCTC 17100

Qy 22681 CATTAATACCGCGCGCCCGGGCCCGCTCGACGGAACAGAGCGGTGTAAGCACTGAC 22740
D 17101 CATTAATACCGCGCGCCCGGGCCCGCTCGACGGAACAGAGCGGTGTAAGCACTGAC 17160
Qy 22741 GCAGTGTCTCCGTCAGATGTGGCATTTGCGAGTCCCAAAACGGCGTGTCTAATACG 22800
D 17161 GCAGTGTCTCCGTCAGATGTGGCATTTGCGAGTCCCAAAACGGCGTGTCTAATACG 17220
Qy 22801 GTGCGCGGGGTTCAAAAGAACGGGATGCCCCCAACAGGTAATAACCTTTTCCAAA 22860
D 17221 GTGCGCGGGGTTCAAAAGAACGGGATGCCCCCAACAGGTAATAACCTTTTCCAAA 17280
Qy 22861 CAGAAAGCAACAGCAACCCGAAAGAAATCTCCAAAGCAAGCAAGTCCGTGCGCGGA 22920
D 17281 CAGAAAGCAACAGCAACCCGAAAGAAATCTCCAAAGCAAGCAAGTCCGTGCGCGGA 17340
Qy 22921 TAAAGGAAATTTTCCCTACCTTAACACAGCGCGCGGTAACTGTTAAACAGCAAT 22980
D 17341 TAAAGGAAATTTTCCCTACCTTAACACAGCGCGCGGTAACTGTTAAACAGCAAT 17400
Qy 22981 ACTTCTAGGCTGTGTTAATAAACAACAGAGGTTGTAATTCGGGGGCGCTTTGG 23040
D 17401 ACTTCTAGGCTGTGTTAATAAACAACAGAGGTTGTAATTCGGGGGCGCTTTGG 17460
Qy 23041 GCCCGCGCGTGTGGGGGTGGCTGTGCTGTTGTGTGCAATCACACCCCGCTGGC 23100
D 17461 GCCCGCGCGTGTGGGGGTGGCTGTGCTGTTGTGTGCAATCACACCCCGCTGGC 17520
Qy 23101 CGAAACAGGGCAACAAACCCCTGTGCTAGTTTAACTTAAACCTTAACACGGGGA 23160
D 17521 CGAAACAGGGCAACAAACCCCTGTGCTAGTTTAACTTAAACCTTAACACGGGGA 17580
Qy 23161 GAGGGAGAGGGGGGCGGCTTAATGGGCTGTACAGCAACCGAGGGGAAAAAAG 23220
D 17581 GAGGGAGAGGGGGGCGGCTTAATGGGCTGTACAGCAACCGAGGGGAAAAAAG 17640
Qy 23221 GGGCAAAAGCGCGGTTAAACAAACAGCAACAGGCGCAACCCCAATTAACACAGCA 23280
D 17641 GGGCAAAAGCGCGGTTAAACAAACAGCAACAGGCGCAACCCCAATTAACACAGCA 17700
Qy 23281 TATTCGCTGTGTTTCGGGGGGGCGGTCGATACGGCTTAACCCGTTGGGCTTGCACA 23340
D 17701 TATTCGCTGTGTTTCGGGGGGGCGGTCGATACGGCTTAACCCGTTGGGCTTGCACA 17760
Qy 23341 AGCAGCGCCCGCGCTGACCGCGCTCCCGAGGTCAACGAGGCTGAGAAACATAGTT 23400
D 17761 AGCAGCGCCCGCGCTGACCGCGCTCCCGAGGTCAACGAGGCTGAGAAACATAGTT 17820
Qy 23401 TTACAGGTGCGCAGTGCAGCGCGGTGGCAACATCTTGGGTCCCTCGAAGACCGGAA 23460
D 17821 TTACAGGTGCGCAGTGCAGCGCGGTGGCAACATCTTGGGTCCCTCGAAGACCGGAA 17880
Qy 23461 AAATCCCGCGCGCGCGGTGTCGAGAGGCAACGAAATATCCCAACGCAACTA 23520
D 17881 AAATCCCGCGCGCGCGGTGTCGAGAGGCAACGAAATATCCCAACGCAACTA 17940
Qy 23521 AAGCATGATGTTGGGTTTCGATGACGCGCGCGCAAGAGGCGCGGTGTGCGCTGG 23580
D 17941 AAGCATGATGTTGGGTTTCGATGACGCGCGCGCGCAAGAGGCGCGGTGTGCGCTGG 18000
Qy 23581 CGAAGATAGTGGCGCAGAGCAGGTTTCGATAGTACGCGCTGAGCGGCTCCACT 23640
D 18001 CGAAGATAGTGGCGCAGAGCAGGTTTCGATAGTACGCGCTGAGCGGCTCCACT 18060
Qy 23641 GCGAGCAGGCCAAAAACAGGGCGCGCGAGCGCGCAAGTGGCGCGCTTCCCC 23700
D 18061 GCGAGCAGGCCAAAAACAGGGCGCGCGAGCGCGCAAGTGGCGCGCTTCCCC 18120
Qy 23701 CACGCGGATTTGGCAAAATGGCGACCGCGCGGTGAGAGCGCGGAGCTCAA 23760
D 18121 CACGCGGATTTGGCAAAATGGCGACCGCGCGGTGAGAGCGCGGAGCTCAA 18180
Qy 23761 TCACGACGAGAGAGCAAGCTGTTGTCCTCGTCAATCACGAGGGCGCGCGG 23820

Dp	18181	TCAGACGAGAGAAAGCGCAGTTGGTAGTTCGCCGTCAATACCAGAGGCCGCGCCG	18240
Oy	23821	TTGGCGGATAATGAACCGCGCGCGCCATTGGAGCGTGGCGGACCAATGGCGCGT	23880
Dp	18241	TTGGCGGATAATGAACCGCGCGCGCCATTGGAGCGCTGGCGGACCAATGGCGCGT	18300
Oy	23881	TGGGTTTTGTTACAACTGCCCTATATATATATATATACCTTCCCTGTAAAGGAATC	23940
Dp	18301	TGGGTTTTGTTACAACTGCCCTATATATATATATATACCTTCCCTGTAAAGGAATC	18360
Oy	23941	CCAGTCTCTTAAATCTAATACGCTGGGTATATATATAGAAATTCAGTATATATTC	24000
Dp	18361	CCAGTCTCTTAAATCTAATACGCTGGGTATATATATAGAAATTCAGTATATATTC	18420
Oy	24001	TACTGATCTTGCGT	24060
Dp	18421	TACTGATCTTGCGT	18480
Oy	24061	TATATATGAATACAGATACCTGGGAAATCTACCCAGTTTATATATATATATATAT	24120
Dp	18481	TATATATGAATACAGATACCTGGGAAATCTACCCAGTTTATATATATATATATAT	18540
Oy	24121	CTATTATAGTGGGGGTCTFAAATATATGTACAAAACAATATTTTATATATATATC	24180
Dp	18541	CTATTATAGTGGGGGTCTFAAATATATGTACAAAACAATATTTTATATATATC	18600
Oy	24181	TAAAAATGCTCCATTCTTACCTGTGACGTACATGTTAGAAATGTGGAGTGGTTGTAA	24240
Dp	18601	TAAAAATGCTCCATTCTTACCTGTGACGTACATGTTAGAAATGTGGAGTGGTTGTAA	18660
Oy	24241	TATGTTTCAACACACACCTTTTGGGCGCTCTGAATCTATATAAAGCGAAGCTCGCG	24300
Dp	18661	TATGTTTCAACACACACCTTTTGGGCGCTCTGAATCTATATAAAGCGAAGCTCGCG	18720
Oy	24301	GTTAATGCGACAGTGGCGGTACACAGTCCAGTGGAGTTTATATGTCGCTTA	24360
Dp	18721	GTTAATGCGACAGTGGCGGTACACAGTCCAGTGGAGTTTATATGTCGCTTA	18780
Oy	24361	TGCGTTTACCTCGCATTCGCGGACACAAGCTGATTTACGTAGACAGCATTTGGGGTTTAA	24420
Dp	18781	TGCGTTTACCTCGCATTCGCGGACACAAGCTGATTTACGTAGACAGCATTTGGGGTTTAA	18840
Oy	24421	CCGGTTAATTTAGTGTGTGACGCTGTAAAAAGCCCAACGAGCGTTGGCTTAAAGCGT	24480
Dp	18841	CCGGTTAATTTAGTGTGTGACGCTGTAAAAAGCCCAACGAGCGTTGGCTTAAAGCGT	18900
Oy	24481	TTTAAAGGTGCGGTTTTTATACATGCGATTTAATGTATAGGAGCTAGCTGTATTC	24540
Dp	18901	TTTAAAGGTGCGGTTTTTATACATGCGATTTAATGTATAGGAGCTAGCTGTATTC	18960
Oy	24541	CGCATGCTTTCGGTTTTAGTAGTTGTACAAAACGAATTTAGCCGCAATTTGTTACTGG	24600
Dp	18961	CGCATGCTTTCGGTTTTAGTAGTTGTACAAAACGAATTTAGCCGCAATTTGTTACTGG	19020
Oy	24601	TACCCAAAACGGCAAGCCGCTTAAACAGCCCGCGCTGGCTTTTGTCTACGCCGC	24660
Dp	19021	TACCCAAAACGGCAAGCCGCTTAAACAGCCCGCGCTGGCTTTTGTCTACGCCGC	19080
Oy	24661	TCCGAATACATGAGATTTTAAATTTAAATGGGGAATGGGTAGCGCAATTTAAAGC	24720
Dp	19081	TCCGAATACATGAGATTTTAAATTTAAATGGGGAATGGGTAGCGCAATTTAAAGC	19140
Oy	24721	CGTCAAAAATTTAAATNGACATACGTAACCGGTGCTTTTACTGACCTATGGCGAATTTT	24780
Dp	19141	CGTCAAAAATTTAAATNGACATACGTAACCGGTGCTTTTACTGACCTATGGCGAATTTT	19200
Oy	24781	AAAAATTTAAAGCCGTGGTTTTTAAACAACAAGCTGCAGCTTTATATAGCTTGCATATCA	24840
Dp	19201	AAAAATTTAAAGCCGTGGTTTTTAAACAACAAGCTGCAGCTTTATATAGCTTGCATATCA	19260
Oy	24841	GTGCGCTGTGATTTTATGAGTTAAAGTAATTTTAAACATTTGTAATGTGTACAC	24900

Db	19261	GTGCCGTTGTCATTTTATGTTAGTTCAGATTTTAACTTAATTTTGTATGCTACAC	19320
QY	24901	GTGGATTTTAAATTTGAATTTAAATTTGTAATTACGTGCAGCGGTGGAATTTTAAATTTGAT	24960
Db	19321	GTGATTTTAAATTTGAATTTAAATTTGTAATTCACGTGCAGCGGTGGAATTTTAAATTTGAT	19380
QY	24961	TTATGTAACTTTGTTAAATTTTAACTGCGTTATGTTGTATTTTGGTTAAATTTATGTAT	25020
Db	19381	TTATGTAACTTTGTTAAATTTTAACTGCGTTATGTTGTATTTTGGTTAAATTTATGTAT	19440
QY	25021	TTTGGTTTACATTTGTTCCGGGTGTGAATTCAGACAGGTAAAGCCTACCTCTAATGT	25080
Db	19441	TTTGGCTTTAGATTTGTTCCGGGTGTGAATTCAGACAGGTAAAGCCTACCTCTAATGT	19500
QY	25081	TTGCTTTGCCGCTACGCTCCTAATGTTTGGCTTTGCCGCTACGCTCCTAATGTTGGCTTG	25140
Db	19501	TTGCTTTGCCGCTACGCTCCTAATGTTTGGCTTTGCCGCTACGCTCCTAATGTTGGCTTG	19560
QY	25141	CCGCCCTACCTCTATGTTTGCTTTGCCGCTACGCTCTAATGTTTGCTTTGCCGCTACG	25200
Db	19561	CCGCCCTACCTCTAATGTTTGCTTTGCCGCTACGCTCTAATGTTTGCTTTGCCGCTACG	19620
QY	25201	CTCCTAATGTTTGCTTTGCCGCTACGCTCCTAATGTTTGCTTTGCCGCTACGCTCCTAAT	25260
Db	19621	CTCCTAATGTTTGCTTTGCCGCTACGCTCCTAATGTTTGCTTTGCCGCTACGCTCCTAAT	19680
QY	25261	GTTTGCCCTTGGCGGCTACGCTCTAATGTTTGGCTTTGGCGGCTACGCTCTAATGTTGGCT	25320
Db	19681	GTTTGCCCTTGGCGGCTACGCTCTAATGTTTGGCTTTGGCGGCTACGCTCTAATGTTGGCT	19740
QY	25321	TGCGGCTACGCTCTAATGTTTGCTTTGCCGCTACGCTCTAATGTTTAAACAATTAAT	25380
Db	19741	TGCGGCTACGCTCTAATGTTTGCTTTGCCGCTACGCTCTAATGTTTAAACAATTAAT	19800
QY	25381	GTTTAAAGACACTAAATTTAAAGAGCTTGTGTGGTTTATGACACAGCTTGACAA	25440
Db	19801	GTTTAAAGACACTAAATTTAAAGAGCTTGTGTGGTTTATGACACAGCTTGACAA	19860
QY	25441	AACCTGCTGGTGATTTTATCCCAACAATAATTAATAAAGTTAAACCTTATTTCTG	25500
Db	19861	AACCTGCTGGTGATTTTATCCCAACAATAATTAATAAAGTTAAACCTTATTTCTG	19920
QY	25501	TTGTCTGTGTAATTTGGGTTCCCGAGAGGTCCCGGCTCCCGTTCCCGAGAGGTCCCG	25560
Db	19921	TTGTCTGTGTAATTTGGGTTCCCGAGAGGTCCCGGCTCCCGTTCCCGAGAGGTCCCG	19980
QY	25561	GCTCCCGGTTCCCGAGAGGTCCCGGAGTCCCGGTTCCCGAGAGGTCCCGGAGTCCCGGTT	25620
Db	19981	GCTCCCGGTTCCCGAGAGGTCCCGGAGTCCCGGTTCCCGAGAGGTCCCGGAGTCCCGGTT	20040
QY	25621	CCCGAGAGGTCCCGGAGTCCCGGTTCCCGAGAGGTCCCGGAGTCCCGGTTCCCGAGAGGT	25680
Db	20041	CCCGAGAGGTCCCGGAGTCCCGGTTCCCGAGAGGTCCCGGAGTCCCGGTTCCCGAGAGGT	20100
QY	25681	CCCGGAGTCCCGGTTCCCGAGAGGTCCCGGAGTCCCGGTTCCCGAGAGGTCCCGGAGTCC	25740
Db	20101	CCCGGAGTCCCGGTTCCCGAGAGGTCCCGGAGTCCCGGTTCCCGAGAGGTCCCGGAGTCC	20160
QY	25741	CCGTTTCCCGAGAGGTCCCGGAGTCCCGGTTCCCGAGAGGTCCCGGAGTCCCGGTTCCCGG	25800
Db	20161	CCGTTTCCCGAGAGGTCCCGGAGTCCCGGTTCCCGAGAGGTCCCGGAGTCCCGGTTCCCGG	20220
QY	25801	AGGGTCCCGGAGTCCCGGTTCCCGAGAGGTCCCGGTTCCCGAGAGGTCCCGGTTCCCGG	25860
Db	20221	AGGGTCCCGGAGTCCCGGTTCCCGAGAGGTCCCGGTTCCCGAGAGGTCCCGGTTCCCGG	20280
QY	25861	GCTTCCCGGTTCCCGGAGTCCCGGAGTCCCGGTTCCCGAGAGGTCCCGGAGTCCCGGTT	25920
Db	20281	GCTTCCCGGTTCCCGGAGTCCCGGAGTCCCGGTTCCCGAGAGGTCCCGGAGTCCCGGTT	20340
QY	25921	CCCGAGAGGTCCCGGAGTCCCGGTTCCCGAGAGGTCCCGGAGTCCCGGTTCCCGAGAGGT	25980
Db	20341	CCCGAGAGGTCCCGGAGTCCCGGTTCCCGAGAGGTCCCGGAGTCCCGGTTCCCGAGAGGT	20400

QY	23981	CCGGG6CTCCCGCTTCCCGAGG6CTCCGG6CTCCCGTTC	CCCGAGG6CTCCGG6CTCCCGGAGG6CTCCCGGAGG6CTCC	26400
Db	20401	CCCCGG6CTCCCGCTTCCCGAGG6CTCCGG6CTCCCGTTC	CCCCGG6CTCCCGGAGG6CTCCCGGAGG6CTCCCGGAGG6CTCC	20460
QY	26041	CCGTTTCCCGAGG6CTCCGG6CTCCCGTTC	CCCGAGG6CTCCGG6CTCCCGGAGG6CTCCGG6CTCCCGGAGG6CTCC	26100
Db	20461	CCGTTTCCCGAGG6CTCCGG6CTCCCGTTC	CCCGAGG6CTCCGG6CTCCCGGAGG6CTCCGG6CTCCCGGAGG6CTCC	20520
QY	26101	AGG6TCCCGG6CTCCCGTTC	CCCGAGG6CTCCGG6CTCCCGGAGG6CTCCGG6CTCCCGGAGG6CTCC	26160
Db	20521	AGG6TCCCGG6CTCCCGTTC	CCCGAGG6CTCCGG6CTCCCGGAGG6CTCCGG6CTCCCGGAGG6CTCC	20580
QY	26161	GCTCCCGGCTCCCGAGG6CTCCGG6CTCCCGTTC	CCCGAGG6CTCCGG6CTCCCGGAGG6CTCCGG6CTCCCGGAGG6CTCC	26220
Db	20581	GCTCCCGGCTCCCGAGG6CTCCGG6CTCCCGTTC	CCCGAGG6CTCCGG6CTCCCGGAGG6CTCCGG6CTCCCGGAGG6CTCC	20640
QY	26221	CCCGGAGG6CTCCGG6CTCCCGTTC	CCCGAGG6CTCCGG6CTCCCGGAGG6CTCCGG6CTCCCGGAGG6CTCC	26280
Db	20641	CCCGGAGG6CTCCGG6CTCCCGTTC	CCCGAGG6CTCCGG6CTCCCGGAGG6CTCCGG6CTCCCGGAGG6CTCC	20700
QY	26281	CCCGGAGG6CTCCCGTTC	CCCGAGG6CTCCGG6CTCCCGGAGG6CTCCGG6CTCCCGGAGG6CTCC	26340
Db	20701	CCCGGAGG6CTCCCGTTC	CCCGAGG6CTCCGG6CTCCCGGAGG6CTCCGG6CTCCCGGAGG6CTCC	20760
QY	26341	CCGTTTCCCGAGG6CTCCGG6CTCCCGTTC	CCCGAGG6CTCCGG6CTCCCGGAGG6CTCCGG6CTCCCGGAGG6CTCC	26400
Db	20761	CCGTTTCCCGAGG6CTCCGG6CTCCCGTTC	CCCGAGG6CTCCGG6CTCCCGGAGG6CTCCGG6CTCCCGGAGG6CTCC	20820
QY	26401	AGG6TCCCGG6CTCCCGTTC	CCCGAGG6CTCCGG6CTCCCGGAGG6CTCCGG6CTCCCGGAGG6CTCC	26460
Db	20821	AGG6TCCCGG6CTCCCGTTC	CCCGAGG6CTCCGG6CTCCCGGAGG6CTCCGG6CTCCCGGAGG6CTCC	20880
QY	26461	GCTCCCGGCTCCCGAGG6CTCCGG6CTCCCGTTC	CCCGAGG6CTCCGG6CTCCCGGAGG6CTCCGG6CTCCCGGAGG6CTCC	26520
Db	20881	GCTCCCGGCTCCCGAGG6CTCCGG6CTCCCGTTC	CCCGAGG6CTCCGG6CTCCCGGAGG6CTCCGG6CTCCCGGAGG6CTCC	20940
QY	26521	CCCGGATTC	CCCGAGG6CTCCGG6CTCCCGGAGG6CTCCGG6CTCCCGGAGG6CTCC	26580
Db	20941	CCCGGATTC	CCCGAGG6CTCCGG6CTCCCGGAGG6CTCCGG6CTCCCGGAGG6CTCC	21000
QY	26581	TTGTACATPACACGCGG6CTCCGG6CTCCCGTTC	CCCGAGG6CTCCGG6CTCCCGGAGG6CTCCGG6CTCCCGGAGG6CTCC	26640
Db	21001	TTGTACATPACACGCGG6CTCCGG6CTCCCGTTC	CCCGAGG6CTCCGG6CTCCCGGAGG6CTCCGG6CTCCCGGAGG6CTCC	21060
QY	26641	GAAACGCGTACGCTTTC	CCCGAGG6CTCCGG6CTCCCGGAGG6CTCCGG6CTCCCGGAGG6CTCC	26700
Db	21061	GAAACGCGTACGCTTTC	CCCGAGG6CTCCGG6CTCCCGGAGG6CTCCGG6CTCCCGGAGG6CTCC	21120
QY	26701	GTTTTTGGTACGCAATGCAACGAGTACGCTTC	CCCGAGG6CTCCGG6CTCCCGGAGG6CTCCGG6CTCCCGGAGG6CTCC	26760
Db	21121	GTTTTTGGTACGCAATGCAACGAGTACGCTTC	CCCGAGG6CTCCGG6CTCCCGGAGG6CTCCGG6CTCCCGGAGG6CTCC	21180
QY	26761	CCGCAAGTACGCGG6CTCCGG6CTCCCGTTC	CCCGAGG6CTCCGG6CTCCCGGAGG6CTCCGG6CTCCCGGAGG6CTCC	26820
Db	21181	CCGCAAGTACGCGG6CTCCGG6CTCCCGTTC	CCCGAGG6CTCCGG6CTCCCGGAGG6CTCCGG6CTCCCGGAGG6CTCC	21240
QY	26821	TACCTTAAGTTACGCTACGCAATATATGCGGCTTC	CCCGAGG6CTCCGG6CTCCCGGAGG6CTCCGG6CTCCCGGAGG6CTCC	26880
Db	21241	TACCTTAAGTTACGCTACGCAATATATGCGGCTTC	CCCGAGG6CTCCGG6CTCCCGGAGG6CTCCGG6CTCCCGGAGG6CTCC	21300
QY	26881	GGAAGAAATGAAATCTTTCGCAAGTACGCTTTC	CCCGAGG6CTCCGG6CTCCCGGAGG6CTCCGG6CTCCCGGAGG6CTCC	26940
Db	21301	GGAAGAAATGAAATCTTTCGCAAGTACGCTTTC	CCCGAGG6CTCCGG6CTCCCGGAGG6CTCCGG6CTCCCGGAGG6CTCC	21360
QY	26941	CTGTGGGCTCCGCGAGG6CTCCGG6CTCCCGTTC	CCCGAGG6CTCCGG6CTCCCGGAGG6CTCCGG6CTCCCGGAGG6CTCC	27000
Db	21361	CTGTGGGCTCCGCGAGG6CTCCGG6CTCCCGTTC	CCCGAGG6CTCCGG6CTCCCGGAGG6CTCCGG6CTCCCGGAGG6CTCC	21420
QY	27001	TATCAGCGCTTTC	CCCGAGG6CTCCGG6CTCCCGGAGG6CTCCGG6CTCCCGGAGG6CTCC	27060
Db	21421	TATCAGCGCTTTC	CCCGAGG6CTCCGG6CTCCCGGAGG6CTCCGG6CTCCCGGAGG6CTCC	21480

QY	27061	TTACCGCTCTCTGCGGGGACCTAAACGCCATAGGCCAAGGATGCTCAATAATAACACGGA	27120
Db	21481	TTACCGCTCTCTGCGGGGACCTAAACGCCAATAGGCCAAGGATGCTCAATAATAACACGGA	21540
QY	27121	CGGACGGCCAAACCTGGGGGTGGCGCTTTGGCCGCTTGGGCTTTGGGCTATGTGGTGA	27180
Db	21541	CGGACGGCCAAACCTGGGGGTGGCGCTTTGGCCGCTTGGGCTTTGGGCTATGTGGTGA	21600
QY	27181	TAAAGTTAAAGACAGCAGCGCTCTTTTAAAGTTACGGCATAGCCGTCTACCCGTGTACGC	27240
Db	21601	TAAAGTTAAAGACAGCAGCGCTCTTTTAAAGTTACGGCATAGCCGTCTACCCGTGTACGC	21660
QY	27241	GTAAGAGCGCGCTGAGTCTCAAGTGGTTTGGTTTCAACAGCGGAATGGAGGAGCTACAGAA	27300
Db	21661	GTAAGAGCGCGCTGAGTCTCAAGTGGTTTGGTTTCAACAGCGGAATGGAGGAGCTACAGAA	21720
QY	27301	TTACTGGAGGAATACTGAGGGCATGGCCGCAACGGGAGAGACATATGCTACGGAAAT	27360
Db	21721	TTACTGGAGGAATACTGAGGGCATGGCCGCAACGGGAGAGACATATGCTACGGAAAT	21780
QY	27361	TGCGGCTGCTCTTCTGGCGCTAAGTGGCGCTGTTTGCATCAGGCGATAGTGTGGCTTTA	27420
Db	21781	TGCGGCTGCTCTTCTGGCGCTAAGTGGCGCTGTTTGCATCAGGCGATAGTGTGGCTTTA	21840
QY	27421	ACCGCGTATTTCCCGACCCCTGACCTTAAGTGAAGCCGATGTGTATATGACCAATAAACA	27480
Db	21841	ACCGCGTATTTCCCGACCCCTGACCTTAAGTGAAGCCGATGTGTATATGACCAATAAACA	21900
QY	27481	AAACAGCTAACGAGTATTCGTTGGTGAACATTTTATTTATGACAACTTCTCGCAGAAC	27540
Db	21901	AAACAGCTAACGAGTATTCGTTGGTGAACATTTTATTTATGACAACTTCTCGCAGAAC	21960
QY	27541	TTTTTTGTATCTGTGACACAGGGGGCCGGCTGTGCGCTGCGCTTACACGGGGCCCGCGCGG	27600
Db	21961	TTTTTTGTATCTGTGACACAGGGGGCCGGCTGTGCGCTGCGCTTACACGGGGCCCGCGCGG	22020
QY	27601	ACTGTCCGCAATTCGTGATCGAAGGGGGCGGCGACGCCAGCGCGGGGGCGAGAGGCTGAAG	27660
Db	22021	ACTGTCCGCAATTCGTGATCGAAGGGGGCGGCGACGCCAGCGCGGGGGCGAGAGGCTGAAG	22080
QY	27661	GAAAGCGGTTTGAATATACAGATTCTTGGGCGGGGGCGGTGAGTTGGCGGGCTGGGTGG	27720
Db	22081	GAAAGCGGTTTGAATATACAGATTCTTGGGCGGGGGCGGTGAGTTGGCGGGCTGGGTGG	22140
QY	27721	CGAGACCGGCGCTGTGTGCTCGCGCGGCTGCGGGGGCGGTGTGCTGCTGTGATGCCCT	27780
Db	22141	CGAGACCGGCGCTGTGTGCTCGCGCGGCTGCGGGGGCGGTGTGCTGCTGTGATGCCCT	22200
QY	27781	GCGGCGCTGTGTACAGGCTGTGGGGCGTGGAGATGGGTGTCTCCGGAATACCACTGCGG	27840
Db	22201	GCGGCGCTGTGTACAGGCTGTGGGGCGTGGAGATGGGTGTCTCCGGAATACCACTGCGG	22260
QY	27841	GCTGTGAGCGTATAGGTACGGGCGACAGCCGTAAGGCTGTGTGGCCACGAGAACTGAACGGGG	27900
Db	22261	GCTGTGAGCGTATAGGTACGGGCGACAGCCGTAAGGCTGTGTGGCCACGAGAACTGAACGGGG	22320
QY	27901	GTTGGTTGCGGCTGTGTGTCGGGCTGTGTCTCGCCGCGAGAGCTGTGACAGCGGCTGTTTTA	27960
Db	22321	GTTGGTTGCGGCTGTGTGTCGGGCTGTGTCTCGCCGCGAGAGCTGTGACAGCGGCTGTTTTA	22380
QY	27961	GGTCCTTCAGATCCGCGCTGAATGTCAATATGTTTTTGAACAGCGCCATATGACGTCCTTGT	28020
Db	22381	GGTCCTTCAGATCCGCGCTGAATGTCAATATGTTTTTGAACAGCGCCATATGACGTCCTTGT	22440
QY	28021	GTAATGCCGACCTCTCGCCTGTGAAACACAGGGGCTGTGTGGAAGCTCCACAGTCCGTTTGC	28080
Db	22441	GTAATGCCGACCTCTCTCGCCTGTGAAACACAGGGGCTGTGTGGAAGCTCCACAGTCCGTTTGC	22500
QY	28081	GCTTCTGTTGGCGAGAGGTGTGCGGAGCGTAAGCGCTAAGTCGAGAGAAATAGTACGTGGCGG	28140
Db	22501	GCTTCTGTTGGCGAGAGGTGTGCGGAGCGTAAGCGCTAAGTCGAGAGAAATAGTACGTGGCGG	22560
QY	28141	CATACGAGAGAGGTGTGGGGGCAAAACCCCACTGTGGAAGGGAACGGTGTGCGGACGGCGG	28200

|||||
Db 22561 CATACGAGAGGGTTGGGGGCAACGCCACTGGAAAGGAGCGGGGCGACGGCG 22620
QY 28201 GTGCTACGATGGAGCGGTACAGCTCAGGGCGGTATCCAGATGATACGCCGGTTC 28260
Db 22621 GTGCTACGATGGAGCGGTACAGCTCAGGGCGGTATCCAGATGATACGCCGGTTC 22680
QY 28261 CCGGCATTCGAGGGTGGCGCAAGAACGTACGTGCGGTGGCCCTGGTTCGATTTATCGA 28320
Db 22681 CCGGCATTCGAGGGTGGCGCAAGAACGTACGTGCGGTGGCCCTGGTTCGATTTATCGA 22740
QY 28321 GACTGCTGACCATGATGATGAGAAAGGTGCTTGGGAATGATGATGCTCTCCGGGA 28380
Db 22741 GACTGCTGACCATGATGATGAGAAAGGTGCTTGGGAATGATGATGCTCTCCGGGA 22800
QY 28381 GGGCGCTCATGTTGCGGTGTGCGGGTTACCGCAGTGTGAGCGCAGGAAATGGCTTG 28440
Db 22801 GGGCGCTCATGTTGCGGTGTGCGGGTTACCGCAGTGTGAGCGCAGGAAATGGCTTG 22860
QY 28441 CCTTTAAATACGTACTTCTGCGGACGTGCGCCACGCCCTTATCTGTTTGAGCAGGTCTG 28500
Db 22861 CCTTTAAATACGTACTTCTGCGGACGTGCGCCACGCCCTTATCTGTTTGAGCAGGTCTG 22920
QY 28501 TGGCATCTGGATAAATCCGGGGTGGATGGCTTGGCCATCACTGTCTCAAGAGGGCGG 28560
Db 22921 TGGCATCTGGATAAATCCGGGGTGGATGGCTTGGCCATCACTGTCTCAAGAGGGCGG 22980
QY 28561 CGAATTCGCGGGTGTACCTGACCTGACCTTCCGCAAGATCTAAACATTAAGACCTTATTTAC 28620
Db 22981 CGAATTCGCGGGTGTACCTGACCTGACCTTCCGCAAGATCTAAACATTAAGACCTTATTTAC 23040
QY 28621 CGGCTTCCTCTGCGGTGAAGAAATCAAACTTGGAGACGACCATTGATGGTCTGTCCTG 28680
Db 23041 CGGCTTCCTCTGCGGTGAAGAAATCAAACTTGGAGACGACCATTGATGGTCTGTCCTG 23100
QY 28681 AAACGGCGATTGACCCCTACGCGCTCCGACAGTGCAGACAGAGAGATGGTGAAGAGCGG 28740
Db 23101 AAACGGCGATTGACCCCTACGCGCTCCGACAGTGCAGACAGAGAGATGGTGAAGAGCGG 23160
QY 28741 GTGGGTGATTGGGGTCTTGCAGCTCTTGGGTGAAGGAGACGAGAGAGAGCTCCGGGA 28800
Db 23161 GTGGGTGATTGGGGTCTTGCAGCTCTTGGGTGAAGGAGACGAGAGAGAGCTCCGGGA 23220
QY 28801 GGCATCTGTGTAAACATCTCCACACAGGGGGTCCCGAGAGCATGGGGTTTACGTGATCTGGG 28860
Db 23221 GGCATCTGTGTAAACATCTCCACACAGGGGGTCCCGAGAGCATGGGGTTTACGTGATCTGGG 23280
QY 28861 CCGCTCGCAGTCCCGCGGAGCGGTGACGCCAGGSCCAAGAAATGTGGCTGTAGCT 28920
Db 23281 CCGCTCGCAGTCCCGCGGAGCGGTGACGCCAGGSCCAAGAAATGTGGCTGTAGCT 23340
QY 28921 TGGCCAGGCAAAATATCCCGTGTATCTTGGAAAGACCGATTTGTGACCTACGTGGG 28980
Db 23341 TGGCCAGGCAAAATATCCCGTGTATCTTGGAAAGACCGATTTGTGACCTACGTGGG 23400
QY 28981 GTTGGGGAGCGTCTATGTTTANCGGTAAGAGGTCCTATACGGGAGCAGGCTGCCA 29040
Db 23401 GTTGGGGAGCGTCTATGTTTANCGGTAAGAGGTCCTATACGGGAGCAGGCTGCCA 23460
QY 29041 CGATTAGAGGCTTAATACAGCTCTTTTCTATCTTTGTAGTACGACACGTCCACGT 29100
Db 23461 CGATTAGAGGCTTAATACAGCTCTTTTCTATCTTTGTAGTACGACACGTCCACGT 23520
QY 29101 ATCCGCCAACGTACACGGGAGTCATGTTGGTGGTGTGCTGCGTGAAGCGAAGAGATGA 29160
Db 23521 ATCCGCCAACGTACACGGGAGTCATGTTGGTGGTGTGCTGCGTGAAGCGAAGAGATGA 23580
QY 29161 GGGCGGCTCTGGGGGCTGATGTGGCGGCTTATCCGTGTGAGATTTAATACGTTTC 29220
Db 23581 GGGCGGCTCTGGGGGCTGATGTGGCGGCTTATCCGTGTGAGATTTAATACGTTTC 23640
QY 29221 TCCCTGGGAGGCTCAGGTTCTTACCTGTGCTGGCAAAATGTACAATACGGCTTA 29280
|||||

Db 23641 TCCCTGGGAGGCTCAGGTTTCTTACCTGCTGTGCGAAATGTACACTACGGCTTA 23700
QY 29281 ACCTGTACCTTCTGAAGAGCAATTCCTAATACCGGAACGAGAGCATATTTGCTCG 29340
Db 23701 ACCTGTACCTTCTGAAGAGCAATTCCTAATACCGGAACGAGAGCATATTTGCTCG 23760
QY 29341 GGGGTAAAGTTCCGGTGAAGTTCTGCAAAATCGTTTACATGGGTTTAAAGACATGGGG 29400
Db 23761 GGGGTAAAGTTCCGGTGAAGTTCTGCAAAATCGTTTACATGGGTTTAAAGACATGGGG 23820
QY 29401 TTTCTGACGACGTTGCTCTGCAAAACCAAAAGGGGGCTGTGGCTTACTTCAACG 29460
Db 23821 TTTCTGACGACGTTGCTCTGCAAAACCAAAAGGGGGCTGTGGCTTACTTCAACG 23880
QY 29461 GGGCTCGTGGCTGTTAAAGGTCTAGGGCACTACGTTTTCCTCAACTGGGTTAAGCC 29520
Db 23881 GGGCTCGTGGCTGTTAAAGGTCTAGGGCACTACGTTTTCCTCAACTGGGTTAAGCC 23940
QY 29521 ACAGCGTACCGGTGTCCGGAACCAACGATGGGAATTTCTATTAATACCTAGGCA 29580
Db 23941 ACAGCGTACCGGTGTCCGGAACCAACGATGGGAATTTCTATTAATACCTAGGCA 24000
QY 29581 GCGTCAATACATGTGCGCTGCTGTGGCACGTAGCTACGTTTGGGGTGGGGCAGC 29640
Db 24001 GCGTCAATACATGTGCGCTGCTGTGGCACGTAGCTACGTTTGGGGTGGGGCAGC 24060
QY 29641 CTGACCAAGACCCCTGGGTGAGGTGTTCGCCGCAAGATTTTATACGTACTTAATA 29700
Db 24061 CTGACCAAGACCCCTGGGTGAGGTGTTCGCCGCAAGATTTTATACGTACTTAATA 24120
QY 29701 TTTCCGGCCACATTAATGCCAGCAATCTTAATAACAGTGGGAGCTCCGGGTACG 29760
Db 24121 TTTCCGGCCACATTAATGCCAGCAATCTTAATAACAGTGGGAGCTCCGGGTACG 24180
QY 29761 GTGGCTTCGAGGAGAGTGTGTGCGGATTTGCCGAGTACACGGGATTCGCGCTGGG 29820
Db 24181 GTGGCTTCGAGGAGAGTGTGTGCGGATTTGCCGAGTACACGGGATTCGCGCTGGG 24240
QY 29821 ATTTTGCCTCCGGCTCCGGCTGTAAAGTCTGACAGACGACTTGTTCGCTCA 29880
Db 24241 ATTTTGCCTCCGGCTCCGGCTGTAAAGTCTGACAGACGACTTGTTCGCTCA 24300
QY 29881 ATTAACGCGTACGTAGGCGTGCCTACACTACCGAGTGGCGACCGGAGATGCCAG 29940
Db 24301 ATTAACGCGTACGTAGGCGTGCCTACACTACCGAGTGGCGACCGGAGATGCCAG 24360
QY 29941 GACCAAAAATAAATCTGTCTGATGCTGTAACTCCGAATTTGGCTTTCTATATCTC 30000
Db 24361 GACCAAAAATAAATCTGTCTGATGCTGTAACTCCGAATTTGGCTTTCTATATCTC 24420
QY 30001 GTGTGCCAGACCGGGGGCGAGTGGTCGAAGAGATGGCGCCAGGCTTCTCGGCCGT 30060
Db 24421 GTGTGCCAGACCGGGGGCGAGTGGTCGAAGAGATGGCGCCAGGCTTCTCGGCCGT 24480
QY 30061 TTAACGTACGACGTTGAGCTGAGCTGCAATCGAGGCTCCCTAAGCGTGGCTTTG 30120
Db 24481 TTAACGTACGACGTTGAGCTGAGCTGCAATCGAGGCTCCCTAAGCGTGGCTTTG 24540
QY 30121 GTTCAGAGATCAAAATTTGTTAAATCTGGAACCGGTACAGTTGACGAACGAGAGT 30180
Db 24541 GTTCAGAGATCAAAATTTGTTAAATCTGGAACCGGTACAGTTGACGAACGAGAGT 24600
QY 30181 GTGTTTTAAGTGGATATGGCTTTTGCCTCCACGCGCTAGATACGACCCGGGAACAA 30240
Db 24601 GTGTTTTAAGTGGATATGGCTTTTGCCTCCACGCGCTAGATACGACCCGGGAACAA 24660
QY 30241 AAACGAGTGGGGGCTGTGGCGGCGCAAAATTTGGGAGATTAATTTCTGTCAG 30300
Db 24661 AAACGAGTGGGGGCTGTGGCGGCGCAAAATTTGGGAGATTAATTTCTGTCAG 24720
QY 30301 GAAATCAAAAAGTTGCCCTTTTAAAGTATTTGTGGACCCGGAGGGTCTTCACTT 30360
Db 24721 GAAATCAAAAAGTTGCCCTTTTAAAGTATTTGTGGACCCGGAGGGTCTTCACTT 24780
|||||

OY	30361	GGAAATCTCCACCCAGAGGAGGCGACAGTTGAGCGCCCGGTGGGCGGATCTGGTGT	30420
Db	24781	GGAAAACTCTCCACCCAGAGGAGGCGACAGTTGAGCGCCCGGTGGGCGGATCTGGTGT	24840
OY	30421	GATTTGGGCGGAGCTCCAAATGACAGTAAACCAAAACTAAACAGCCATGAGCGGAGAGGCG	30480
Db	24841	GATTTGGGCGGAGCTCCAAATGACAGTAAACCAAAACTAAACAGCCATGAGCGGAGAGGCG	24900
OY	30481	GGCTCGGAGGTTCCATTGGTAGCTTGAAGGGGAGGACAGTCTTCGCTAACCAAGTGT	30540
Db	24901	GGCTCGGAGGTTCCATTGGTAGCTTGAAGGGGAGGACAGTCTTCGCTAACCAAGTGT	24960
OY	30541	CGCAGAGATATATACAGAGATCTGTCCAGTGGCTACCCGGTATACGGGGTCTTGGAGAC	30600
Db	24961	CGCAGAGATATATACAGAGATCTGTCCAGTGGCTACCCGGTATACGGGGTCTTGGAGAC	25020
OY	30601	GGGTAGCAGTCCGCTGTGCGCAACGTCGGCTATATCAGCTGGTTGTAAAGAGTCGCG	30660
Db	25021	GGGTAGCAGTCCGCTGTGCGCAACGTCGGCTATATCAGCTGGTTGTAAAGAGTCGCG	25080
OY	30661	GTTGTACTTTGTTTCTTTGTTTAGGGGCGCTAGAGAGGCGGTTGGCTTGGATTGGATA	30720
Db	25081	GTTGTACTTTGTTTCTTTGTTTAGGGGCGCTAGAGAGGCGGTTGGCTTGGATTGGATA	25140
OY	30721	TGTAAACTCGAAACCCAGGCGCTTCGTTGTTTGTAAAGTGAACAAAGGTCGCCAG	30780
Db	25141	TGTAAACTCGAAACCCAGGCGCTTCGTTGTTTGTAAAGTGAACAAAGGTCGCCAG	25200
OY	30781	CTTTGTGCGGAGTTATCCAGAGGCGTTTCGATTTGGCGGCAACGGGGTATCTGTCCG	30840
Db	25201	CTTTGTGCGGAGTTATCCAGAGGCGTTTCGATTTGGCGGCAACGGGGTATCTGTCCG	25260
OY	30841	GTCACATAGTACCCGCTGAGAGGAGCAACGCGGCGTCGTCGATACGTTGGGAGC	30900
Db	25261	GTCACATAGTACCCGCTGAGAGGAGCAACGCGGCGTCGTCGATACGTTGGGAGC	25320
OY	30901	ATCCGCGTAAAGTCTTGTGTGATCGAGGCGGCTGTTGAGATTATACGGCAGACATTAGCTT	30960
Db	25321	ATCCGCGTAAAGTCTTGTGTGATCGAGGCGGCTGTTGAGATTATACGGCAGACATTAGCTT	25380
OY	30961	TAGAGACGTGAGTTTGAAGAATTTGTTGTGCTCGCAAAATCTCTGGGAAACACCTCGCG	31020
Db	25381	TAGAGACGTGAGTTTGAAGAATTTGTTGTGCTCGCAAAATCTCTGGGAAACACCTCGCG	25440
OY	31021	TTGCATGCGCTTATCTGTGAGGCTACTGTCACACGCGCGTATTTGGGAGGCATTGGTT	31080
Db	25441	TTGCATGCGCTTATCTGTGAGGCTACTGTCACACGCGCGTATTTGGGAGGCATTGGTT	25500
OY	31081	TTGGTTCATGTACAGGCTTGGCAGAGCTCCAGACGAGATCTGTGTTTACCGTGAATCC	31140
Db	25501	TTGGTTCATGTACAGGCTTGGCAGAGCTCCAGACGAGATCTGTGTTTACCGTGAATCC	25560
OY	31141	CGGGTCTCCGGGGGCTTGTGACAAAGAAAGGCTGCCATGTGTCGGGGGCGATTTT	31200
Db	25561	CGGGTCTCTCGGGGCTATTTGTACAAAGAAAGGCTGCCATGTGTCGGGGGCGATTTT	25620
OY	31201	GGGTTGGGGTTTAGTGATGTTTGGGCAATGGCGGTTTCCCTGCGCGGGAGACCGCAGATC	31260
Db	25621	GGGTTGGGGTTTAGTGATGTTTGGGCAATGGCGGTTTCCCTGCGCGGGAGACCGCAGATC	25680
OY	31261	CCGCACCATGTTTGAATTTGTTTCTAGGTGGCGCATGACACACTTCTGTTTCCCGTTGGTG	31320
Db	25681	CCGCACCATGTTTGAATTTGTTTCTAGGTGGCGCATGACACACTTCTGTTTCCCGTTGGTG	25740
OY	31321	CGTTTGCAGACGTTGTCATGTTCTTACCGGACAGATTTTTCGAGCGTGGAAACCTT	31380
Db	25741	CGTTTGCAGACGTTGTCATGTTCTTACCGGACAGATTTTTCGAGCGTGGAAACCTT	25800
OY	31381	TAGCGCAGCTGTTGATTTGCAATCACAAACGCGTTTCTTCTTCTATCAGAGATGG	31440
Db	25801	TAGCGCAGCTGTTGATTTGCAATCACAAACGCGTTTCTTCTTCTATCAGAGATGG	25860

QY	31441	TTTGTGAATAAACAGACGTTGTTTGGATGGGGGCCCAAAAGTTGGCGTAAATTTGGCG	31500
Db	25861	TTTGTGAATAAACAGACGTTGTTTGGATGGGGGCCCAAAAGTTGGCGTAAATTTGGCG	25920
QY	31501	CGCGGTTTTCGGGGGATCTCATACAGATTTTTTCGACGGGCGATCTCCCAATTGGC	31560
Db	25921	CGCGGTTTTCGGGGGATCTCATACAGATTTTTTCGACGGGCGATCTCCCAATTGGC	25980
QY	31561	TAAAAAACCCGTTAAGGGCCGCCAGCGTGGTGTGTAATATGATAGCGGAACGCTGATG	31620
Db	25981	TAAAAAACCCGTTAAGGGCCGCCAGCGTGGTGTGTAATATGATAGCGGAACGCTGATG	26040
QY	31621	ACTCAGTATGAAATGTTTAAAGTGTTCGTGTTCTTAAATAGCAGCCAGGCGCTTACCG	31680
Db	26041	ACTCAGTATGAAATGTTTAAAGTGTTCGTGTTCTTAAATAGCAGCCAGGCGCTTACCG	26100
QY	31681	ACCGATTTCGGTCCCTTGGGGGGCCCTGGCTATATATGCGACCGGAATCTGTCAGTT	31740
Db	26101	ACCGATTTCGGTCCCTTGGGGGGCCCTGGCTATATATGCGACCGGAATCTGTCAGTT	26160
QY	31741	GGTTAAGCCCTGCGCATCGCTGATATATTTTATTCAGTTGGCGGAATATACAGCGCGC	31800
Db	26161	GGTTAAGCCCTGCGCATCGCTGATATATTTTATTCAGTTGGCGGAATATACAGCGCGC	26220
QY	31801	TTAGCGACGTCCTGAGTTCAATTACGTAGCAGCTTTTGTGATGTTGCTATTACGGTAA	31860
Db	26221	TTAGCGACGTCCTGAGTTCAATTACGTAGCAGCTTTTGTGATGTTGCTATTACGGTAA	26280
QY	31861	GCACACAAATCTGCTATTGCGGCTACCTAAGGAAACCTCGAAAAAAATCCTAAATTTAACCT	31920
Db	26281	GCACACAAATCTGCTATTGCGGCTACCTAAGGAAACCTCGAAAAAAATCCTAAATTTAACCT	26340
QY	31921	TTTTGGTTGGCCCTAGTGTGGGCGAATTAAAGAAACCTTAAATATATCATAAGGAGAC	31980
Db	26341	TTTTGGTTGGCCCTAGTGTGGGCGAATTAAAGAAACCTTAAATATATCATAAGGAGAC	26400
QY	31981	GGTGTATTGATTAAACCGTGGTATACGTAAAGTGGGCGGAGTTCCAGCCGTTTGGCGTG	32040
Db	26401	GGTGTATTGATTAAACCGTGGTATACGTAAAGTGGGCGGAGTTCCAGCCGTTTGGCGTG	26460
QY	32041	AGGCCGGAAGGGCTTCAGAGGTCGCGACGTCCTTAATGTGATTTGGAAACGCGATGGCGG	32100
Db	26461	AGGCCGGAAGGGCTTCAGAGGTCGCGACGTCCTTAATGTGATTTGGAAACGCGATGGCGG	26520
QY	32101	AAGAGGGGTCGGGTTTGGGAGAGAGTTTCCGTCAGATGGCGGATCGGAAGCCTAAGAT	32160
Db	26521	AAGAGGGGTCGGGTTTGGGAGAGAGTTTCCGTCAGATGGCGGATCGGAAGCCTAAGAT	26580
QY	32161	GGGACGAGTCTCCGACGATACTGATAGCCTGTGACACCGAAGCACCGATCTTGAATAG	32220
Db	26581	GGGACGAGTCTCCGACGATACTGATAGCCTGTGACACCGAAGCACCGATCTTGAATAG	26640
QY	32221	ATGATGTGTTCCTCCGTCGTAGATACGACGCGCTTAATGAGCCTCGGAAGTCAAACTATG	32280
Db	26641	ATGATGTGTTCCTCCGTCGTAGATACGACGCGCTTAATGAGCCTCGGAAGTCAAACTATG	26700
QY	32281	ACGATACCCAGCTCTCCGTCGCGGAACGCGCGGGAATTACTGACCCCGGACGCCCTGTATG	32340
Db	26701	ACGATACCCAGCTCTCCGTCGCGGAACGCGCGGGAATTACTGACCCCGGACGCCCTGTATG	26760
QY	32341	CACATCCGAGTGGCCCTTAAAGAGGGCGGTGTGTCGGGGCGGTGGCGCGCTCCCAAG	32400
Db	26761	CACATCCGAGTGGCCCTTAAAGAGGGCGGTGTGTCGGGGCGGTGGCGCGCGCTCCCAAG	26820
QY	32401	TGTCCGCGTTCGCGCTAGACCTTCATATGTGTGGACACAGAGTTTGGGGATAGAGAGA	32460
Db	26821	TGTCCGCGTTCGCGCTAGACCTTCATATGTGTGGACACAGAGTTTGGGGATAGAGAGA	26880
QY	32461	CGGGGACGCTTACCGGGGGCTCAGTTTTCCTCGAAGGCGGACGAAATTTGGGGAATATC	32520
Db	26881	CGGGGACGCTTACCGGGGGCTCAGTTTTCCTCGAAGGCGGACGAAATTTGGGGAATATC	26940
QY	32521	CGGAGCGCTACTACTACAGCGCCGCTTGAAGGCGGTACAAAGAAATTTTCACCTCCGGCG	32580

|||||
Db 26941 CGGACGCTACTACTACAGCCCGGTGAAGCGGTGACAGGAATTTCCACTCCGGC 27000
OY 32581 GTAGGGGTGCAATCTCGGGACCTCTGCGACAAAACCTAGTCAGGTCGGGGTTAACAC 32640
Db 27001 GTAGGGGTGCAATCTCGGGACCTCTGCGACAAAACCTAGTCAGGTCGGGGTTAACAC 27060
OY 32641 GTAAAGCTAAAAAGCGCGTGTAGCTTTAAACTGTGTGGGATAAAGGACGATG 32700
Db 27061 GTAAAGCTAAAAAGCGCGTGTAGCTTTAAACTGTGTGGGATAAAGGACGATG 27120
OY 32701 ATGTAGAGTTGATGTACCCAGGCGGTACCGTCGGGTTCAATCTCATGACGCCATC 32760
Db 27121 ATGTAGAGTTGATGTACCCAGGCGGTGTACCGTCGGGTTCAATCTCATGACGCCATC 27180
OY 32761 CTATACGGAATATGAAATGCTTTTATCTATCTAGAGGGGTCATGGGTGTGAA 32820
Db 27181 CTATACGGAATATGAAATGCTTTTATCTATCTAGAGGGGTCATGGGTGTGAA 27240
OY 32821 AAACAGCGCTATTAATTCATAGACTGGCATGGTCCGAGGAAAAGCTTAACCTGC 32880
Db 27241 AAACAGCGCTATTAATTCATAGACTGGCATGGTCCGAGGAAAAGCTTAACCTGC 27300
OY 32881 CCGAGCCCATGAATTTTGGAGCGTGTATTATTCAAATTTGCTTAAGACAGCCAGCA 32940
Db 27301 CCGAGCCCATGAATTTTGGAGCGTGTATTATTCAAATTTGCTTAAGACAGCCAGCA 27360
OY 32941 TAGTTAAGCAAGGCCACCGGGAATTTGATCATCTTCTGCTGCTATACGGGTCTAGA 33000
Db 27361 TAGTTAAGCAAGGCCACCGGGAATTTGATCATCTTCTGCTGCTATACGGGTCTAGA 27420
OY 33001 GCAAGTTTGGCTTACCGTTTGTGCGACAGCCCGCATGGTGGCAACCTGCAACGCT 33060
Db 27421 GCAAGTTTGGCTTACCGTTTGTGCGACAGCCCGCATGGTGGCAACCTGCAACGCT 27480
OY 33061 GCGTGTGGGAAACGGTAGCACAAGCAGCGAATTTGATTTTGAACAGACACCTAC 33120
Db 27481 GCGTGTGGGAAACGGTAGCACAAGCAGCGAATTTGATTTTGAACAGACACCTAC 27540
OY 33121 TGTCCGCAACGGTGTGTTTCCGTGCTACGTTAAATATACAGAGGCTAACGCCGATC 33180
Db 27541 TGTCCGCAACGGTGTGTTTCCGTGCTACGTTAAATATACAGAGGCTAACGCCGATC 27600
OY 33181 ATCTGTTCAAAATCTATCTCTTTTCTCGGCACAGCGGCGATGTGCTTTGCTAAA 33240
Db 27601 ATCTGTTCAAAATCTATCTCTTTTCTCGGCACAGCGGCGATGTGCTTTGCTAAA 27660
OY 33241 CGCTCACAAGTTCGAGGCGCAGAGCGCATTTCAAAAGTCGAGGCCGTAAAGAGAAAAG 33300
Db 27661 CGCTCACAAGTTCGAGGCGCAGAGCGCATTTCAAAAGTCGAGGCCGTAAAGAGAAAAG 27720
OY 33301 GAATCAGCGAAATCTACTTGGAGAGGTAGCGTGGGCGTACCATGCCGTCTCTAGCT 33360
Db 27721 GAATCAGCGAAATCTACTTGGAGAGGTAGCGTGGGCGTACCATGCCGTCTCTAGCT 27780
OY 33361 GGGGTGATGATCAATATCTCAGCAGCGAGCAAAATGTTCAAGTGTGTACAAATGCTGT 33420
Db 27781 GGGGTGATGATCAATATCTCAGCAGCGAGCAAAATGTTCAAGTGTGTGTACAAATGCTGT 27840
OY 33421 CCATAGAGCATATGCAATATGAAATTCAGATTGACTATCGTTTCTAACCCCTAACAA 33480
Db 27841 CCATAGAGCATATGCAATATGAAATTCAGATTGACTATCGTTTCTAACCCCTAACAA 27900
OY 33481 AACTACATGAACAGAGTATGATACCATGTGGGAGAAATGTATATCGGTTAAAGAAC 27960
Db 27901 AACTACATGAACAGAGTATGATACCATGTGGGAGAAATGTATATCGGTTAAAGAAC 27960
OY 33541 ACGTACCTTAATGGAGGTGTTGGAGCTCTTTAAAGAGCTACGAAGGCTCAAAATTT 33600
Db 27961 ACGTACCTTAATGGAGGTGTTGGAGCTCTTTAAAGAGCTACGAAGGCTCAAAATTT 28020
OY 33601 TAATTTGTGACGAGGAGACATCTAGATGATGCTGTGGCTCTGGGAAATATTTATG 33660
|||||

Db 28021 TAATTTGTGACGAGGAGAACATCTAGATGATGCTGTGGCTCTGGGAAATATTTATG 28080
OY 33661 GCGAGGTGATGTCAATATGAGCTATTAAACGAGCAGTGAACCTGGCCAGCTTTGAAA 33720
Db 28081 GCGAGGTGATGTCAATATGAGCTATTAAACGAGCAGTGAACCTGGCCAGCTTTGAAA 28140
OY 33721 GCTACATTCAAAAGCTTAACCAATTTGGAAGGCAATGGCGGATATGATTTATTTT 33780
Db 28141 GCTACATTCAAAAGCTTAACCAATTTGGAAGGCAATGGCGGATATGATTTATTTT 28200
OY 33781 TTTACTATTAATGAGTGTCTGTAAAGCAAAATGCTATAGATGAAATTAATGTA 33840
Db 28201 TTTACTATTAATGAGTGTCTGTAAAGCAAAATGCTATAGATGAAATTAATGTA 28260
OY 33841 GAGTTGCAATTTAATGGAACAATTTACCAATTTAATTTGAGAAACGTAAAGCAAAATTA 33900
Db 28261 GAGTTGCAATTTAATGGAACAATTTACCAATTTAATTTGAGAAACGTAAAGCAAAATTA 28320
OY 33901 ACATCTATTGTATGAGAGATGCGGTGATGACATTTCTTACTGTGGAACATGTCTGTG 33960
Db 28321 ACATCTATTGTATGAGAGATGCGGTGATGACATTTCTTACTGTGGAACATGTCTGTG 28380
OY 33961 ACTTTGAAAAAAGAAAAAGTTTGTGCGATCAAGTATATGTTAATGTCATATATATGAC 34020
Db 28381 ACTTTGAAAAAAGAAAAAGTTTGTGCGATCAAGTATATGTTAATGTCATATATGAC 28440
OY 34021 TATACATTTTGTAAATCTTCAAGTACCATGATGAATTAACCTTACGTTGATTTATATAC 34080
Db 28441 TATACATTTTGTAAATCTTCAAGTACCATGATGAATTAACCTTACGTTGATTTATATAC 28500
OY 34081 AGTTCTTTGACAGTTTACTGTGGAATTTATGTAAAGACACATGCTTTAAACACAGC 34140
Db 28501 AGTTCTTTGACAGTTTACTGTGGAATTTATGTAAAGACACATGCTTTAAACACAGC 28560
OY 34141 GTTTTATTAAGAAAAGTGAATTTATTAACCACTGACAAACATTAATGATCTTTTATAC 34200
Db 28561 GTTTTATTAAGAAAAGTGAATTTATTAACCACTGACAAACATTAATGATCTTTTATAC 28620
OY 34201 GCGGAAAAATTAATGCAAGAAATGTTCAAGATTTACTTTGATTTCAATGATATAT 34260
Db 28621 GCGGAAAAATTAATGCAAGAAATGTTCAAGATTTACTTTGATTTCAATGATATAT 28680
OY 34261 TCCGCAATTAATACGAAATTTGATATAGTATACGTTAACAAATTAAGTATAATCA 34320
Db 28681 TCCGCAATTAATACGAAATTTGATATAGTATACGTTAACAAATTAAGTATAATCA 28740
OY 34321 AATATGCAATGTGTGCACTGTGTTGGTGTCTTACACATTTCCAGCGTTAAAGGC 34380
Db 28741 AATATGCAATGTGTGCACTGTGTTGGTGTCTTACACATTTCCAGCGTTAAAGGC 28800
OY 34381 TATGTATCTTATCGTATTTATGTTGCTTAAATTTCAAACTATGCTGGGTATAT 34440
Db 28801 TATGTATCTTATCGTATTTATGTTGCTTAAATTTCAAACTATGCTGGGTATAT 28860
OY 34441 GCGCGGAATCTTATATATCTCTGATTTGGCATTTTACCAAAAAATTTTACAGAAATG 34500
Db 28861 GCGCGGAATCTTATATATCTCTGATTTGGCATTTTACCAAAAAATTTTACAGAAATG 28920
OY 34501 TTTGTTTCAATTATATATATGATGCTTAAATGCTTATATCTCAAAAGAAACTTTTG 34560
Db 28921 TTTGTTTCAATTATATATATGATGCTTAAATGCTTATATCTCAAAAGAAACTTTTG 28980
OY 34561 GCTATGGAAGAAAGGTCCTGTCAAAATCCTTCAATGAAATGATATCTATCTTC 34620
Db 28981 GCTATGGAAGAAAGGTCCTGTCAAAATCCTTCAATGAAATGATATCTATCTTC 29040
OY 34621 TTTTGTGAAGTTACGACGTAATTTTATTTATTAATAATCTTCAAAACAGCAATTA 34680
Db 29041 TTTTGTGAAGTTACGACGTAATTTTATTTATTAATAATCTTCAAAACAGCAATTA 29100
OY 34681 GTTAAAGTTGGGTGTGTGTACAGGATGTTACAGGCTTGAAGATTTAATGCAATTTATTA 34740
Db 29101 GTTAAAGTTGGGTGTGTGTGTACAGGATGTTACAGGCTTGAAGATTTAATGCAATTTATTA 29160
|||||

DE RRV macrophage inflammatory protein (MIP) DNA sequence SEQ ID NO:22.
 XX
 XX Macaca mulatta rhadinovirus 17577; RRV; rhesus macaque rhadinovirus;
 KW genome; Kaposi's sarcoma-associated herpesvirus; KSHV; interleukin 6;
 KW IL-6; macrophage inflammatory protein; MIP; diagnosis; vaccine;
 KW cytostatic; anti-HIV; gene therapy; infection; Kaposi's sarcoma;
 KW lymphoproliferative disorder; B-cell hyperplasia; lymphadenopathy;
 KW splenomegaly; hypergammaglobulinemia; autoimmune hemolytic anaemia;
 KW ds.
 XX
 OS Macaca mulatta rhadinovirus 17577.
 XX
 XX WO200028040-A2.
 PN
 XX 18-MAY-2000.
 PD
 XX 05-NOV-1999; 99WO-US26260.
 XX
 XX 06-NOV-1998; 98US-0107507.
 PR 20-NOV-1998; 98US-0109409.
 XX
 XX (UYOR-) UNIV OREGON HEALTH SCI.
 PA
 XX Wong SW, Axthelm MK, Searles RP;
 PI
 XX MPI: 2000-376552/32.
 DR P-PSDB: AAB53213.
 XX
 XX New rhesus rhadino virus for producing non-human primate model useful
 PT for testing potential treatments and efficacy of the candidate vaccine
 PT for conditions associated with RRV infection -
 XX
 XX Claim 9; Fig 11; 141pp; English.
 PS
 XX The present invention describes a novel rhesus macaque rhadinovirus
 CC called macaca mulatta rhadinovirus 17577 (RRV). AAC64754 represents the
 CC RRV genome sequence, and AAB53123 to AAB53204 represent the proteins
 CC encoded by the genome sequence. The present invention also specifically
 CC claims the individual open reading frame (ORF) nucleotide sequences from
 CC the genome which encode the individual proteins, but these sequences are
 CC not given. A non-human animal infected with RRV can be used for testing
 CC the efficacy of drug in the treatment of condition associated with
 CC infection with RRV such as Kaposi's sarcoma, lymphoproliferative
 CC disorders, B-cell hyperplasia, lymphadenopathy, splenomegaly,
 CC hypergammaglobulinemia or autoimmune hemolytic anaemia, by
 CC administering the drug to an immuno-compromised non-human primate
 CC preferably Rhesus macaque monkey obtained by as a result of infection
 CC by Simian Immunodeficiency Virus (SIV). RRV is useful for producing
 CC non-human primate model for testing potential treatments for conditions
 CC associated with RRV infection. It is also useful for testing the
 CC efficacy of the candidate vaccine against RRV infection or conditions
 CC associated with its infection by administering the vaccine to the
 CC subject capable of infection with RRV, inoculating the subject with RRV
 CC and observing the effect of vaccine. AAC64755 to AAC64765 and AAB53205
 CC to AAB53213 represent sequence used in the exemplification of the
 CC present invention.
 CC
 XX Sequence 348 BP; 67 A; 91 C; 105 G; 85 T; 0 other;
 SQ
 Query Match 1.0%; Score 348; DB 21; Length 348;
 Best Local Similarity 100.0%; Pred. No. 5,8e-134;
 Matches 348; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 228 ATTGGCACACACTTTTACCCGGCGAGTGTTTATATACAGCGGTCCACGACACTG 169
 QY 22425 CGACGAGTGTGGAGTAAGACACCTAAACCGGGTGGCGCAGATGATTACATACC 22484
 DB 168 CGACGAGTGTGGAGTAAGACACCTAAACCGGGTGGCGCAGATGATTACATACC 109
 QY 22485 CAACACGACGAGTTGGGGCGGGTCCGTCTATGAGCCCATAGGAAAGGCAATATCAG 22544
 DB 108 CAACACGACGAGTTGGGGCGGGTCCGTCTATGAGCCCATAGGAAAGGCAATATCAG 49
 QY 22545 TACACACGCGACACCGCAAAAACGACACGAAAGGCCCTCAT 22592
 DB 48 TACACACGCGAACCACCGCAAAAACGACACGAAAGGCCCTCAT 1
 RESULT 5
 AA164294
 ID AA164294 standard; DNA; 630 BP.
 AC AA164294;
 XX
 XX 22-APR-2002 (first entry)
 DT
 XX JMHV nucleotide sequence from cosmid 3 fragment 5 T7.
 DE
 XX RRV; rhesus rhadinovirus; Japanese macaque virus; multiple sclerosis;
 KW JMHV; cytostatic; antiallergic; antiallergic; dermatological;
 KW vulnerrary; gene therapy; leucopenia; thrombocytopenia;
 KW inflammatory disease; asthma; allergy; dermatitis; ds.
 XX
 OS Japanese macaque herpesvirus.
 XX
 XX WO200188203-A1.
 PN
 XX 22-NOV-2001.
 PD
 XX 17-MAY-2001; 2001WO-US16274.
 PF
 XX 18-MAY-2000; 2000US-205652P.
 PR
 XX (UYOR-) UNIV OREGON HEALTH SCI.
 PA
 XX Wong SW, Axthelm MK;
 PI
 XX MPI: 2002-075323/10.
 DR
 XX New Japanese macaque virus (JMHV) and nucleic acid sequences of open
 XX reading frames in virus, useful for producing animal models for
 PT assessing efficacy of drugs for treatment or prevention of multiple
 PT sclerosis -
 XX
 XX Claim 9; Page 67; 175pp; English.
 PS
 XX The invention relates to an isolated virus (Japanese macaque virus (JMHV)
 XX as deposited with ATCC as deposit accession number PTA-1884. Non-human
 XX primate models infected with the new virus are useful for testing the
 XX efficacy of a drug for treating a condition associated with JMHV,
 XX preferably a drug used to treat multiple sclerosis. This involves
 XX administering the drug to a non-human primate infected with JMHV and
 XX observing the non-human primate to determine if the drug prevents or
 XX reduces the presentation of one or more symptoms associated with JMHV
 XX infection. Methods of the invention are also useful for testing the
 XX efficacy of candidate vaccine against JMHV infection, or conditions
 XX associated with JMHV infection e.g., multiple sclerosis. Methods of the
 XX invention are useful for diagnosing the presence of JMHV or a related
 XX virus in a biological specimen. JMHV genome possesses an interleukin
 XX (IL)-6 gene which encodes IL-6 proteins. The IL-6 proteins may be used
 XX to induce stimulation of haematopoietic stem cells to enhance
 XX proliferation, differentiation and terminal maturation of erythroid
 XX cells from haematopoietic cells. Thus, JMHV IL-6 may be used in vivo or
 XX ex vivo to treat diseases involving leukaemia or thrombocytopenia.
 XX The JMHV IL-6 may also be used to stimulate growth of megakaryocytes
 XX and platelets, and for the inhibition of tumour growth and for treating

DE JMHV cosmid 3 EcoRI fragment 1 Kpn 1 fragment 2 SP6.
 XX
 XX RRV; rhesus rhadinovirus; Japanese macaque virus; multiple sclerosis;
 KM JMHV; cytostatic; antiallergic; antiallergic; dermatological;
 KM vulnery; gene therapy; leucopenia; thrombocytopenia;
 KM inflammatory disease; asthma; allergy; dermatitis; ds.
 XX
 OS Japanese macaque herpesvirus.
 XX
 FH Key Location/Qualifiers
 FT 2..496
 FT CDS /*tag= a
 FT /partial
 FT /product= "DNA polymerase"
 FT /transl_except= (pos:440..442, aa:Xaa)
 FT /note= "no start or stop codon present; Xaa is unknown"
 XX
 PN W0200188203-A1.
 PD 22-NOV-2001.
 XX
 PF 17-MAY-2001; 2001WO-US16274.
 XX
 PR 18-MAY-2000; 2000US-205652P.
 XX
 PA (UYOR-) UNIV OREGON HEALTH SCT.
 XX
 PI Wong SW, Axthelm MK;
 XX
 DR WPI: 2002-075323/10.
 DR P-PSDB: AAG78588.
 XX
 PT New Japanese macaque virus (JMHV) and nucleic acid sequences of open
 PT reading frames in virus, useful for producing animal models for
 PT assessing efficacy of drugs for treatment or prevention of multiple
 PT sclerosis
 XX
 PS Claim 9; Page 70; 175pp; English.
 CC The invention relates to an isolated virus (Japanese macaque virus (JMHV)
 CC as deposited with ATCC as deposit accession number PTA-1884. Non-human
 CC primate models infected with the new virus are useful for testing the
 CC efficacy of a drug for treating a condition associated with JMHV,
 CC preferably a drug used to treat multiple sclerosis. This involves
 CC administering the drug to a non-human primate infected with JMHV and
 CC observing the non-human primate to determine if the drug prevents or
 CC reduces the presentation of one or more symptoms associated with JMHV
 CC infection. Methods of the invention are also useful for testing the
 CC efficacy of candidate vaccine against JMHV infection, or conditions
 CC associated with JMHV infection e.g., multiple sclerosis. Methods of the
 CC invention are useful for diagnosing the presence of JMHV or a related
 CC virus in a biological specimen. JMHV genome possesses an interleukin
 CC (IL)-6 gene which encodes IL-6 proteins. The IL-6 proteins may be used
 CC to induce stimulation of haematopoietic stem cells to enhance
 CC proliferation, differentiation and terminal maturation of erythroid
 CC cells from haematopoietic cells. Thus, JMHV IL-6 may be used in vivo or
 CC ex vivo to treat diseases involving leukopenia or thrombocytopenia.
 CC The JMHV IL-6 may also be used to stimulate growth of megakaryocytes
 CC and platelets, and for the inhibition of tumour growth and for treating
 CC leukemia. Additionally, JMHV IL-6 may be used for research, diagnostic
 CC purposes, to produce antibodies for diagnostic purposes to diagnose
 CC diseases characterized by increased or decreased production of IL-6,
 CC and as a targeting molecule for identifying cells with receptors for
 CC IL-6, etc. The JMHV macrophage inflammatory protein (MIP protein) is
 CC useful for treating wounds and other inflammatory diseases including
 CC asthma, allergies and dermatitis. They are also useful for producing
 CC antibodies for diagnostic purposes, and as a targeting molecule for
 CC identifying cells with receptors for MIP, etc. Nucleic acids encoding
 CC the JMHV proteins are useful in gene therapy techniques for treating
 CC the above mentioned conditions. The current sequence represents the
 CC JMHV Orf1 nucleotide sequence from cosmid 3 EcoRI fragment Kpn 1
 CC fragment 2 SP6. Orf 10 encodes a DNA polymerase.
 CC Note: In example 22 of the specification there is a protein sequence

CC (see AAG78599) that has been allocated the same sequence identification
 CC number as this sequence. This sequence is also from Orf 10.
 CC
 XX
 SQ Sequence 497 BP; 98 A; 162 C; 146 G; 90 T; 1 other;
 Query Match 0.3%; Score 107; DB 24; Length 497;
 Best Local Similarity 100.0%; Pred. No. 7.8e-34;
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 14746 GAAATCAGCTATCGTCCGGTTCATGCTTCGACCTTCAGACCGCCTGTCGCGTGC 14805
 DB 269 GAAATCAGCTATCGTCCGGTTCATGCTTCGACCTTCAGACCGCCTGTCGCGTGC 328
 QY 14806 GGGTCGAGGCTTTCGAGTCAAGCTGACGCGCTTCCCGGTTGCT 14852
 DB 329 GGGTCGAGGCTTTCGAGTCAAGCTGACGCGCGTTCGCGTTCGT 375
 RESULT 8
 AAI64298
 ID AAI64298 standard; DNA; 398 BP.
 XX
 AC AAI64298;
 XX
 DT 22-APR-2002 (first entry)
 XX
 DE JMHV Orf7 nucleotide sequence from cosmid 3 fragment 1 T7.
 XX
 XX RRV; rhesus rhadinovirus; Japanese macaque virus; multiple sclerosis;
 KM JMHV; cytostatic; antiallergic; antiallergic; dermatological;
 KM vulnery; gene therapy; leucopenia; thrombocytopenia;
 KM inflammatory disease; asthma; allergy; dermatitis; ds.
 XX
 OS Japanese macaque herpesvirus.
 XX
 FH Key Location/Qualifiers
 FT 1..396
 FT CDS /*tag= a
 FT /product= "transport protein"
 FT /partial
 FT /note= "no start or stop codon present"
 XX
 PN W0200188203-A1.
 PD 22-NOV-2001.
 XX
 PF 17-MAY-2001; 2001WO-US16274.
 XX
 PR 18-MAY-2000; 2000US-205652P.
 XX
 PA (UYOR-) UNIV OREGON HEALTH SCT.
 XX
 PI Wong SW, Axthelm MK;
 XX
 DR WPI: 2002-075323/10.
 DR P-PSDB: AAG78586.
 XX
 PT New Japanese macaque virus (JMHV) and nucleic acid sequences of open
 PT reading frames in virus, useful for producing animal models for
 PT assessing efficacy of drugs for treatment or prevention of multiple
 PT sclerosis
 XX
 PS Claim 9; Page 69; 175pp; English.
 CC The invention relates to an isolated virus (Japanese macaque virus (JMHV)
 CC as deposited with ATCC as deposit accession number PTA-1884. Non-human
 CC primate models infected with the new virus are useful for testing the
 CC efficacy of a drug for treating a condition associated with JMHV,
 CC preferably a drug used to treat multiple sclerosis. This involves
 CC administering the drug to a non-human primate infected with JMHV and
 CC observing the non-human primate to determine if the drug prevents or
 CC reduces the presentation of one or more symptoms associated with JMHV
 CC infection. Methods of the invention are also useful for testing the

CC efficacy of candidate vaccine against JMHV infection, or conditions
CC associated with JMHV infection e.g., multiple sclerosis. Methods of the
CC invention are useful for diagnosing the presence of JMHV or a related
CC virus in a biological specimen. JMHV genome possesses an interleukin
CC (IL)-6 gene which encodes IL-6 proteins. The IL-6 proteins may be used
CC to induce stimulation of hematopoietic stem cells to enhance
CC proliferation, differentiation and terminal maturation of erythroid
CC cells from hematopoietic cells. Thus, JMHV IL-6 may be used in vivo or
CC ex vivo to treat diseases involving leukopenia or thrombocytopenia.
CC The JMHV IL-6 may also be used to stimulate growth of megakaryocytes
CC and platelets, and for the inhibition of tumour growth and for treating
CC leukemia. Additionally, JMHV IL-6 may be used for research, diagnostic
CC purposes, to produce antibodies for diagnostic purposes to diagnose
CC diseases characterized by increased or decreased production of IL-6,
CC and as a targeting molecule for identifying cells with receptors for
CC IL-6, etc. The JMHV macrophage inflammatory protein (MIP protein) is
CC useful for treating wounds and other inflammatory diseases including
CC asthma, allergies and dermatitis. They are also useful for producing
CC antibodies for diagnostic purposes, and as a targeting molecule for
CC identifying cells with receptors for MIP, etc. Nucleic acids encoding
CC the JMHV proteins are useful in gene therapy techniques for treating
CC the above mentioned conditions. The current sequence represents the
CC JMHV Orf7 nucleotide sequence from cosmid 3 fragment 1 T7. Orf 7
CC encodes a transport protein.

XX Sequence 398 BP; 111 A; 107 C; 108 G; 72 T; 0 other;

Query Match 0.2%; Score 74; DB 24; Length 398;
Best Local Similarity 100.0%; Pred. No. 4.1e-20;

Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10731 TATCGCAAGAACAGTACATGAAAGAGTGGCGGCGCTTTAAAAAATAACAGAG 10790
DB 265 TATCGCAAGAACAGTACATGAAAGAGTGGCGGCGCTTTAAAAAATAACAGAG 324

OY 10791 TGTCTGCAGACGCA 10804
DB 325 TGTCTGCAGACGCA 338

RESULT 9

AA164292/C
ID AA164292 standard; DNA; 426 BP.

XX AA164292;

XX AC
XX 22-APR-2002 (first entry)

DE JMHV Orf21 nucleotide sequence from cosmid 3 fragment 7 T7.

XX RRV: rhesus rhadinovirus; Japanese macaque virus; multiple sclerosis;
XX JMHV: cytostatic; antileukemic; antiallergic; dermatological;
XX inflammatory; gene therapy; leucopenia; thrombocytopenia;
XX inflammatory disease; asthma; allergy; dermatitis; ds.

OS Japanese macaque herpesvirus.

XX WO20018203-A1.

XX 22-NOV-2001.

XX 17-MAY-2001; 2001WO-US16274.

XX 18-MAY-2000; 2000US-205652P.

XX (UYOR-) UNIV OREGON HEALTH SCI.

XX Mong SW, Axthelm MK;

XX WPI; 2002-075323/10.

PT New Japanese macaque virus (JMHV) and nucleic acid sequences of open
reading frames in virus, useful for producing animal models for

PT assessing efficacy of drugs for treatment or prevention of multiple
PT sclerosis
XX
XX Claim 9; Page 66; 175pp; English.

XX The invention relates to an isolated virus (Japanese macaque virus (JMHV))
CC as deposited with ATCC as deposit accession number PTA-1884. Non-human
CC primate models infected with the new virus are useful for testing the
CC efficacy of a drug for treating a condition associated with JMHV,
CC preferably a drug used to treat multiple sclerosis. This involves
CC administering the drug to a non-human primate infected with JMHV and
CC observing the non-human primate to determine if the drug prevents or
CC reduces the presentation of one or more symptoms associated with JMHV
CC infection. Methods of the invention are also useful for testing the
CC efficacy of candidate vaccine against JMHV infection, or conditions
CC associated with JMHV infection e.g., multiple sclerosis. Methods of the
CC invention are useful for diagnosing the presence of JMHV or a related
CC virus in a biological specimen. JMHV genome possesses an interleukin
CC (IL)-6 gene which encodes IL-6 proteins. The IL-6 proteins may be used
CC to induce stimulation of hematopoietic stem cells to enhance
CC proliferation, differentiation and terminal maturation of erythroid
CC cells from hematopoietic cells. Thus, JMHV IL-6 may be used in vivo or
CC ex vivo to treat diseases involving leukopenia or thrombocytopenia.
CC The JMHV IL-6 may also be used to stimulate growth of megakaryocytes
CC and platelets, and for the inhibition of tumour growth and for treating
CC leukemia. Additionally, JMHV IL-6 may be used for research, diagnostic
CC purposes, to produce antibodies for diagnostic purposes to diagnose
CC diseases characterized by increased or decreased production of IL-6,
CC and as a targeting molecule for identifying cells with receptors for
CC IL-6, etc. The JMHV macrophage inflammatory protein (MIP protein) is
CC useful for treating wounds and other inflammatory diseases including
CC asthma, allergies and dermatitis. They are also useful for producing
CC antibodies for diagnostic purposes, and as a targeting molecule for
CC identifying cells with receptors for MIP, etc. Nucleic acids encoding
CC the JMHV proteins are useful in gene therapy techniques for treating
CC the above mentioned conditions. The current sequence represents the
CC JMHV Orf21 nucleotide sequence from cosmid 3 fragment 7 T7. Orf 21
CC encodes a thymidine kinase.
CC Note: In the specification the deduced amino acid sequence of this
CC fragment is also given (see AMG78581). However, the sequence here does
CC not decode to the amino acid sequence in that record.

XX Sequence 426 BP; 101 A; 111 C; 104 G; 110 T; 0 other;

Query Match 0.2%; Score 71; DB 24; Length 426;
Best Local Similarity 99.2%; Pred. No. 7.2e-19;

Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 33222 GATGTGCTGTTTGTAAACGCTCAACAGTTTCGAGGCGACAGCGCATTTCAAGTGA 33281
DB 227 GATGTGCTGTTTGTAAACGCTCAACAGTTTCGAGGCGACAGCGCATTTCAAGTGA 168

OY 33282 GCCCGTAAGGAAGAAAGAAATCAGCGAAACTTCTGCGACAGGTAGCGTGGCGTAC 33341
DB 167 GCCCGTAAGGAAGAAAGAAATCAGCGAAACTTCTGCGACAGGTAGCGTGGCGTAC 108

OY 33342 CA 33343

DB 107 CA 106

RESULT 10

AA164293
ID AA164293 standard; DNA; 524 BP.

XX AA164293;

XX 22-APR-2002 (first entry)

XX JMHV Orf21 nucleotide sequence from cosmid 3 fragment 7 SP6.

XX RRV: rhesus rhadinovirus; Japanese macaque virus; multiple sclerosis;
XX JMHV: cytostatic; antileukemic; antiallergic; dermatological;
XX

KM vulnery; gene therapy; leucopenia; thrombocytopenia;
KM inflammatory disease; asthma; allergy; dermatitis; ds.
XX Japanese macaque herpesvirus.
XX
FH Key Location/Qualifiers
FT CDS 2.523
FT /tag= a
FT /product= "thymidine kinase"
FT /partial
FT /note= "no start or stop codon present"
XX
XX MO200188203-A1.
XX
XX 22-NOV-2001.
XX
XX 17-MAY-2001; 2001WO-US16274.
XX
XX 18-MAY-2000; 2000US-205652P.
XX
XX (UYOR-) UNIV OREGON HEALTH SCI.
XX
XX Wong SW, Axthelm MK;
XX
XX MPI: 2002-075323/10.
XX P-PSDB; AAG78582.
XX
XX
XX New Japanese macaque virus (JMHV) and nucleic acid sequences of open
XX reading frames in virus, useful for producing animal models for
XX assessing efficacy of drugs for treatment or prevention of multiple
XX sclerosis
XX
XX
XX Claim 9; Page 66-67; 175pp; English.
XX
XX The invention relates to an isolated virus (Japanese macaque virus (JMHV)
XX as deposited with ATCC as deposit accession number PTA-1884. Non-human
XX primate models infected with the new virus are useful for testing the
XX efficacy of a drug used for treating a condition associated with JMHV,
XX preferably a drug used to treat multiple sclerosis. This involves
XX administering the drug to a non-human primate infected with JMHV and
XX observing the non-human primate to determine if the drug prevents or
XX reduces the presentation of one or more symptoms associated with JMHV
XX infection. Methods of the invention are also useful for testing the
XX efficacy of candidate vaccine against JMHV infection, or conditions
XX associated with JMHV infection e.g., multiple sclerosis. Methods of the
XX invention are useful for diagnosing the presence of JMHV or a related
XX virus in a biological specimen. JMHV genome possesses an interleukin
XX (IL)-6 gene which encodes IL-6 proteins. The IL-6 proteins may be used
XX to induce stimulation of haematopoietic stem cells to enhance
XX proliferation, differentiation and terminal maturation of erythroid
XX cells from haematopoietic cells. Thus, JMHV IL-6 may be used in vivo or
XX ex vivo to treat diseases involving leukopenia or thrombocytopenia.
XX The JMHV IL-6 may also be used to stimulate growth of megakaryocytes
XX and platelets, and for the inhibition of tumour growth and for treating
XX leukemia. Additionally, JMHV IL-6 may be used for research, diagnostic
XX purposes, to produce antibodies for diagnostic purposes to diagnose
XX diseases characterized by increased or decreased production of IL-6,
XX and as a targeting molecule for identifying cells with receptors for
XX IL-6, etc. The JMHV macrophage inflammatory protein (MIP protein) is
XX useful for treating wounds and other inflammatory diseases including
XX asthma, allergies and dermatitis. They are also useful for producing
XX antibodies for diagnostic purposes, and as a targeting molecule for
XX identifying cells with receptors for MIP, etc. Nucleic acids encoding
XX the JMHV proteins are useful in gene therapy techniques for treating
XX the above mentioned conditions. The current sequence represents the
XX JMHV Orf21 nucleotide sequence from cosmid 3 fragment 7 Sp6. Orf 21
XX encodes a thymidine kinase.
XX
XX Sequence 524 BP; 131 A; 132 C; 136 G; 125 T; 0 other;
XX
XX Query Match 0.2%; Score 71; DB 24; Length 524;
XX Best Local Similarity 99.2%; Pred. No. 7.1e-19;
XX Matches 121; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 33222 GATGTGTCGTTTGTCTAAGCTCAACAGTTCGAGCGCACAGCGCATTCGAAGTGA 33281
OY |||||||
Db 389 GATGTGTCGTTTGTCTAAGCTCAACAGTTCGAGCGCACAGCGCATTCGAAGTGA 448
OY 33282 GGCCGCTAAGGAGAAAGAAAGCATTCACGCAAACTCTTCCGACAGTACCCTGGCGCTAC 33341
OY |||||||
Db 449 GGCCGCAAGGAGAAAGAAAGCATTCACGCAAACTCTTCCGACAGTACCCTGGCGCTAC 508
OY 33342 CA 33343
OY ||
Db 509 CA 510
XX
XX RESULT 11
XX ABA97191/C
XX ID ABA97191 standard; DNA; 314 BP.
XX
XX ABA97191;
XX
XX 22-APR-2002 (first entry)
XX
XX JMHV cosmid 3 EcoRI fragment 1 kpn 1 fragment 2 T7.
XX
XX RRV; rhesus rhadinovirus; Japanese macaque virus; multiple sclerosis;
XX JMHV; cytostatic; antileukemic; antiallergic; dermatological;
XX vulnery; gene therapy; leucopenia; thrombocytopenia;
XX inflammatory disease; asthma; allergy; dermatitis; ds.
XX
XX Japanese macaque herpesvirus.
XX
XX WO200188203-A1.
XX
XX 22-NOV-2001.
XX
XX 17-MAY-2001; 2001WO-US16274.
XX
XX 18-MAY-2000; 2000US-205652P.
XX
XX (UYOR-) UNIV OREGON HEALTH SCI.
XX
XX Wong SW, Axthelm MK;
XX
XX MPI: 2002-075323/10.
XX
XX
XX New Japanese macaque virus (JMHV) and nucleic acid sequences of open
XX reading frames in virus, useful for producing animal models for
XX assessing efficacy of drugs for treatment or prevention of multiple
XX sclerosis
XX
XX
XX Claim 9; Page 71; 175pp; English.
XX
XX The invention relates to an isolated virus (Japanese macaque virus (JMHV)
XX as deposited with ATCC as deposit accession number PTA-1884. Non-human
XX primate models infected with the new virus are useful for testing the
XX efficacy of a drug used for treating a condition associated with JMHV,
XX preferably a drug used to treat multiple sclerosis. This involves
XX administering the drug to a non-human primate infected with JMHV and
XX observing the non-human primate to determine if the drug prevents or
XX reduces the presentation of one or more symptoms associated with JMHV
XX infection. Methods of the invention are also useful for testing the
XX efficacy of candidate vaccine against JMHV infection, or conditions
XX associated with JMHV infection e.g., multiple sclerosis. Methods of the
XX invention are useful for diagnosing the presence of JMHV or a related
XX virus in a biological specimen. JMHV genome possesses an interleukin
XX (IL)-6 gene which encodes IL-6 proteins. The IL-6 proteins may be used
XX to induce stimulation of haematopoietic stem cells to enhance
XX proliferation, differentiation and terminal maturation of erythroid
XX cells from haematopoietic cells. Thus, JMHV IL-6 may be used in vivo or
XX ex vivo to treat diseases involving leukopenia or thrombocytopenia.
XX The JMHV IL-6 may also be used to stimulate growth of megakaryocytes
XX and platelets, and for the inhibition of tumour growth and for treating
XX leukemia. Additionally, JMHV IL-6 may be used for research, diagnostic

CC purposes, to produce antibodies for diagnostic purposes to diagnose
CC diseases characterized by increased or decreased production of IL-6,
CC and as a targeting molecule for identifying cells with receptors for
CC IL-6, etc. The JMHV macropage inflammatory protein (MIP protein) is
CC useful for treating wounds and other inflammatory diseases including
CC asthma, allergies and dermatitis. They are also useful for producing
CC antibodies for diagnostic purposes, and as a targeting molecule for
CC identifying cells with receptors for MIP, etc. Nucleic acids encoding
CC the JMHV proteins are useful in gene therapy techniques for treating
CC the above mentioned conditions. The current sequence represents the
CC JMHV Orf10 nucleotide sequence from cosmid 3 fragment 1 kpn 1 fragment 2
CC 17. Orf10 encodes an unknown protein.
CC Note: In the specification the deduced amino acid sequence of this
CC fragment is also given (see AAG78589). However, the sequence here does
CC not decode to the amino acid sequence in that record. There are also two
CC amino acid sequences (see AAG78597 and AAG78598) given in example 22 of
CC the specification that have the same sequence identification number as
CC the current sequence, but are said to be from Orf 9.

XX Sequence 314 BP; 59 A; 83 C; 108 G; 64 T; 0 other;

Query Match 0.2%; Score 70; DB 24; Length 314;

Best Local Similarity 99.2%; Pred. No. 1.9e-18;

Matches 120; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 18027 TGGGCGACATCGGACCGCTCTGCCACACACCGGCGCGCTATTGGGGGTCTACG 18086
DB 260 TGGGCGACATCGGACCGCTCTGCCACACACCGGCGCGCTATTGGGGGTCTACG 201

QY 18087 CCGAGCGCGGAAAAAACATCCACACCTGGAGCTCCGGCGGAGTCCGCTTCACTTAATCT 18146
DB 200 CCGAGCGCGGAAAAAACATCCACACCTGGAGCTCCGGCGGAGTCCGCTTCACTTAATCT 141

QY 18147 T 18147
DB 140 T 140

RESULT 12

ABA97194/C
ID ABA97194 standard; DNA; 330 BP.

XX ABA97194;

DT 22-APR-2002 (first entry)

XX JMHV cosmid 3 EcoRI fragment 1 kpn 1 fragment 4 T7.

XX RRV; rhesus rhadinovirus; Japanese macaque virus; multiple sclerosis;

KW JMHV; cytostatic; antiasthmatic; antiallergic; dermatological;

KW vulnerrary; gene therapy; leucopenia; thrombocytopenia;

KW inflammatory disease; asthma; allergy; dermatitis; ds.

OS Japanese macaque herpesvirus.

XX WO200188203-A1.

XX 22-NOV-2001.

XX 17-MAY-2001; 2001WO-US16274.

XX 18-MAY-2000; 2000US-205652P.

XX (UOYR-) UNIV OREGON HEALTH SCI.

XX Wong SW, Axthelm MK;

XX WPI; 2002-075323/10.

XX New Japanese macaque virus (JMHV) and nucleic acid sequences of open
PT reading frames in virus, useful for producing animal models for
PT assessing efficacy of drugs for treatment or prevention of multiple
PT sclerosis

XX Claim 9; Page 72; 175pp; English.

PS The invention relates to an isolated virus (Japanese macaque virus (JMHV))
XX as deposited with ATCC as deposit accession number PTV-1884. Non-human
CC primate models infected with the new virus are useful for testing the
CC efficacy of a drug for treating a condition associated with JMHV,
CC preferably a drug used to treat multiple sclerosis. This involves
CC administering the drug to a non-human primate infected with JMHV and
CC observing the non-human primate to determine if the drug prevents or
CC reduces the presentation of one or more symptoms associated with JMHV
CC infection. Methods of the invention are also useful for testing the
CC efficacy of candidate vaccine against JMHV infection, or conditions
CC associated with JMHV infection e.g., multiple sclerosis. Methods of the
CC invention are useful for diagnosing the presence of JMHV or a related
CC virus in a biological specimen. JMHV genome possesses an interleukin
CC (IL)-6 gene which encodes IL-6 proteins. The IL-6 proteins may be used
CC to induce stimulation of haematopoietic stem cells to enhance
CC proliferation, differentiation and terminal maturation of erythroid
CC cells from haematopoietic cells. Thus, JMHV IL-6 may be used in vivo or
CC ex vivo to treat diseases involving leukopenia or thrombocytopenia.
CC The JMHV IL-6 may also be used to stimulate growth of megakaryocytes
CC and platelets, and for the inhibition of tumour growth and for treating
CC leukemia. Additionally, JMHV IL-6 may be used for research, diagnostic
CC purposes, to produce antibodies for diagnostic purposes to diagnose
CC diseases characterized by increased or decreased production of IL-6,
CC and as a targeting molecule for identifying cells with receptors for
CC IL-6, etc. The JMHV macropage inflammatory protein (MIP protein) is
CC useful for treating wounds and other inflammatory diseases including
CC asthma, allergies and dermatitis. They are also useful for producing
CC antibodies for diagnostic purposes, and as a targeting molecule for
CC identifying cells with receptors for MIP, etc. Nucleic acids encoding
CC the JMHV proteins are useful in gene therapy techniques for treating
CC the above mentioned conditions. The current sequence represents the
CC JMHV Orf8 nucleotide sequence from cosmid 3 fragment 1 kpn 1 fragment 4
CC T7. Orf 8 encodes glycoprotein B.
CC Note: In the specification the deduced amino acid sequence of this
CC fragment is also given (see AAG78592). However, the sequence here does
CC not decode to the amino acid sequence in that record.

XX Sequence 330 BP; 58 A; 89 C; 104 G; 78 T; 1 other;

Query Match 0.2%; Score 59; DB 24; Length 330;

Best Local Similarity 100.0%; Pred. No. 7.1e-14;

Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11692 AAGTTCCGCGTGTGACGCGCTCGGCGGACGCTTACGTTTAACTGGAAAA 11750

DB 157 AAGTTCCGCGTGTGACGCGCTCGGCGGACGCTTACGTTTAACTGGAAAA 99

RESULT 13

ABA97192
ID ABA97192 standard; DNA; 681 BP.

XX ABA97192;

DT 22-APR-2002 (first entry)

XX JMHV cosmid 3 EcoRI fragment 1 kpn fragment 3 SP6.

XX RRV; rhesus rhadinovirus; Japanese macaque virus; multiple sclerosis;

KW JMHV; cytostatic; antiasthmatic; antiallergic; dermatological;

KW vulnerrary; gene therapy; leucopenia; thrombocytopenia;

KW inflammatory disease; asthma; allergy; dermatitis; ds.

OS Japanese macaque herpesvirus.

XX Key Location/Qualifiers

XX CDS 3..680
XX /*tag= a
XX /partial= 1
XX /product= "glycoprotein B"

FT /note- "no start or stop codon present"

PN WO200188203-A1.

XX 22-NOV-2001.

PD

XX 17-MAY-2001; 2001WO-US16274.

PF

XX 18-MAY-2000; 2000US-205652P.

PR

XX (UYOR-) UNIV OREGON HEALTH SCI.

PA

XX Mong SW, Axtheim MK;

PI

XX WPI; 2002-075323/10.

DR

XX P-PSDB; AAG78590.

DR

XX

XX New Japanese macaque virus (JMHV) and nucleic acid sequences of open

PT reading frames in virus, useful for producing animal models for

PT assessing efficacy of drugs for treatment or prevention of multiple

PT sclerosis -

PS

XX Claim 9; Page 71; 175pp; English.

PS

XX The invention relates to an isolated virus (Japanese macaque virus (JMHV)

CC as deposited with ATCC as deposit accession number PTA-1884. Non-human

CC primate models infected with the new virus are useful for testing the

CC efficacy of a drug for treating a condition associated with JMHV,

CC preferably a drug used to treat multiple sclerosis. This involves

CC administering the drug to a non-human primate infected with JMHV and

CC observing the non-human primate to determine if the drug prevents or

CC reduces the presentation of one or more symptoms associated with JMHV

CC infection. Methods of the invention are also useful for testing the

CC efficacy of candidate vaccine against JMHV infection, or conditions

CC associated with JMHV infection e.g., multiple sclerosis. Methods of the

CC invention are useful for diagnosing the presence of JMHV or a related

CC virus in a biological specimen. JMHV genome possesses an interleukin

CC (IL)-6 gene which encodes IL-6 proteins. The IL-6 proteins may be used

CC to induce stimulation of haematopoietic stem cells to enhance

CC proliferation, differentiation and terminal maturation of erythroid

CC cells from haematopoietic cells. Thus, JMHV IL-6 may be used in vivo or

CC ex vivo to treat diseases involving leukopenia or thrombocytopenia.

CC The JMHV IL-6 may also be used to stimulate growth of megakaryocytes

CC and platelets, and for the inhibition of tumour growth and for treating

CC leukemia. Additionally, JMHV IL-6 may be used for research, diagnostic

CC purposes, to produce antibodies for diagnostic purposes to diagnose

CC diseases characterized by increased or decreased production of IL-6,

CC and as a targeting molecule for identifying cells with receptors for

CC IL-6, etc. The JMHV macrophage inflammatory protein (MIP protein) is

CC useful for treating wounds and other inflammatory diseases including

CC asthma, allergies and dermatitis. They are also useful for producing

CC antibodies for diagnostic purposes, and as a targeting molecule for

CC identifying cells with receptors for MIP, etc. Nucleic acids encoding

CC the JMHV proteins are useful in gene therapy techniques for treating

CC the above mentioned conditions. The current sequence represents the

CC JMHV Orf8 nucleotide sequence from cosmid 3 EcoRI fragment Kpn 1

CC fragment 3 SP6. Orf 8 encodes glycoprotein B.

XX

XX Sequence 681 BP; 163 A; 203 C; 186 G; 129 T; 0 other;

SQ

Query Match 0.2%; Score 58; DB 24; Length 681;

Best Local Similarity 100.0%; Pred. No. 1.7e-13;

Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12152 GAACCGCGTCAACTCGAGATGATGATCGGCGGTCGGAACCGTACTC 12209

DB 310 GAACCGCGTCAACTCGAGATGATGATCGGCGGTCGGAACCGTACTC 367

RESULT 14

AA164300

ID AA164300 standard; DNA; 438 BP.

XX

AC AA164300;

XX

XX 22-APR-2002 (first entry)

DT

XX

XX JMHV cosmid 3 EcoRI fragment 1 Kpn 1 fragment 1 T7.

DE

XX

XX RRV; Rhesus rhadinovirus; Japanese macaque virus; multiple sclerosis;

KW JMHV; cytostatic; antiallergic; dermatologic;

KW vulnery; gene therapy; leucopenia; thrombocytopenia;

KW inflammatory disease; asthma; allergy; dermatitis; ds.

XX

OS Japanese macaque herpesvirus.

XX

XX Key Location/Qualifiers

FH 1..231

FT CDS /*tag- a

FT /partial

FT /note- "no start codon present"

FT

XX WO200188203-A1.

XX

XX 22-NOV-2001.

XX

XX 17-MAY-2001; 2001WO-US16274.

PF

XX

XX 18-MAY-2000; 2000US-205652P.

PR

XX (UYOR-) UNIV OREGON HEALTH SCI.

PA

XX Mong SW, Axtheim MK;

PI

XX WPI; 2002-075323/10.

DR

XX P-PSDB; AAG78587.

DR

XX

XX New Japanese macaque virus (JMHV) and nucleic acid sequences of open

PT reading frames in virus, useful for producing animal models for

PT assessing efficacy of drugs for treatment or prevention of multiple

PT sclerosis -

PS

XX Claim 9; Page 70; 175pp; English.

PS

XX The invention relates to an isolated virus (Japanese macaque virus (JMHV)

CC as deposited with ATCC as deposit accession number PTA-1884. Non-human

CC primate models infected with the new virus are useful for testing the

CC efficacy of a drug for treating a condition associated with JMHV,

CC preferably a drug used to treat multiple sclerosis. This involves

CC administering the drug to a non-human primate infected with JMHV and

CC observing the non-human primate to determine if the drug prevents or

CC reduces the presentation of one or more symptoms associated with JMHV

CC infection. Methods of the invention are also useful for testing the

CC efficacy of candidate vaccine against JMHV infection, or conditions

CC associated with JMHV infection e.g., multiple sclerosis. Methods of the

CC invention are useful for diagnosing the presence of JMHV or a related

CC virus in a biological specimen. JMHV genome possesses an interleukin

CC (IL)-6 gene which encodes IL-6 proteins. The IL-6 proteins may be used

CC to induce stimulation of haematopoietic stem cells to enhance

CC proliferation, differentiation and terminal maturation of erythroid

CC cells from haematopoietic cells. Thus, JMHV IL-6 may be used in vivo or

CC ex vivo to treat diseases involving leukopenia or thrombocytopenia.

CC The JMHV IL-6 may also be used to stimulate growth of megakaryocytes

CC and platelets, and for the inhibition of tumour growth and for treating

CC leukemia. Additionally, JMHV IL-6 may be used for research, diagnostic

CC purposes, to produce antibodies for diagnostic purposes to diagnose

CC diseases characterized by increased or decreased production of IL-6,

CC and as a targeting molecule for identifying cells with receptors for

CC IL-6, etc. The JMHV macrophage inflammatory protein (MIP protein) is

CC useful for treating wounds and other inflammatory diseases including

CC asthma, allergies and dermatitis. They are also useful for producing

CC antibodies for diagnostic purposes, and as a targeting molecule for

CC identifying cells with receptors for MIP, etc. Nucleic acids encoding

CC the JMHV proteins are useful in gene therapy techniques for treating

CC the above mentioned conditions. The current sequence represents the

CC JMHV Orf10 nucleotide sequence from cosmid 3 EcoRI fragment Kpn 1

CC fragment 1 T7. Orf 10 encodes an unknown protein.
 XX Sequence 438 BP; 76 A; 146 C; 142 G; 74 T; 0 other;
 SO Query Match 0.1%; Score 50; DB 24; Length 438;
 Best Local Similarity 100.0%; Pred. No. 3.8e-10;
 Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 18571 GTGGACACAGCGAGCGGTACAGCTCCCTGTGTGGGCGCCACTAT 18620
 DB 291 GTGGACACAGCGAGCGGTACAGCTCCCTGTGTGGGCGCCACTAT 340
 RESULT 15
 ABA97193/C
 ID ABA97193 standard; DNA; 389 BP.
 AC ABA97193;
 DT 22-APR-2002 (first entry)
 XX JMHV cosmid 3 EcorI fragment 1 kpn 1 fragment 3 T7.
 DE JMHV cosmid 3 EcorI fragment 1 kpn 1 fragment 3 T7.
 XX RRV; rhesus rhadinovirus; Japanese macaque virus; multiple sclerosis;
 KM JMHV; cytostatic; antiallergic; dermatological;
 KM vulnery; gene therapy; leucopenia; thrombocytopenia;
 KM inflammatory disease; asthma; allergy; dermatitis; ds.
 XX Japanese macaque herpesvirus.
 OS WO20018203-A1.
 PN 22-NOV-2001.
 XX 17-MAY-2001; 2001WO-US16274.
 PF 18-MAY-2000; 2000US-205652P.
 XX (UYOR-) UNIV OREGON HEALTH SCI.
 PA Wong SM, Axthelm MK;
 PI Mong SM, Axthelm MK;
 XX WPI: 2002-075323/10.
 DR New Japanese macaque virus (JMHV) and nucleic acid sequences of open
 PT reading frames in virus, useful for producing animal models for
 PT assessing efficacy of drugs for treatment or prevention of multiple
 PT sclerosis -
 XX Claim 9; Page 72; 175pp; English.
 PS The invention relates to an isolated virus (Japanese macaque virus (JMHV))
 CC as deposited with ATCC as deposit accession number PTA-1884. Non-human
 CC primate models infected with the new virus are useful for testing the
 CC efficacy of a drug for treating a condition associated with JMHV,
 CC preferably a drug used to treat multiple sclerosis. This involves
 CC administering the drug to a non-human primate infected with JMHV and
 CC observing the non-human primate to determine if the drug prevents or
 CC reduces the presentation of one or more symptoms associated with JMHV
 CC infection. Methods of the invention are also useful for testing the
 CC efficacy of candidate vaccine against JMHV infection, or conditions
 CC associated with JMHV infection e.g., multiple sclerosis. Methods of the
 CC invention are useful for diagnosing the presence of JMHV or a related
 CC virus in a biological specimen. JMHV genome possesses an interleukin
 CC (IL)-6 gene which encodes IL-6 proteins. The IL-6 proteins may be used
 CC to induce stimulation of hematopoietic stem cells to enhance
 CC proliferation, differentiation and terminal maturation of erythroid
 CC cells from hematopoietic cells. Thus, JMHV IL-6 may be used in vivo or
 CC ex vivo to treat diseases involving leukopenia or thrombocytopenia.
 CC The JMHV IL-6 may also be used to stimulate growth of megakaryocytes
 CC and platelets, and for the inhibition of tumour growth and for treating
 CC leukemia. Additionally, JMHV IL-6 may be used for research, diagnostic
 CC purposes, to produce antibodies for diagnostic purposes to diagnose

CC diseases characterized by increased or decreased production of IL-6,
 CC and as a targeting molecule for identifying cells with receptors for
 CC IL-6, etc. The JMHV macrophage inflammatory protein (MIP protein) is
 CC useful for treating wounds and other inflammatory diseases including
 CC asthma, allergies and dermatitis. They are also useful for producing
 CC antibodies for diagnostic purposes, and as a targeting molecule for
 CC identifying cells with receptors for MIP, etc. Nucleic acids encoding
 CC the JMHV proteins are useful in gene therapy techniques for treating
 CC the above mentioned conditions. The current sequence represents the
 CC JMHV Orf9 nucleotide sequence from cosmid 3 fragment 1 kpn 1 fragment 3
 CC T7. Orf 9 encodes a DNA polymerase.
 CC Note: In the specification the deduced amino acid sequence of this
 CC fragment is also given (see AAG78591). However, the sequence here does
 CC not decode to the amino acid sequence in that record. There is also an
 CC amino acid sequence (see AAG78596) given in example 22 of the
 CC specification that has the same sequence identification number as the
 CC current sequence, but is said to be from Orf 8.
 CC Sequence 389 BP; 61 A; 114 C; 147 G; 67 T; 0 other;
 SO Query Match 0.1%; Score 41; DB 24; Length 389;
 Best Local Similarity 100.0%; Pred. No. 2.1e-06;
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 14269 GGGGACAGCGGAGATCCGCGTCACGATCCCGTTCCGCC 14309
 DB 215 GGGGACAGCGGAGATCCGCGTCACGATCCCGTTCCGCC 175
 RESULT 16
 AA164296
 ID AA164296 standard; DNA; 630 BP.
 XX AA164296;
 AC 22-APR-2002 (first entry)
 DT JMHV Orf21 nucleotide sequence from cosmid 3 fragment 3 T7.
 XX RRV; rhesus rhadinovirus; Japanese macaque virus; multiple sclerosis;
 KM JMHV; cytostatic; antiallergic; dermatological;
 KM vulnery; gene therapy; leucopenia; thrombocytopenia;
 KM inflammatory disease; asthma; allergy; dermatitis; ds.
 XX Japanese macaque herpesvirus.
 OS Key Location/Qualifiers
 FH CDS 153..527
 FT /*tag= a
 FT /product= "thymidine kinase"
 FT /partial
 FT /note= "no start codon present"
 XX WO20018203-A1.
 PN 22-NOV-2001.
 XX 17-MAY-2001; 2001WO-US16274.
 PF 18-MAY-2000; 2000US-205652P.
 XX (UYOR-) UNIV OREGON HEALTH SCI.
 PA Wong SM, Axthelm MK;
 PI Wong SM, Axthelm MK;
 XX WPI: 2002-075323/10.
 DR P-PSDB; AAG78584.
 DR New Japanese macaque virus (JMHV) and nucleic acid sequences of open
 PT reading frames in virus, useful for producing animal models for
 PT assessing efficacy of drugs for treatment or prevention of multiple
 PT sclerosis -
 XX

PS Claim 9; Page 68; 175bp; English.

XX The invention relates to an isolated virus (Japanese macaque virus (JMHV))
CC as deposited with ATCC as deposit accession number PTA-1884. Non-human
CC primate models infected with the new virus are useful for testing the
CC efficacy of a drug for treating a condition associated with JMHV,
CC preferably a drug used to treat multiple sclerosis. This involves
CC administering the drug to a non-human primate infected with JMHV and
CC observing the non-human primate to determine if the drug prevents or
CC reduces the presentation of one or more symptoms associated with JMHV
CC infection. Methods of the invention are also useful for testing the
CC efficacy of candidate vaccine against JMHV infection, or conditions
CC associated with JMHV infection e.g., multiple sclerosis. Methods of the
CC invention are useful for diagnosing the presence of JMHV or a related
CC virus in a biological specimen. JMHV genome possesses an interleukin
CC (IL)-6 gene which encodes IL-6 proteins. The IL-6 proteins may be used
CC to induce stimulation of haematopoietic stem cells to enhance
CC proliferation, differentiation and terminal maturation of erythroid
CC cells from haematopoietic cells. Thus, JMHV IL-6 may be used in vivo or
CC ex vivo to treat diseases involving leukaemia or thrombocytopenia.
CC The JMHV IL-6 may also be used to stimulate growth of megakaryocytes
CC and platelets, and for the inhibition of tumour growth and for treating
CC leukaemia. Additionally, JMHV IL-6 may be used for research, diagnostic
CC purposes, to produce antibodies for diagnostic purposes to diagnose
CC diseases characterized by increased or decreased production of IL-6,
CC and as a targeting molecule for identifying cells with receptors for
CC IL-6, etc. The JMHV macrophage inflammatory protein (MIP protein) is
CC useful for treating wounds and other inflammatory diseases including
CC asthma, allergies and dermatitis. They are also useful for producing
CC antibodies for diagnostic purposes, and as a targeting molecule for
CC identifying cells with receptors for MIP, etc. Nucleic acids encoding
CC the JMHV proteins are useful in gene therapy techniques for treating
CC the above mentioned conditions. The current sequence represents the
CC JMHV Orf21 nucleotide sequence from cosmid 3 fragment 3 T7. Orf 21
CC encodes a thymidine kinase.

SQ Sequence 630 BP; 179 A; 133 C; 156 G; 159 T; 3 other;

Query Match 0.1%; Score 40; DB 24; Length 630;
Best Local Similarity 100.0%; Pred. No. 5.3e-06;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 33529 CGGTTAAGACACGCTGACCTTAATGAGAGCTGTTGGG 33568
|||||
DB 289 CGGTTAAGACACGCTGACCTTAATGAGAGCTGTTGGG 328

RESULT 17
AA164299/C
ID AA164299 standard; DNA; 524 BP.
XX
AC AA164299;
XX
DT 22-APR-2002 (first entry)
XX
DE JMHV nucleotide sequence from cosmid 3 fragment 1 SP6.
XX
KM RRV, rhesus rhadinovirus; Japanese macaque virus; multiple sclerosis;
KM JMHV; cytostatic; antiallergic; antiallergic; dermatological;
KM vulnery; gene therapy; leucopenia; thrombocytopenia;
KM inflammatory disease; asthma; allergy; dermatitis; ds.
XX
OS Japanese macaque herpesvirus.
XX
PN WO20018203-A1.
XX
PD 22-NOV-2001.
XX
PE 17-MAY-2001; 2001WO-US16274.
XX
PR 18-MAY-2000; 2000US-205652P.
XX
PA (UOR-) UNIV OREGON HEALTH SCI.

XX Wong SW, Axthelm MK;
PI
CC
DR WPI: 2002-075323/10.
XX
XX
PT New Japanese macaque virus (JMHV) and nucleic acid sequences of open
PT reading frames in virus, useful for producing animal models for
PT assessing efficacy of drugs for treatment or prevention of multiple
PT sclerosis
XX
PS Claim 9; Page 69-70; 175bp; English.

XX The invention relates to an isolated virus (Japanese macaque virus (JMHV))
CC as deposited with ATCC as deposit accession number PTA-1884. Non-human
CC primate models infected with the new virus are useful for testing the
CC efficacy of a drug for treating a condition associated with JMHV,
CC preferably a drug used to treat multiple sclerosis. This involves
CC administering the drug to a non-human primate infected with JMHV and
CC observing the non-human primate to determine if the drug prevents or
CC reduces the presentation of one or more symptoms associated with JMHV
CC infection. Methods of the invention are also useful for testing the
CC efficacy of candidate vaccine against JMHV infection, or conditions
CC associated with JMHV infection e.g., multiple sclerosis. Methods of the
CC invention are useful for diagnosing the presence of JMHV or a related
CC virus in a biological specimen. JMHV genome possesses an interleukin
CC (IL)-6 gene which encodes IL-6 proteins. The IL-6 proteins may be used
CC to induce stimulation of haematopoietic stem cells to enhance
CC proliferation, differentiation and terminal maturation of erythroid
CC cells from haematopoietic cells. Thus, JMHV IL-6 may be used in vivo or
CC ex vivo to treat diseases involving leukaemia or thrombocytopenia.
CC The JMHV IL-6 may also be used to stimulate growth of megakaryocytes
CC and platelets, and for the inhibition of tumour growth and for treating
CC leukaemia. Additionally, JMHV IL-6 may be used for research, diagnostic
CC purposes, to produce antibodies for diagnostic purposes to diagnose
CC diseases characterized by increased or decreased production of IL-6,
CC and as a targeting molecule for identifying cells with receptors for
CC IL-6, etc. The JMHV macrophage inflammatory protein (MIP protein) is
CC useful for treating wounds and other inflammatory diseases including
CC asthma, allergies and dermatitis. They are also useful for producing
CC antibodies for diagnostic purposes, and as a targeting molecule for
CC identifying cells with receptors for MIP, etc. Nucleic acids encoding
CC the JMHV proteins are useful in gene therapy techniques for treating
CC the above mentioned conditions. The current sequence represents the
CC JMHV nucleotide sequence from cosmid 3 fragment 1 SP6. There is no Orf
CC in this fragment, but it is similar to the sequence to the left of the
CC RRV repeat rDL-B1.

SQ Sequence 524 BP; 191 A; 104 C; 84 G; 145 T; 0 other;

Query Match 0.1%; Score 37; DB 24; Length 524;
Best Local Similarity 100.0%; Pred. No. 9.5e-05;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 25015 TGTAAATTTGCTTTAGATTGTTGGGTGCAATTC 25051
|||||
DB 37 TGTAAATTTGCTTTAGATTGTTGGGTGCAATTC 1

RESULT 18
AA164291/C
ID AA164291 standard; DNA; 128139 BP.
XX
AC AA164291;
XX
DT 22-APR-2002 (first entry)
XX
DE RRV genome nucleotide sequence.
XX
PE RRV, rhesus rhadinovirus; Japanese macaque virus; multiple sclerosis;
KM JMHV; cytostatic; antiallergic; antiallergic; dermatological;
KM vulnery; gene therapy; leucopenia; thrombocytopenia;
KM inflammatory disease; asthma; allergy; dermatitis; virus; ds.
XX

OS Macaca mulatta rhadinovirus 17577.
 XX Key Location/Qualifiers
 FT CDS 1353..2674
 FT /*tag- a
 FT /product- "RV R1"
 FT /note- "complement (2692..3258)"
 FT /*tag- b
 FT /product- "dihydrofolate reductase"
 FT /label- RV_ORF2
 FT /note- "has similarity to Kaposi's sarcoma-associated
 virus (KSHV) open reading frame (ORF) 2"
 FT CDS 3676..5613
 FT /*tag- c
 FT /product- "complement binding protein"
 FT /label- RV_ORF4
 FT /note- "has similarity to KSHV ORF4"
 FT 6045..9443
 FT /*tag- d
 FT /product- "sADNA binding protein"
 FT /label- RV_ORF6
 FT /note- "has similarity to KSHV ORF6"
 FT 9468..11528
 FT /*tag- e
 FT /product- "transport protein"
 FT /label- RV_ORF7
 FT /note- "has similarity to KSHV ORF7"
 FT 11515..14004
 FT /*tag- f
 FT /product- "glycoprotein B"
 FT /label- RV_ORF8
 FT /note- "has similarity to KSHV ORF8"
 FT 1412..17166
 FT /*tag- g
 FT /product- "DNA polymerase protein"
 FT /label- RV_ORF9
 FT /note- "has similarity to KSHV ORF9"
 FT 17261..18511
 FT /*tag- h
 FT /label- RV_ORF10
 FT /note- "has similarity to KSHV ORF10"
 FT 18520..19749
 FT /*tag- i
 FT /label- RV_ORF11
 FT /note- "has similarity to KSHV ORF11"
 FT complement (19921..20544)
 FT /*tag- j
 FT /product- "RV R2"
 FT /label- RV_ORF
 FT /note- "has similarity to KSHV Interleukin (IL)-6 gene"
 FT complement (20777..21778)
 FT /*tag- k
 FT /product- "thymidylate synthase"
 FT /label- RV_ORF70
 FT /note- "has similarity to KSHV ORF70"
 FT complement (22245..22592)
 FT /*tag- l
 FT /product- "RV R3"
 FT /note- "has similarity to KSHV K4 viral MIP gene"
 FT 26846..27409
 FT /*tag- m
 FT /product- "Bcl2-homologue"
 FT /label- RV_ORF16
 FT /note- "has similarity to KSHV ORF16"
 FT complement (27515..29125)
 FT /*tag- n
 FT /label- RV_ORF17
 FT /note- "has similarity to KSHV ORF17"
 FT 28998..29897
 FT /*tag- o
 FT /label- RV_ORF18
 FT /note- "has similarity to KSHV ORF18"
 FT complement (29905..31548)
 FT CDS

FT /*tag- p
 FT /product- "tegument protein"
 FT /label- RV_ORF19
 FT /note- "has similarity to KSHV ORF19"
 FT complement (31043..32095)
 FT /*tag- q
 FT /label- RV_ORF20
 FT /note- "has similarity to KSHV ORF20"
 FT 32094..33767
 FT /*tag- r
 FT /product- "thymidine kinase"
 FT /label- RV_ORF21
 FT /note- "has similarity to KSHV ORF21"
 FT 33754..35868
 FT /*tag- s
 FT /product- "glycoprotein H"
 FT /label- RV_ORF22
 FT /note- "has similarity to KSHV ORF22"
 FT complement (35865..37073)
 FT /*tag- t
 FT /label- RV_ORF23
 FT /note- "has similarity to KSHV ORF23"
 FT complement (37123..39321)
 FT /*tag- u
 FT /label- RV_ORF24
 FT /note- "has similarity to KSHV ORF24"
 FT 39323..43459
 FT /*tag- v
 FT /product- "major capsid protein"
 FT /label- RV_ORF25
 FT /note- "has similarity to KSHV ORF25"
 FT 43491..44408
 FT /*tag- w
 FT /product- "capsid protein"
 FT /label- RV_ORF26
 FT /note- "has similarity to KSHV ORF26"
 FT 44433..45242
 FT /*tag- x
 FT /label- RV_ORF27
 FT /note- "has similarity to KSHV ORF27"
 FT 45408..45683
 FT /*tag- y
 FT /label- RV_ORF28
 FT /note- "has similarity to KSHV ORF28"
 FT complement (45733..46779)
 FT /*tag- z
 FT /label- RV_ORF29b
 FT /note- "has similarity to KSHV ORF29b"
 FT 46905..47135
 FT /*tag- aa
 FT /label- RV_ORF30
 FT /note- "has similarity to KSHV ORF30"
 FT 47093..47746
 FT /*tag- ab
 FT /label- RV_ORF31
 FT /note- "has similarity to KSHV ORF31"
 FT 47683..49077
 FT /*tag- ac
 FT /label- RV_ORF32
 FT /note- "has similarity to KSHV ORF32"
 FT 49049..50059
 FT /*tag- ad
 FT /label- RV_ORF33
 FT /note- "has similarity to KSHV ORF33"
 FT complement (49977..50960)
 FT /*tag- ae
 FT /label- RV_ORF29a
 FT /note- "has similarity to KSHV ORF29a"
 FT 50959..51942
 FT /*tag- af
 FT /label- RV_ORF34
 FT /note- "has similarity to KSHV ORF34"
 FT 51923..52372
 FT CDS

PD		18-MAY-2000.
PE	05-NOV-1999;	99WO-US26260.
PR	06-NOV-1998;	98US-0107507.
XX	20-NOV-1998;	98US-0109409.
PA	(UNOR-) UNIV OREGON HEALTH SCI.	
PI	Mong SW, Axthelm MK, Searles RP;	
DR	WPI; 2000-376552/32.	
PT	New rhesus rhadino virus for producing non-human primate model useful	
PT	for testing potential treatments and efficacy of the candidate vaccine	
PT	for conditions associated with RRV infection	
PS	Claim 2; Page 83-122; 141pp; English.	
XX		
CC	The present invention describes a novel rhesus macaque rhadinovirus	
CC	called macaca mulatta rhadinovirus 17577 (RRV). AAC64754 represents the	
CC	RRV genome sequence, and AAB53123 to AAB53204 represent the proteins	
CC	encoded by the genome sequence. The present invention also specifically	
CC	claims the individual open reading frame (ORF) nucleotide sequences from	
CC	the genome which encode the individual proteins, but these sequences are	
CC	not given. A non-human animal infected with RRV can be used for testing	
CC	the efficacy of drug in the treatment of condition associated with	
CC	infection with RRV such as Kaposi's sarcoma, lymphoproliferative	
CC	disorders, B-cell hyperplasia, lymphadenopathy, splenomegaly,	
CC	hyperimmunoglobulinemia or autoimmune haemolytic anaemia, by	
CC	administering the drug to a immuno-compromised non-human primate	
CC	preferably Rhesus macaque monkey obtained by as a result of infection	
CC	by Simian Immunodeficiency Virus (SIV). RRV is useful for producing	
CC	non-human primate model for testing potential treatments for conditions	
CC	associated with RRV infection. It is also useful for testing the	
CC	efficacy of the candidate vaccine against RRV infection or conditions	
CC	associated with its infection by administering the vaccine to the	
CC	subject capable of infection with RRV, inoculating the subject with RRV	
CC	and observing the effect of vaccine. AAC64755 to AAC64765 and AAB53205	
CC	to AAB53213 represent sequence used in the exemplification of the	
CC	present invention.	
SQ	Sequence 133719 BP; 32746 A; 35648 C; 34521 G; 30804 T; 0 other;	
Query Match	0.1%; Score 33; DB 21; Length 133719;	
Best Local Similarity	100.0%; Pred. No. 0.0029;	
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
Yy	23879 GTTGGCTTTGTTACAAAGTCCTATATATAT 23911	
Db		
	117575 GTTGCGTTTGTTCACAAAGTCCCTAATATAT 117543	
RESULT 20		
ID	AAT51553	
XX	AAT51553 standard; DNA: 2511 BP.	
AC	AAT51553:	
DT	06-NOV-1997 (first entry)	
DE	Herpes virus DNA polymerase segment KSHV encoding DNA.	
KM	Retroperitoneal fibromatosis herpes virus; detection; infection;	
KW	Kapost's sarcoma herpes virus; viral DNA; viral RNA; vaccine;	
XX	antigen; antibody; ss.	
OS	Kaposi's sarcoma herpes virus.	
FH	Key location/Qualifiers	
FT	CDS 1..2511	
FT	/tag= a	
FT	/product= DNA_polymerase	

```

FT XX /note- "No stop codon given"
PR PN MO9704105-A1.
XX XX
PD PD 06-FEB-1997.
XX XX
PF PF 12-JUL-1996; 96WO-US11688.
XX XX
PR PR 11-JUL-1996; 96US-0001148.
XX XX
PR PR 14-JUL-1995; 95US-0001148.
XX XX
PA PA (UNIW ) UNIV WASHINGTON.
XX XX
PI PI Bosch ML, Rose TM, Strand K, Todaro GJ;
XX XX
DR DR WPI: 1997-132644/12.
XX XX
PT PT P-P-SDB; AAM11995.
XX XX
PT PT Herpes virus DNA polymerase and corresponding nucleotide sequence -
XX XX used in the detection and treatment of herpes virus infection
PS PS Claim 9; Page 88-90; 132pp; English.
XX XX
CC CC The present sequence represents a novel isolated polynucleotide
CC CC with a region encoding a DNA polymerase designated KSHV of a
CC CC herpes virus. This DNA polymerase was isolated from Kaposi's
CC CC sarcoma herpes virus (KSHV) found in tissue samples taken from
CC CC humans. Primers used in the amplification of polynucleotides
CC CC encoding DNA polymerases may be used for detecting viral DNA or
CC CC RNA in a sample of primate origin, especially in the diagnosis of
CC CC herpes viral infection. Herpes virus DNA polymerases of this
CC CC infection, may be used in vaccines for the protection against
CC CC infection by a herpes virus of the RFHV/KSHV family. They may also
CC CC be used in the design and screening of anti-viral drugs. Antibodies
CC CC raised against the polymerase or fragments of it, may be used in the
CC CC detection of herpes virus infection and for drug targeting for the
CC CC therapy of herpes virus infection.
XX XX
SQ SQ Sequence 2511 BP; 624 A; 708 C; 662 G; 513 T; 4 other;

Query Match 0.1%; Score 29; DB 18; Length 2511;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14938 CTGGAGTTTGACTGCAGCTGGAGGACCT 14966
DB 391 CTGGAGTTTGACTGCAGCTGGAGGACCT 419

RESULT 21
AAV73802
ID AAV73802 standard; DNA: 35100 BP.
XX XX
AC AC AAV73802;
XX XX
DT DT 25-FEB-1999 (first entry)
XX XX
DE DE KSHV LUR DNA (nucleotides 1-35,100).
XX XX
XX Kaposi's sarcoma; acquired immune deficiency syndrome; AIDS; DHFR; Bcl-2;
XX K dihydrofolate reductase; LUR; long unique region; vacuole; prophylaxis;
XX K diagnosis; treatment; HHV8; complement binding protein; v-CBP; SSBP;
XX K ssDNA binding protein; transport protein; glycoprotein B; pol; vIL-6;
XX K DNA polymerase; viral interleukin-6; BHV4-IE1 I; thymidylate synthase;
XX K vMIP-II; BHV4-IE1 II; vMIP-I; capsid protein I; tegument protein I; ds.
XX OS Kaposi's sarcoma-associated herpesvirus.
XX PN US5849564-A.
XX PD 15-DEC-1998.
XX PF 29-NOV-1996; 96US-0770379.

```

```

XX XX 29-NOV-1996; 96US-0770379.
PR XX (UYCO ) UNIV COLUMBIA NEW YORK.
XX XX
PA PA Bohenzky RA, Chang Y, Edelman IS, Moore PS, Russo JU;
XX XX WPI: 1999-069741/06.
XX XX
DR DR WPI: 1999-069741/06.
XX XX
PT PT Kaposi's sarcoma-associated herpes virus nucleic acid - encodes
XX XX dihydrofolate reductase and is useful for treatment, prophylaxis
XX XX or diagnosis of Kaposi's sarcoma
PS PS Disclosure; Column 67-96; 109pp; English.
XX XX
CC CC This sequence is a fragment of the Kaposi's sarcoma-associated
CC CC herpesvirus (KSHV) LUR (long unique region). This fragment contains
CC CC coding regions for K1, ORF4 which encodes the complement binding protein
CC CC v-CBP, ORF6 which encodes a ssDNA binding protein (SSBP), ORF7 which
CC CC encodes a transport protein, ORF8 which encodes glycoprotein B, ORF9
CC CC which encodes DNA polymerase (pol), ORF10, ORF11, K2 which encodes viral
CC CC interleukin-6 (vIL-6), ORF02 which encodes dihydrofolate reductase
CC CC (DHFR), K3 which encodes BHV4-IE1 I, ORF70 which encodes thymidylate
CC CC synthase, K4 which encodes vMIP-II, K5 which encodes BHV4-IE1 II, K6
CC CC which encodes vMIP-I, K7, ORF16 which encodes Bcl-2, ORF17 which encodes
CC CC capsid protein I, ORF18 and ORF19 which encodes tegument protein I.
CC CC KSHV is a new human Herpesvirus (HHV8) believed to cause Kaposi's sarcoma
CC CC (KS) which is the most common form of neoplasm occurring in persons with
CC CC acquired immune deficiency syndrome (AIDS). The DHFR protein is useful
CC CC for vaccination, prophylaxis, diagnosis and treatment of a subject with
CC CC Kaposi's sarcoma and for detecting expression of a DNA virus associated
CC CC with Kaposi's sarcoma in a cell.
XX XX
SQ SQ Sequence 35100 BP; 8703 A; 9395 C; 8921 G; 8081 T; 0 other;

Query Match 0.1%; Score 29; DB 20; Length 35100;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14938 CTGGAGTTTGACTGCAGCTGGAGGACCT 14966
DB 12167 CTGGAGTTTGACTGCAGCTGGAGGACCT 12195

RESULT 22
AAV19941
ID AAV19941 standard; DNA: 137507 BP.
XX XX
AC AC AAV19941;
XX XX
DT DT 03-AUG-1998 (first entry)
XX XX
DE DE KSHV long unique coding region and terminal repeat.
XX XX
XX KSHV; HHV8; human herpes virus 8; macrophage inflammatory protein II;
XX K interleukin-6; IL-6; interferon regulatory factor; rheumatoid arthritis;
XX K complement-binding protein; glycoprotein; capsid protein IV; infection;
XX K immediate early protein; Kaposi's sarcoma; protective vaccine; lymphoma;
XX K lymphoproliferative disease; leukaemia; splenomegaly; mycosis fungoides;
XX K HIV immune status; anti-inflammatory agent; therapy; ds.
XX OS Kaposi's sarcoma-associated herpes virus.
XX FH Key Location/Qualifiers
XX FT 1142..2794
XX FT /*tag- a
XX FT /product- complement-binding protein
XX FT 8699..11236
XX FT /*tag- b
XX FT /product- glycoprotein B
XX FT complement (17261..17875)
XX FT /*tag- c
XX FT /product- interleukin 6
FT FT

```

```

FT CDS complement (21548..21832)
FT /tag= d
FT /product= macrophage inflammatory protein II
FT CDS complement (27137..27424)
FT /tag= e
FT /product= interferon regulatory factor 1
FT CDS 28661..29741
FT /tag= f
FT /product= protein T1.1
FT CDS complement (58976..60175)
FT /tag= g
FT /product= glycoprotein M
FT CDS complement (69412..69915)
FT /tag= h
FT /product= glycoprotein L
FT CDS complement (88410..88910)
FT /tag= i
FT /product= interferon regulatory factor 2
FT CDS 89600..90541
FT /tag= j
FT /product= interferon regulatory factor 3
FT CDS 90173..90643
FT /tag= k
FT /product= glycoprotein X
FT CDS complement (93636..94127)
FT /tag= l
FT /product= interferon regulatory factor 4
FT CDS complement (111931..112443)
FT /tag= m
FT /product= capsid protein IV
FT CDS complement (123808..127296)
FT /tag= n
FT /product= immediate early protein

XX WO9804576-A1.
XX
XX 05-FEB-1998.
XX
XX 22-JUL-1997; 97WO-US13346.
XX
XX 29-NOV-1996; 96US-0757669.
XX PR 25-JUL-1996; 96US-0686243.
XX PR 25-JUL-1996; 96US-0686349.
XX PR 25-JUL-1996; 96US-0686350.
XX PR 25-JUL-1996; 96US-0687253.
XX PR 25-JUL-1996; 96US-0688814.
XX PR 05-SEP-1996; 96US-0708678.
XX PR 10-OCT-1996; 96US-0728323.
XX PR 13-NOV-1996; 96US-0747887.
XX PR 13-NOV-1996; 96US-0748640.
XX
XX (UNIV ) UNIV COLUMBIA NEW YORK.
XX
XX Bohenzky RA, Chang Y, Edelman IS, Moore PS, Russo JJ;
XX
XX WPI; 1998-130615/12.
XX
XX New nucleic acid encoding Kaposi's sarcoma associated herpes virus
XX proteins - useful for, e.g. detecting levels of HHV8 in, and
XX preparation of vaccines for treatment of, HIV patients
XX
XX Example 2; Page 135-203; 230pp; English.
XX
XX This sequence represents the long unique region and terminal repeat of
XX the Kaposi's sarcoma-associated herpes virus (KSHV). KSHV is also known
XX as human herpes virus 8 (HHV8). This sequence contains the DNAs of the
XX invention which encode KSHV polypeptides selected from: (a) viral
XX macrophage inflammatory protein (MIP) II; (b) viral interleukin-6 (IL-6);
XX (c) viral IRF 1; (d) complement-binding protein; glycoproteins B, M or L;
XX (d) capsid protein IV encoded by ORF5; and (e) immediate early protein
XX encoded by ORF73. Labelled probes for the nucleic acid, proteins encoded
XX by it, and antibodies (Ab) specific for the proteins are useful for
XX detecting HHV8, specifically for diagnosis of Kaposi's sarcoma, in body

```

```

CC fluids or tissue samples. HHV8 infections can be treated with antisense
CC or triplex forming molecules or agents that bind specifically to the
CC protein. Ab may be used for prophylaxis or treatment of HHV8 infection,
CC while the protein can be used in protective vaccines. Ab may also be used
CC to differentiate between lymphomas, and HHV8 may be implicated in many
CC other lymphoproliferative diseases such as lymphomas, leukemia,
CC splenomegaly and mycosis fungoides. Cells and animals containing the
CC nucleic acid are useful for drug screening. HHV8-derived peptides can be
CC used as targets for antiviral drugs, e.g. dihydrofolate reductase gene
CC can be inhibited with methotrexate. These can also be used to determine
CC the immune status of a patient infected with HIV. HHV8 derived protein
CC viral MIP III may be used as an anti-inflammatory agent for,
CC e.g. treating rheumatoid arthritis. This sequence is stated as containing
CC 81 open reading frames.
XX
XX Sequence 137507 BP; 32579 A; 37795 C; 35758 G; 31375 T; 0 other;
XX
XX Query Match 0.1%; Score 29; DB 19; Length 137507;
XX Best Local Similarity 100.0%; Pred No. 0.14;
XX Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 14938 CTGAGTTTGACTGCAGCTGGAGGACCT 14966
XX |||||||||||||||||||||||||||
XX Db 12167 CTGAGTTTGACTGCAGCTGGAGGACCT 12195
XX
XX RESULT 23
XX AAT51545
XX ID AAT51545 standard; DNA; 536 BP.
XX
XX AC AAT51545;
XX
XX DT 06-NOV-1997 (first entry)
XX
XX DE Herpes virus DNA polymerase PCR segment RFHV encoding DNA.
XX
XX KW Retroperitoneal fibromatosis herpes virus; detection; infection;
XX Kaposi's sarcoma herpes virus; viral DNA; viral RNA; vaccine;
XX antigen; antibody; polymerase chain reaction; ss.
XX
XX OS Retroperitoneal fibromatosis herpes virus.
XX
XX FH Key Location/Qualifiers
XX FT 1..536
XX FT CDS /tag= a
XX FT /product= DNA_polymerase
XX FT /note= "No stop codon given"
XX
XX PN WO9704105-A1.
XX
XX PD 06-FEB-1997.
XX
XX PF 12-JUL-1996; 96WO-US11688.
XX
XX PR 11-JUL-1996; 96US-0001148.
XX PR 14-JUL-1995; 95US-0001148.
XX
XX (UNIV ) UNIV WASHINGTON.
XX
XX Bosch ML, Rose TM, Strand K, Todaro GJ;
XX
XX WPI; 1997-132644/12.
XX P-PSDB; AAM11993.
XX
XX Herpes virus DNA polymerase and corresponding nucleotide sequence -
XX used in the detection and treatment of herpes virus infection
XX
XX Claim 1; Page 78; 132pp; English.
XX
XX The present sequence represents a novel isolated polynucleotide with
XX a region encoding a DNA polymerase designated RFHV of a herpes virus.
XX This DNA polymerase was isolated from Retroperitoneal fibromatosis
XX herpes virus (RFHV) found in tissue samples taken from Macaque

```

CC nemestrina monkeys. Primers used in the amplification of
CC polynucleotides encoding DNA polymerases may be used for detecting
CC viral DNA or RNA in a sample of primate origin, especially in the
CC diagnosis of herpes viral infection. Herpes virus DNA polymerases of
CC this invention, may be used in vaccines for the protection against
CC infection by a herpes virus of the RRV/KSHV family. They may also be
CC used in the design and screening of anti-viral drugs. Antibodies
CC raised against the polymerase or fragments of it, may be used in the
CC detection of herpes virus infection and for drug targeting for the
CC therapy of herpes virus infection.

XX
SQ Sequence 536 BP; 137 A; 165 C; 134 G; 100 T; 0 other;
Query Match 0.1%; Score 26; DB 18; Length 536;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 16150 GATTAACACAGCTGCCATCAGCT 16175
Db 274 GATTAACACAGCTGCCATCAGCT 299
|||||

RESULT 24
AAS84956/C
ID AAS84956 standard; CDNA: 651 BP.
XX
AC AAS84956;
XX
DT 13-FEB-2002 (first entry)
XX
DE DNA encoding novel human diagnostic protein #20760.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US08631.
XX
PR 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI: 2001-639362/73.
DR P-PSDB: ABG20769.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX
PS Claim 1; SEQ ID NO 20760; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and
XX polypeptide (II) sequences. (I) is useful as hybridisation probes,
XX polymerase chain reaction (PCR) primers, oligomers, and for chromosome
XX and gene mapping, and in recombinant production of (II). The
XX polynucleotides are also used in diagnostics as expressed sequence tags
XX for identifying expressed genes. (I) is useful in gene therapy techniques
XX to restore normal activity of (II) or to treat disease states involving
XX (II). (II) is useful for generating antibodies against it, detecting or
XX quantitating a polypeptide in tissue, as molecular weight markers and as
XX a food supplement. (II) and its binding partners are useful in medical
XX imaging of sites expressing (II). (I) and (II) are useful for treating
XX disorders involving aberrant protein expression or biological activity.
XX The polypeptide and polynucleotide sequences have applications in

CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human
CC diagnostic coding sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pcr_sequences.
XX
SQ Sequence 651 BP; 152 A; 86 C; 241 G; 172 T; 0 other;
Query Match 0.1%; Score 26; DB 23; Length 651;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 21075 CTCGTGTCACGTGCAGACAGCTC 21100
Db 425 CTCGTGTCACGTGCAGACAGCTC 400
|||||

RESULT 25
AB283296/C
ID AB283296 standard; CDNA: 1024 BP.
XX
AC AB283296;
XX
DT 14-MAY-2003 (first entry)
XX
DE Toxicologically relevant human nucleotide sequence #455.
XX
KW Toxicologically relevant gene; toxicological response; gene; ss.
XX
OS Homo sapiens.
XX
PN WO2003016500-A2.
XX
PD 27-FEB-2003.
XX
PF 16-AUG-2002; 2002WO-US26514.
XX
PR 16-AUG-2001; 2001US-313080P.
XX
PA (PHAS-) PHASE-1 MOLECULAR TOXICOLOGY INC.
XX
PI Neft RE, Dunn RT, Adkins K, Pickett GG, Klier LD, Schmeisler K;
PI Alen P;
XX
DR WPI: 2003-268322/26.
XX
PT Determining a toxicological response to an agent, useful for screening
PT of drugs, comprises comparing the expression profile of one or more
PT human toxic response genes to a reference gene expression profile
PT indicative of toxicity -
XX
PS Claim 1; Page 162; 455pp; English.

XX The present invention describes a method (M1) for determining a
XX toxicological response to an agent, which comprises comparing the
XX expression profile of one or more human toxic response genes to a
XX reference gene expression profile indicative of toxicity, and so
XX determining the presence of a toxic response to the agent. Also
XX described: (1) an array comprising one or more polynucleotides selected
XX from the genes corresponding to the partial sequences given in AB282842
XX to AB284764, or their fragments of at least 20 nucleotides, or
XX homologues; and (2) determining if a gene putatively identified to be a
XX toxic response gene plays a role on toxic response pathways by
XX determining the expression profile of the gene after exposure of cells
XX or a human subject to a known toxic pharmaceutical or industrial agent,
XX comprising: (a) exposing cells to an agent or isolating cells from a
XX human subject who was exposed to an agent; (b) obtaining the test gene
XX expression profile for a putatively identified toxic response gene after
XX exposure to a known toxic pharmaceutical or industrial agent; and
XX (c) comparing the test profile to the expression profile of a gene with

CC TS and/or ERCC1 mRNA in the amplified sample and the threshold level for
CC TS and/or ERCC1 gene expression. The method is useful in medicine,
CC particularly cancer chemotherapy, i.e. treating tumours, e.g. colorectal
CC adenocarcinoma and in assessing tumour cell gene expression in a patient
CC and may also be used in prognosticating the efficacy of 5-Fluorouracil
CC and oxaliplatin-based therapies. This sequence represents the human TS
CC gene.
XX
SQ Sequence 1536 BP; 390 A; 369 C; 399 G; 378 T; 0 other;
Query Match 0.1%; Score 26; DB 24; Length 1536;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 21075 CTCGTACAGCTGCAGACAGCTC 21100
|||||
Db 749 CTCGTACAGCTGCAGACAGCTC 724

RESULT 28
ABK43335/C
ID ABK43335 standard; CDNA: 1536 BP.
XX
AC ABK43335;
XX
DT 05-JUN-2002 (first entry)
XX
DE Human Thymidylate synthase cDNA sequence.
XX
KW HKMG1; ss: gene: chromosome 18p; bipolar affective disorder: BAD;
KW severe bipolar affective (mood) disorder: BP-I; schizophrenia: TS;
KW Hong Kong new gene 1; antimanic; antidepressant; neuroleptic;
KW Thymidylate synthase.
XX
OS Homo sapiens.
XX
PN WO200210366-A2.
XX
PD 07-FEB-2002.
XX
PE 02-AUG-2001; 2001WO-US24417.
XX
PR 02-AUG-2000; 2000US-0631275.
PR 28-NOV-2000; 2000US-0722544.
XX
XX
PA (MILL-) MILENNIUM PHARM INC.
PA (REGC) UNIV CALIFORNIA.
XX
PI Chen H, Frelmer NB, Novak T;
XX
DR WPI: 2002-195962/25.
DR P-PSDB; AAU87071.
XX
PT New nucleic acid molecule Hong Kong New Gene 1 (HKNG1), useful for
PT screening for molecules which modulate HKNG1 expression for the
PT treatment of bipolar disorder and schizophrenia -
XX
PS Disclosure: Fig 45; 367pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule comprising a
CC nucleotide sequence that encodes a Hong Kong New Gene (HKNG) 1 gene
CC product. The human gene for HKNG1 is located on chromosome 18p in
CC an area associated with bipolar affective disorder, BAD. Also
CC included are an expression vector comprising the nucleic acid, a
CC host cell expressing the nucleic acid, an anti-HKNG1 antibody, a method
CC of identifying modulators of HKNG1, and identifying an individual (at
CC risk of) having HKNG1-mediated disorder comprising detecting the presence
CC or absence of a polymorphism that correlates with an HKNG1 allele
CC associated with the disorder, where the presence of the polymorphism
CC indicates that the individual (is at risk of) having HKNG1-mediated
CC disorder. A (small molecule) compound which modulates (inhibits or
CC potentiates) expression of a HKNG1 gene or gene product in a human
CC individual is useful for the treatment of a HKNG1-mediated disorder

CC such as bipolar affective disorder (BAD), severe bipolar affective (mood)
CC disorder (BP-I) and schizophrenia. The present sequence is the cDNA
CC encoding thymidylate synthase, TS. The gene for TS
CC overlaps that of HKMG1 and therefore TS may also be involved in the
CC diseases listed above.
XX
SQ Sequence 1536 BP; 390 A; 369 C; 399 G; 378 T; 0 other;
Query Match 0.1%; Score 26; DB 24; Length 1536;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 21075 CTCGTACAGCTGCAGACAGCTC 21100
|||||
Db 749 CTCGTACAGCTGCAGACAGCTC 724

RESULT 29
AAT84648
ID AAT84648 standard; DNA: 3056 BP.
XX
AC AAT84648;
XX
DT 02-JAN-1998 (first entry)
XX
DE KSHV capsid maturation and glycoprotein B genes.
XX
KW KSHV; gamma herpes virus; glycoprotein B; vaccine; infection;
KW diagnosis; ss.
XX
OS Human Kaposi's sarcoma-associated herpesvirus.
XX
XX
FH Key Location/Qualifiers
FH CDS 2..409
ET /*tag= a
ET /product= capsid/maturation/transport protein
ET 393..2930
FT /*tag= b
FT /product= glycoprotein B
XX
XX WO9712042-A2.
XX
XX 03-APR-1997.
XX
XX 26-SEP-1996; 96WO-US15702.
XX
XX 26-SEP-1995; 95US-0004297.
XX
XX (UNIW) UNIV WASHINGTON.
XX
XX Bosch ML, Rose TM, Strand K;
XX
PI WPI: 1997-212901/19.
DR P-PSDB; AAW26475; AAW26487.
XX
PT DNA encoding glycoprotein B of retroperitoneal fibromatosis and
PT Kaposi's sarcoma associated herpes viruses - useful in vaccines for
PT treatment of herpes infection or for detection of viral DNA
XX
XX Claim 7; Fig 19a-c; 138pp; English.
XX
XX This DNA sequence contains overlapping open reading frames coding
CC for the capsid maturation protein (AAW26487) and claimed glycoprotein
CC B (9B) (AAW26475) of human Kaposi's sarcoma-associated herpes virus
CC (KSHV). It is a consensus of sequences obtained by PCR
CC amplification of Kaposi's sarcoma tissue DNA using primers based on
CC consensus segments of gamma herpes viruses. Herpes viruses
CC glycoprotein B molecules are associated with fibroproliferative and
CC neoplastic conditions in primates, including humans. Glycoprotein
CC B polypeptides and polynucleotides (see also AAT84641-42; AAT84649) can
CC be used in vaccines, e.g. live virus or viral expression vectors,
CC for the treatment of herpes virus infection, or for the detection
CC of viral DNA or RNA in a sample. Polynucleotides can also be used

CC for recombinant production of glycoprotein B. Probes (see AAT84643-46,
CC AAT84650-96) are claimed and can be used for the detection of gamma
CC herpes viruses, of KSHV and retroperitoneal fibromatosis-associated
CC herpes virus (RFHV), or for the specific detection of RFHV or KSHV.
CC Primers based on RFHV or KSHV sequences can be used in the PCR
CC amplification of glycoprotein B polynucleotides.
XX
SQ Sequence 3056 BP; 823 A; 847 C; 741 G; 641 T; 4 other;
Query Match 0.1%; Score 26; DB 18; Length 3056;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DY 11454 GGCTGGATATTTAAAGACCTGTACGC 11479
|||
DB 332 GGCTGGATATTTAAAGACCTGTACGC 357
RESULT 30
AAS94945/C
ID AAS94945 standard; DNA; 3298 BP.
XX
AC AAS94945;
XX
DT 14-FEB-2002 (first entry)
XX
DE Human DNA sequence #200 expressed during foam cell differentiation.
XX
KW Human: foam cell differentiation; atherosclerosis; cerebral stroke;
KW cardiovascular disorder; coronary artery disease; gene therapy; ds.
XX
OS Homo sapiens.
XX
PN WO200177389-A2.
XX
PD 18-OCT-2001.
XX
PF 04-APR-2001; 2001WO-US11128.
XX
PR 05-APR-2000; 2000US-195106P.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Shiffman D, Somogyi R, Lawn R, Sellhammer JJ, Porter GJ, Mikita T;
PI Tai J;
XX
DR WPI; 2002-010925/01.
XX
PT Composition useful for diagnosis of conditions, disorders or diseases
PT associated with atherosclerosis, comprises several polynucleotides that
PT are differentially expressed in foam cell development -
PS
PS Claim 1; Page 250-251; 315pp; English.
XX
CC The present invention relates to the isolation of human polynucleotide
CC sequences that are differentially expressed during foam cell
CC differentiation. The polynucleotide sequences of the invention or a
CC composition comprising these polynucleotides are useful as a high
CC throughput method for detecting altered expression of one or more
CC polynucleotides in a sample. The polynucleotides can be used in the
CC diagnosis of disorders associated with foam cell development such as
CC atherosclerosis, cerebral stroke, and cardiovascular disorders such as
CC coronary artery disease. The polynucleotide sequences can also be used
CC as PCR primers and probes. The polynucleotides of the invention are also
CC useful in gene therapy. AAS94746-AAS95021 represent the human
CC polynucleotide sequences of the invention which are differentially
CC expressed during foam cell differentiation.
XX
SQ Sequence 3298 BP; 898 A; 709 C; 744 G; 919 T; 28 other;
Query Match 0.1%; Score 26; DB 24; Length 3298;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DY 21075 CTCTGTACAGCTGCAGACAGCTC 21100
|||
DB 728 CTCTGTACAGCTGCAGACAGCTC 703
RESULT 31
AAT84697
ID AAT84697 standard; DNA; 3612 BP.
XX
AC AAT84697;
XX
DT 02-JAN-1998 (first entry)
XX
DE KSHV capsid maturation, glycoprotein B, DNA polymerase genes.
XX
KW KSHV; gamma herpes virus; glycoprotein B; vaccine; infection;
KW diagnosis; capsid maturation; DNA polymerase; ss.
XX
OS Human Kaposi's sarcoma-associated herpesvirus.
XX
FH Key Location/Qualifiers
FH CDS 2..409
FT /*tag= a
FT /product= capsid/maturation/transport protein
FT 393..2930
FT CDS /*tag= b
FT /product= glycoprotein B
FT CDS 3057..3611
FT /*tag= c
FT /product= DNA polymerase
XX
PN WO9712042-A2.
XX
PD 03-APR-1997.
XX
PF 26-SEP-1996; 96WO-US15702.
XX
PR 26-SEP-1995; 95US-0004297.
XX
PA (UNITV) UNITV WASHINGTON.
XX
PI Bosch ML, Rose TM, Strand K;
XX
DR WPI; 1997-212901/19.
XX
DR P-PSDB; AAM26475, AAM26487, AAM26488.
XX
PT DNA encoding glycoprotein B of retroperitoneal fibromatosis and
PT Kaposi's sarcoma associated herpes viruses - useful in vaccines for
PT treatment of herpes infection or for detection of viral DNA
XX
PS Example 7; Fig 19a-c; 138pp; English.
XX
CC This DNA sequence contains open reading frames coding for the
CC capsid maturation protein (AAM26487), the claimed glycoprotein
CC B (9b) (AAM26475) and the DNA polymerase (AAM26488) of human Kaposi's
CC sarcoma-associated herpes virus (KSHV). It is a consensus of
CC sequences obtained by PCR amplification of Kaposi's sarcoma tissue
CC DNA using primers based on consensus segments of gamma herpes
CC viruses. Herpes viruses glycoprotein B molecules are associated
CC with fibroproliferative and neoplastic conditions in primates,
CC including humans. Glycoprotein B polypeptides and polynucleotides
CC (see also AAT84641-42, AAT84648-49) can be used in vaccines, e.g. live
CC virus or viral expression vectors, for the treatment of herpes
CC virus infection, or for the detection of viral DNA or RNA in a
CC sample. Polynucleotides can also be used for recombinant
CC production of glycoprotein B. Probes (see AAT84643-46, AAT84650-96)
CC are claimed and can be used for the detection of gamma herpes
CC viruses, of KSHV and retroperitoneal fibromatosis-associated
CC herpes virus (RFHV), or for the specific detection of RFHV or KSHV.
CC Primers based on RFHV or KSHV sequences can be used in the PCR
CC amplification of glycoprotein B polynucleotides.

SO Sequence 3612 BP; 944 A; 1033 C; 883 G; 748 T; 4 other;
Query Match 0.1%; Score 26; DB 18; Length 3612;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11454 GGCTGATATTAAAGACCTGTACGC 11479
|||||
DB 332 GGCTGATATTAAAGACCTGTACGC 357

RESULT 32
AAF31109/c
ID AAF31109 standard; cDNA; 18596 BP.
XX
AC AAF31109;
XX
DT 27-APR-2001 (first entry)
XX
DE Thymidylate synthase coding sequence.
XX
KM Analyte-binding enzyme; analyte analysis; ss.
XX
OS Homo sapiens.
XX
PN WO200102600-A2.
PD 11-JAN-2001.
XX
PF 30-JUN-2000; 2000WO-US18057.
XX
PR 06-JUL-1999; 99US-0347878.
PR 06-DEC-1999; 99US-0457205.
XX
PA (GRAT) GEN ATOMICS.
XX
PI Yuan C;
DR WPI; 2001-071583/08.
XX
XX Assaying method, useful for prognosis and diagnosis of disease,
PT comprises contacting sample with a mutant analyte-binding enzyme and
PT detecting binding -
XX
PS Disclosure: Page -: 187pp; English.
XX
CC The present invention relates to a method for assaying an analyte in a
CC sample comprising: contacting the sample with a mutant analyte-binding
CC enzyme which has binding affinity for the analyte or an immediate
CC analog; enzymatic conversion product but has attenuated catalytic
CC activity; and detecting resulting binding. The method is useful in
CC monitoring biological systems/processes, or prognosis/diagnosis of
CC disease caused by imbalances of the analytes. The present sequence is
CC a coding sequence used in the present invention.
CC Note: the present sequence is not shown in the specification, but was
CC from Genbank, using information given in the specification.
XX
SQ Sequence 18596 BP; 4521 A; 3991 C; 4479 G; 5605 T; 0 other;

Query Match 0.1%; Score 26; DB 22; Length 18596;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 21075 CTCTGTACAGCTGCGACAGACGCTC 21100
|||||
DB 13536 CTCTGTACAGCTGCGACAGACGCTC 13511

RESULT 33
AAC91215/c
ID AAC91215 standard; DNA; 18596 BP.
XX
AC AAC91215;

XX
DT 20-MAR-2001 (first entry)
XX
DE Human thymidylate synthase gene SRQ ID NO: 11.
XX
KM Human; schizophrenia; developmental disorder; spina bifida cystica;
KM Tourette's syndrome; bipolar illness; conduct disorder;
KM attention deficit disorder; obsessive compulsive disorder;
KM chronic multiple tic syndrome; learning disorder; polymorphism; ds.
XX
OS Homo sapiens.
XX
PN WO200071754-A1.
PD 30-NOV-2000.
XX
PF 24-MAY-2000; 2000WO-US14354.
XX
PR 25-MAY-1999; 99US-0318448.
XX
PA (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.
XX
PI Johnson WG, Stenroos ES;
DR WPI; 2001-025174/03.
XX
XX Diagnosing a developmental disorder, e.g. schizophrenia, by forming
PT datasets (DS) of genetic (e.g. genotypes of folate metabolism alleles)
PT and environmental variables affecting an individual and then comparing
PT these DS with reference DS -
XX
PS Disclosure: Page 125-131; 156pp; English.
XX
CC The present invention provides a novel method of estimating the
CC susceptibility of an individual to a developmental disorder using genetic
CC and environmental variables. The method can be used in the diagnosis,
CC prevention and treatment of disorders such as schizophrenia, spina bifida
CC cystica, Tourette's syndrome, bipolar illness, autism, conduct disorders,
CC attention deficit disorder, obsessive compulsive disorder, chronic
CC multiple tic syndrome and learning disorders such as dyslexia.
XX
SQ Sequence 18596 BP; 4521 A; 3991 C; 4479 G; 5605 T; 0 other;

Query Match 0.1%; Score 26; DB 22; Length 18596;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 21075 CTCTGTACAGCTGCGACAGACGCTC 21100
|||||
DB 13536 CTCTGTACAGCTGCGACAGACGCTC 13511

RESULT 34
ABN95092/c
ID ABN95092 standard; DNA; 18596 BP.
XX
AC ABN95092;
XX
DT 13-AUG-2002 (first entry)
XX
DE Gene #1590 used to diagnose liver cancer.
XX
KM Gene; liver cancer; ds; hepatocellular carcinoma; hepatotropic;
KM metastatic liver tumour; cytostatic; expression profile; disease state;
KM disease progression; drug toxicity; drug efficacy; drug metabolism.
XX
OS Homo sapiens.
XX
PN WO200229103-A2.
PD 11-APR-2002.
XX
PF 02-OCT-2001; 2001WO-US30589.

XX		02-OCT-2000; 2000US-237054P.
PR		(GENE-) GENE LOGIC INC.
XX	PA	
XX	P1	Horne D, Alvares C, Peres-Da-Silva S, Vockley JG;
DR		WPI; 2002-426119/45.
XX		
PT		Diagnosing and detecting the progression of liver cancer,
PT		hepatocellular carcinoma or metastatic liver tumor in a patient,
PT		Involves detecting the level of expression of two or more genes in a
PT		liver tissue sample .
XX		
SQ		Claim 1: SEQ ID NO 1590; 298bp; English.
XX		
CC		The invention relates to a novel method for diagnosing and detecting the
CC		progression of liver cancer, hepatocellular carcinoma or metastatic liver
CC		tumour in a patient, and differentiating metastatic liver cancer from
CC		hepatocellular carcinoma in a patient, involving detecting the level of
CC		expression of two or more genes represented in ABN93503-ABN97455 in a
CC		tissue sample. The method of the invention has hepatotropic, and
CC		cytostatic activity. The method is useful for diagnosing and detecting
CC		the progression of liver cancer, hepatocellular carcinoma and metastatic
CC		liver carcinoma in a patient. The method is useful for identifying
CC		expression profiles which serve as useful diagnostic markers as well as
CC		markers that can be used to monitor disease states, disease progression,
CC		drug toxicity, drug efficacy and drug metabolism.
CC		Note: The sequence data for this patent did not form part of the printed
CC		specification, but was obtained in electronic format directly from WIPO
CC		at ftp.wipo.int/pub/published_pct_sequences.
XX		
SQ		Sequence 18596 BP; 4521 A; 3991 C; 4479 G; 5605 T; 0 other;
Query Match		0.1%; Score 26; DB 24; Length 18596;
Best Local Similarity		100.0%; Pred. No. 2.7;
Matches		26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY		21075 CTCGTGACAGCTGCAGACAGCTC 21100
DDB		13536 CTCGTGACAGCTGCAGACAGCTC 13511
RESULT 35		
ABK43334/C		
ID		ABK43334 standard; DNA; 18596 BP.
XX		
AC		ABK43334;
XX		
DT		05-JUN-2002 (first entry)
XX		
DE		Human Thymidylate synthase gene sequence.
XX		
KX		HKNG1; ds; gene; chromosome 18p; bipolar affective disorder; BAD;
KW		severe bipolar affective (mood) disorder; BP-I; schizophrenia; TS;
KM		Hong Kong new gene 1; anti manic; antidepressant; neuroleptic;
KX		Thymidylate synthase.
OS		Homo sapiens.
PN		WO200210366-A2.
PD		07-FEB-2002.
PF		02-AUG-2001; 2001WO-US24417.
PR		02-AUG-2000; 2000US-0631275.
XX		28-NOV-2000; 2000US-0722544.
PA		(MILL-) MILLENNIUM PHARM INC.
PA		(REGC) UNIV CALIFORNIA.
TI		Chen H, Freimer NB, Novak T;

XX	WP1: 2002-195962/25.
DR	New nucleic acid molecule Hong Kong New Gene 1 (HKNG1), useful for
XX	screening for molecules which modulate HKNG1 expression for the
PT	treatment of bipolar disorder and schizophrenia -
PT	
XX	Disclosure; Fig 44; 367pp; English.
PS	
XX	The invention relates to an isolated nucleic acid molecule comprising a
CC	nucleotide sequence that encodes a Hong Kong New Gene (HKNG) 1 gene
CC	product. The human gene for HKNG1 is located on chromosome 18p in
CC	an area associated with bipolar affective disorder, BAD. Also,
CC	included are an expression vector comprising the nucleic acid, a
CC	host cell expressing the nucleic acid, an anti-HKNG1 antibody, a method
CC	of identifying modulators of HKNG1, and identifying an individual (at
CC	risk of) having HKNG1-mediated disorder comprising detecting the presence
CC	or absence of a polymorphism that correlates with an HKNG1 allele
CC	associated with the disorder, where the presence of the polymorphism
CC	indicates that the individual (is at risk of) having HKNG1-mediated
CC	disorder. A (small molecule) compound which modulates (inhibits or
CC	potentiates) expression of a HKNG1 gene or gene product in a human
CC	individual is useful for the treatment of a HKNG1-mediated disorder
CC	such as bipolar affective disorder (BAD), severe bipolar affective (mood)
CC	disorder (BP-I) and schizophrenia. The present sequence is a
CC	thymidylate synthase, TS, genomic DNA sequence. The gene for TS
CC	overlaps that of HKNG1 and therefore TS may also be involved in the
CC	diseases listed above.
XX	
SQ	Sequence 18556 BP; 4521 A; 3991 C; 4479 G; 5605 T; 0 other;
	Query Match 0.1%; Score 26; DB 24; Length 18596;
	Best Local Similarity 100.0%; Pred. No. 2.7;
	Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0
OY	21075 CTGTGATACAGCTGGCAGACAGCTC 21100
DB	13536 CTGTGTRACAGCTGGCAGACAGCTC 13511
RESULT 36	
ABL62854/C	
ID	ABL62854 standard; DNA; 18556 BP.
XX	
AC	ABL62854;
XX	
DT	15-MAY-2002 (first entry)
DE	Breast cancer related gene sequence SEQ ID NO:1191.
XX	
KW	Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
KW	stomach; lung; prostate; pancreas; carcinoma; antitumour; carcinous;
KW	cyclostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
XX	gene; ds.
XX	
OS	Homo sapiens.
PN	WO200194629-A2.
PD	
XX	
XX	13-DEC-2001.
PF	
XX	30-MAY-2001; 2001WO-US10838.
PR	
PR	05-JUN-2000; 2000US-209473P.
PR	05-JUN-2000; 2000US-209531P.
PR	18-SEP-2000; 2000US-233133P.
PR	18-SEP-2000; 2000US-233617P.
PR	20-SEP-2000; 2000US-234009P.
PR	20-SEP-2000; 2000US-234034P.
PR	20-SEP-2000; 2000US-234052P.
PR	22-SEP-2000; 2000US-234509P.
PR	22-SEP-2000; 2000US-234567P.
PR	25-SEP-2000; 2000US-234923P.
RR	

PR 25-SEP-2000; 2000US-234924P.
PR 25-SEP-2000; 2000US-235077P.
PR 25-SEP-2000; 2000US-235082P.
PR 25-SEP-2000; 2000US-235134P.
PR 25-SEP-2000; 2000US-235280P.
PR 26-SEP-2000; 2000US-235637P.
PR 26-SEP-2000; 2000US-235638P.
PR 27-SEP-2000; 2000US-235711P.
PR 27-SEP-2000; 2000US-235720P.
PR 27-SEP-2000; 2000US-235840P.
PR 27-SEP-2000; 2000US-235863P.
PR 28-SEP-2000; 2000US-236028P.
PR 28-SEP-2000; 2000US-236032P.
PR 28-SEP-2000; 2000US-236033P.
PR 28-SEP-2000; 2000US-236034P.
PR 28-SEP-2000; 2000US-236109P.
PR 28-SEP-2000; 2000US-236111P.
PR 29-SEP-2000; 2000US-236842P.
PR 29-SEP-2000; 2000US-236891P.
PR 02-OCT-2000; 2000US-237172P.
PR 02-OCT-2000; 2000US-237173P.
PR 02-OCT-2000; 2000US-237278P.
PR 02-OCT-2000; 2000US-237294P.
PR 02-OCT-2000; 2000US-237295P.
PR 02-OCT-2000; 2000US-237316P.
PR 03-OCT-2000; 2000US-237425P.
PR 03-OCT-2000; 2000US-237598P.
PR 03-OCT-2000; 2000US-237604P.
PR 03-OCT-2000; 2000US-237606P.
PR 03-OCT-2000; 2000US-237608P.
PR 01-NOV-2000; 2000US-244867P.
PR 01-NOV-2000; 2000US-245084P.
XX
XX (AVALON PHARM.
PI Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
PI Soppet DR, Weaver Z;
XX
XX WPI: 2002-188264/24.
XX
XX Screening for anti-neoplastic agent involves exposing cells to a
PT chemical agent to be tested for anti-neoplastic activity and
PT determining a change in expression of a gene of a signature gene set -
XX
XX
XX Claim 1: SEQ ID 1191; 44pp; English.
XX
XX The present invention describes a method (M1) for screening for an
CC anti-neoplastic agent. The method involves exposing cells to a chemical
CC agent to be tested for anti-neoplastic activity, determining a change in
CC expression of at least one gene (I) of a signature gene set, where (I)
CC comprises a sequence (S) selected from 8447 sequences (given in ABL61664
CC to ABL70110), or is at least 95% identical to (S), where a change in
CC expression is indicative of anti-neoplastic activity. (I) has cytostatic
CC activity and can be used in gene therapy. M1 can be used for screening
CC an anti-neoplastic agent, and can be used for producing a product which
CC is the data collected with respect to the anti-neoplastic agent as a
CC result of M1, and the data is sufficient to convey the chemical
CC structure and/or properties of the agent. M1 can be used in the
CC treatment of cancer such as colon, breast, stomach, lung, thyroid,
CC oesophageal, ovarian, kidney, prostate or pancreatic cancer,
CC adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer,
CC infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine
CC carcinoma, papillary carcinoma and Wilms' tumour.
XX
XX Sequence 18596 BP; 4521 A; 3991 C; 4479 G; 5605 T; 0 other;

Query Match 0.1%; Score 26; DB 24; Length 18596;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21075 CTCGTGCTACGCTGCAGACAGCTC 21100
DB 13536 CTCGTGCTACGCTGCAGACAGCTC 13511

RESULT 37
ABL63078/C
ID ABL63078 standard; DNA; 18596 BP.
XX
XX ABL63078;
XX
XX 15-MAY-2002 (first entry)
XX
XX Breast cancer related gene sequence SEQ ID NO:1415.
XX
XX
XX Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
XX stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
XX cytostatic; gene therapy; antineoplastic; Wilms' tumour; adenocarcinoma;
XX gene; ds.
XX
XX Homo sapiens.
XX
XX WO200194629-A2.
XX
XX 13-DEC-2001.
XX
XX 30-MAY-2001; 2001WO-US10838.
XX
XX 05-JUN-2000; 2000US-209473P.
XX 05-JUN-2000; 2000US-209531P.
XX 18-SEP-2000; 2000US-233133P.
XX 18-SEP-2000; 2000US-233617P.
XX 20-SEP-2000; 2000US-234009P.
XX 20-SEP-2000; 2000US-234034P.
XX 20-SEP-2000; 2000US-234052P.
XX 22-SEP-2000; 2000US-234509P.
XX 22-SEP-2000; 2000US-234567P.
XX 25-SEP-2000; 2000US-234923P.
XX 25-SEP-2000; 2000US-234924P.
XX 25-SEP-2000; 2000US-235077P.
XX 25-SEP-2000; 2000US-235082P.
XX 25-SEP-2000; 2000US-235134P.
XX 25-SEP-2000; 2000US-235280P.
XX 26-SEP-2000; 2000US-235637P.
XX 26-SEP-2000; 2000US-235638P.
XX 27-SEP-2000; 2000US-235711P.
XX 27-SEP-2000; 2000US-235720P.
XX 27-SEP-2000; 2000US-235840P.
XX 27-SEP-2000; 2000US-235863P.
XX 28-SEP-2000; 2000US-236028P.
XX 28-SEP-2000; 2000US-236032P.
XX 28-SEP-2000; 2000US-236033P.
XX 28-SEP-2000; 2000US-236034P.
XX 28-SEP-2000; 2000US-236109P.
XX 28-SEP-2000; 2000US-236111P.
XX 29-SEP-2000; 2000US-236842P.
XX 29-SEP-2000; 2000US-236891P.
XX 02-OCT-2000; 2000US-237172P.
XX 02-OCT-2000; 2000US-237173P.
XX 02-OCT-2000; 2000US-237278P.
XX 02-OCT-2000; 2000US-237294P.
XX 02-OCT-2000; 2000US-237295P.
XX 02-OCT-2000; 2000US-237316P.
XX 03-OCT-2000; 2000US-237425P.
XX 03-OCT-2000; 2000US-237598P.
XX 03-OCT-2000; 2000US-237604P.
XX 03-OCT-2000; 2000US-237606P.
XX 03-OCT-2000; 2000US-237608P.
XX 01-NOV-2000; 2000US-244867P.
XX 01-NOV-2000; 2000US-245084P.
XX
XX (AVALON PHARM.
PI Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
PI Soppet DR, Weaver Z;
XX

DR WPI: 2002-188264/24.

XX Screening for anti-neoplastic agent involves exposing cells to a

PT chemical agent to be tested for anti-neoplastic activity, and

PT determining a change in expression of a gene of a signature gene set

XX

PS Claim 1: SEQ ID 1415; 44pp; English.

XX

CC The present invention describes a method (M1) for screening for an

CC anti-neoplastic agent. The method involves exposing cells to a chemical

CC agent to be tested for anti-neoplastic activity, determining a change in

CC expression of at least one gene (I) of a signature gene set, where (I)

CC comprises a sequence (S) selected from 8447 sequences (given in ABL61664

CC to ABL70110), or is at least 95% identical to (S), where a change in

CC expression is indicative of anti-neoplastic activity. (I) has cytostatic

CC activity and can be used in gene therapy. M1 can be used for screening

CC an anti-neoplastic agent, and can be used for producing a product which

CC is the data collected with respect to the anti-neoplastic agent as a

CC result of M1, and the data is sufficient to convey the chemical

CC structure and/or properties of the agent. M1 can be used in the

CC treatment of cancer such as colon, breast, stomach, lung, thyroid,

CC oesophageal, ovarian, kidney, prostate or pancreatic cancer,

CC adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer,

CC infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine

CC carcinoma, papillary carcinoma and Wilm's tumour.

CC

XX

SO Sequence 18596 BP: 4521 A; 3991 C; 4479 G; 5605 T; 0 other:

Query Match 0.1%; Score 26; DB 24; Length 18596;

Best Local Similarity 100.0%; Pred. No. 2.7;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 21075 CTCTGTACAGCTGGCAGACAGCTC 21100

DB 13536 CTCTGTACAGCTGGCAGACAGCTC 13511

RESULT 38

ABL67927/c

ID ABL67927 standard; DNA; 18596 BP.

XX

AC ABL67927;

XX

DT 15-MAY-2002 (first entry)

XX

DE Ovary cancer related gene sequence SEQ ID NO:6264.

XX

KW Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;

KW stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;

KW cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;

KW gene; ds.

XX

OS Homo sapiens.

XX

PN WO200194629-A2.

XX

PD 13-DEC-2001.

XX

PF 30-MAY-2001; 2001WO-US10838.

XX

PR 05-JUN-2000; 2000US-209473P.

PR 05-JUN-2000; 2000US-209531P.

PR 18-SEP-2000; 2000US-233133P.

PR 18-SEP-2000; 2000US-233617P.

PR 20-SEP-2000; 2000US-234009P.

PR 20-SEP-2000; 2000US-234034P.

PR 20-SEP-2000; 2000US-234052P.

PR 22-SEP-2000; 2000US-234509P.

PR 22-SEP-2000; 2000US-234567P.

PR 25-SEP-2000; 2000US-234923P.

PR 25-SEP-2000; 2000US-234924P.

PR 25-SEP-2000; 2000US-235077P.

PR 25-SEP-2000; 2000US-235082P.

PR 25-SEP-2000; 2000US-235134P.

PR 25-SEP-2000; 2000US-235280P.

PR 26-SEP-2000; 2000US-235637P.

PR 26-SEP-2000; 2000US-235638P.

PR 27-SEP-2000; 2000US-235711P.

PR 27-SEP-2000; 2000US-235720P.

PR 27-SEP-2000; 2000US-235840P.

PR 27-SEP-2000; 2000US-235863P.

PR 28-SEP-2000; 2000US-236028P.

PR 28-SEP-2000; 2000US-236032P.

PR 28-SEP-2000; 2000US-236033P.

PR 28-SEP-2000; 2000US-236034P.

PR 28-SEP-2000; 2000US-236109P.

PR 28-SEP-2000; 2000US-236111P.

PR 29-SEP-2000; 2000US-236842P.

PR 29-SEP-2000; 2000US-236891P.

PR 02-OCT-2000; 2000US-237172P.

PR 02-OCT-2000; 2000US-237173P.

PR 02-OCT-2000; 2000US-237278P.

PR 02-OCT-2000; 2000US-237294P.

PR 02-OCT-2000; 2000US-237295P.

PR 02-OCT-2000; 2000US-237295P.

PR 03-OCT-2000; 2000US-237316P.

PR 03-OCT-2000; 2000US-237425P.

PR 03-OCT-2000; 2000US-237598P.

PR 03-OCT-2000; 2000US-237604P.

PR 03-OCT-2000; 2000US-237606P.

PR 03-OCT-2000; 2000US-237608P.

PR 01-NOV-2000; 2000US-244867P.

PR 01-NOV-2000; 2000US-245084P.

XX

PA (AVAL-) AVALON PHARM.

XX

PI Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;

PI Soppet DR, Weaver Z;

XX

DR WPI: 2002-188264/24.

XX

XX Screening for anti-neoplastic agent involves exposing cells to a

PT chemical agent to be tested for anti-neoplastic activity, and

PT determining a change in expression of a gene of a signature gene set

XX

PS Claim 1: SEQ ID 6264; 44pp; English.

XX

CC The present invention describes a method (M1) for screening for an

CC anti-neoplastic agent. The method involves exposing cells to a chemical

CC agent to be tested for anti-neoplastic activity, determining a change in

CC expression of at least one gene (I) of a signature gene set, where (I)

CC comprises a sequence (S) selected from 8447 sequences (given in ABL61664

CC to ABL70110), or is at least 95% identical to (S), where a change in

CC expression is indicative of anti-neoplastic activity. (I) has cytostatic

CC activity and can be used in gene therapy. M1 can be used for screening

CC an anti-neoplastic agent, and can be used for producing a product which

CC is the data collected with respect to the anti-neoplastic agent as a

CC result of M1, and the data is sufficient to convey the chemical

CC structure and/or properties of the agent. M1 can be used in the

CC treatment of cancer such as colon, breast, stomach, lung, thyroid,

CC oesophageal, ovarian, kidney, prostate or pancreatic cancer,

CC adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer,

CC infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine

CC carcinoma, papillary carcinoma and Wilm's tumour.

CC

XX

SO Sequence 18596 BP: 4521 A; 3991 C; 4479 G; 5605 T; 0 other:

Query Match 0.1%; Score 26; DB 24; Length 18596;

Best Local Similarity 100.0%; Pred. No. 2.7;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 21075 CTCTGTACAGCTGGCAGACAGCTC 21100

DB 13536 CTCTGTACAGCTGGCAGACAGCTC 13511

RESULT 39

ABL38559/C	standard; cDNA: 535 BP.
ABL38559	
ABL38559	
08-APR-2002	(first entry)
Human colon tumour antigen polynucleotide SEQ ID NO:2148.	
Human; colon cancer; colon tumour antigen; cytosolic; vaccine; colon tumour metastatic antigen; diagnosis; gene; ss.	
Homo sapiens.	
WO200196388-A2.	
20-DEC-2001.	
08-JUN-2001; 2001WO-US18557.	
09-JUN-2000; 2000US-210899P.	
20-FEB-2001; 2001US-270216P.	
(CORI-) CORIXA CORP.	
Jiang Y, Harlocker SL, Secretist H;	
WPI; 2002-114514/15.	
Novel isolated colon tumor polynucleotide differentially expressed in colon tumor or colon metastatic tumor and polypeptides encoded by them, useful for inhibiting development of cancer in patient -	
Claim 1; SEQ ID 2148; 105pp; English.	
ABL36412 to ABL38645 represent human colon tumour antigen cDNA clones (I) which were isolated from human colon tumour and colon metastatic tumour cDNA libraries. (I) have cytosolic activity and can be used in vaccine production. (I) can be used for stimulating and/or expanding T cells specific for a tumour protein on contact with the T cells. They are also useful for inhibiting the development of cancer in a patient. (I) can be used as probes or primers for nucleic acid hybridisation, for preparing mutant species primers, or primers for use in genetic constructions. (I) can be used in the diagnosis of a colon tumour.	
Sequence 535 BP; 135 A; 129 C; 151 G; 118 T; 2 other;	
Query Match	0.1%; Score 24; DB 24; Length 535;
Best Local Similarity	100.0%; Pred. No. 24;
Matches	24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
21442	TGATAAACACACAGACACTCTCTCA 21465
180	TGATAAACACACAGCACTCTCTCA 157
RESULT 40	
AAS84960	
AAS84960 standard; cDNA: 1539 BP.	
AAS84960;	
13-FEB-2002 (first entry)	
DNA encoding novel human diagnostic protein #20764.	
Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.	
Homo sapiens.	
WO200175067-A2.	

PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US08631.
XX
PR 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX
PA (HYSE-) HYSEQ INC.
XX
XX Drmanac RT, Liu C, Tang YT;
PI WPI: 2001-639362/73.
DR P-PDB: ABG20773.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
PS Claim 1; SEQ ID NO 20764; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human
CC diagnostic coding sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 1539 BP; 396 A; 379 C; 347 G; 417 T; 0 other:

Query Match 0.1%; Score 24; DB 23; Length 1539;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21442 TGATAAACACAGCAACTCTCCA 21465
XXXXXXXXXXXXXXXXXXXXX
DB 1263 TGATAAACACAGCAACTCTCCA 1286

RESULT 41
ABA09660
ID ABA09660 standard; DNA; 1692 BP.
XX
XX ABA09660;
DT 15-JAN-2002 (first entry)
DE Human bone marrow expressed oligonucleotide SEQ ID NO: 169.
XX
XX Human: bone marrow; cytosolic; antirheumatic; antiarthritic; vulnary;
KM antinflammatory; antibacterial; immunosuppressive; vasotropic; cancer;
KM antiParkinsonian; neuroprotective; nootropic; haemostatic; osteopathic;
KM antifungal; antifolate; antidiabetic; antilastmatic; antiallergic;
KM immunostimulant; analgesic; cerebroprotective; antianaemic; infection;
XX nervous system disorder; autoimmune disorder; inflammation; allergy; ds.
OS Homo sapiens.
XX

PN WO200174836-A1.
 XX
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US10472.
 XX
 PR 31-MAR-2000; 2000US-0540217.
 PR 23-AUG-2000; 2000US-0649167.
 PR 23-AUG-2000; 2000US-0649267.
 PR 30-NOV-2000; 2000US-250583P.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Drmanac RT, Ford JE, Boyle BJ;
 DR WPI; 2001-626375/72.
 XX
 XX New bone marrow-expressed nucleic acids and polypeptides, useful for
 PT diagnosis, treatment of inflammatory, autoimmune, neurological, cancer
 PT and increasing hematopoiesis, stem cell survival and bone growth and
 PT remodeling
 XX
 PS Claim 1; Page 249; 380pp; English.
 XX
 CC The present invention relates to bone marrow expressed polynucleotides
 CC and proteins. These sequences can be used in the treatment of
 CC inflammatory conditions (eg arthritis, Crohn's disease), cancer, central
 CC and peripheral nervous system diseases and neuropathies, such as
 CC Alzheimer's, Parkinson's and Huntington's diseases, spinal cord
 CC disorders, head trauma, cerebrovascular diseases, myeloid and lymphoid
 CC cell disorders, platelet disorders, stem cell disorders, bone
 CC degenerative disorders, autoimmune disorders, for example multiple
 CC sclerosis, diabetes and arthritis, viral and bacterial infections,
 CC allergies and blood coagulation disorders. The present sequence is a DNA
 CC of the invention.
 XX
 SQ Sequence 1692 BP; 467 A; 400 C; 410 G; 415 T; 0 other;
 XX
 Query Match 0.1%; Score 24; DB 22; Length 1692;
 Best Local Similarity 100.0%; Pred. No. 22;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 21442 TGATAACGACGACCACTCTCCA 21465
 ||||||||||||||||||||
 DB 1007 TGATAACGACGACCACTCTCCA 1030
 XX
 RESULT 42
 AAS84959
 ID AAS84959 standard; cDNA; 3422 BP.
 XX
 AC AAS84959;
 XX
 DT 13-FEB-2002 (first entry)
 XX
 DE DNA encoding novel human diagnostic protein #20763.
 XX
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200175067-A2.
 XX
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US08631.
 XX
 PR 31-MAR-2000; 2000US-0540217.
 PR 23-AUG-2000; 2000US-0649167.
 XX
 PA (HYSE-) HYSEQ INC.

PI Drmanac RT, Liu C, Tang YT;
 XX
 DR WPI; 2001-639362/73.
 DR P-PSDB; ABG20772.
 XX
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity
 XX
 PS Claim 1; SEQ ID NO 20763; 103pp; English.
 XX
 CC The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. A564197-A594564 represent novel human
 CC diagnostic coding sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 3422 BP; 1012 A; 780 C; 770 G; 860 T; 0 other;
 XX
 Query Match 0.1%; Score 24; DB 23; Length 3422;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 21442 TGATAACGACGACCACTCTCCA 21465
 ||||||||||||||||||||
 DB 1655 TGATAACGACGACCACTCTCCA 1678
 XX
 RESULT 43
 AAV52595
 ID AAV52595 standard; DNA; 24 BP.
 XX
 AC AAV52595;
 XX
 DT 19-NOV-1998 (first entry)
 XX
 DE Primer HTS-2B, used to amplify Thymidylate synthase cDNA.
 XX
 KW Primer; amplification; PCR; thymidylate synthase; TS; HT1080; log phase;
 KW reverse transcription PCR; RT-PCR; mobility shift; SSCP;
 KW Single-Strand Conformation Polymorphism; gene therapy; cancer;
 KW myelotoxicity; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO9833518-A1.
 XX
 PD 06-AUG-1998.
 XX
 PF 03-FEB-1998; 98WO-US02145.
 XX
 PR 04-FEB-1997; 97US-0037163.
 XX
 PA (SLOK) SLOAN KETTERING INST CANCER RES.

PI Banerjee D, Bertino JR, Liu-chen X, Tong Y;
XX
XX WPI: 1998-437173/37.
XX
PT New mutant human thymidylate synthases - used to, e.g. develop
PT products for use in gene therapy and for treating cancers
XX
XX Example 11: Page 17: 78pp; English.
XX
CC Primers AAV52597-V52603 were used to amplify thymidylate synthase (TS)
CC cDNA by using a reverse transcription PCR assay (RT-PCR), in which this
CC particular antisense primer anneals to nucleotides 645-622 of the human
CC TS cDNA. This assay was performed by obtaining RNA coding for the TS
CC enzyme from two different cell types, HT1080 and 41 resistant sublines
CC in log phase. This RNA was then subjected to RT-PCR, thus synthesizing
CC cDNA that could then be amplified by the presence of the 6 pairs of
CC primers. These primers were also used in a DNA-Single-Stranded
CC Conformation Polymorphism (SSCP) assay, whereby mutations within this
CC cDNA can be detected by a mobility shift in the ssDNA as compared to the
CC wt DNA. Mutated TS cDNAs have been found to be resistant to TS specific
CC inhibitors, and to have a high catalytic efficiency and good stability.
CC The mutant TS cDNA can be used in gene therapy to transfer drug
CC resistance to human haematopoietic progenitors, thus allowing
CC dose-intense therapy in cancer patients by protecting normal cells and
CC preventing dose-limiting myelotoxicity.
XX
SQ Sequence 24 BP; 5 A; 6 C; 8 G; 5 T; 0 other;
XX
Query Match 0.1%; Score 23; DB 19; Length 24;
Best Local Similarity 100.0%; Pred. No. 77;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 21075 CTCTGTACAGCTGCAGACAG 21097
Db 2 CTCTGTACAGCTGCAGACAG 24
|||||
RESULT 44
ABQ30240/c
ID ABQ30240 standard; DNA: 542 BP.
XX
XX ABQ30240;
AC
XX
XX 12-JUL-2002 (first entry)
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 16831.
XX
XX Human: cytosine methylation; 5'-CPG-3'; uracil; cytosine; diagnosis;
KW drug; side effect; cancer; central nervous system; cardiovascular;
KW gastrointestinal; respiratory system; single nucleotide polymorphism;
KW SNP; cell differentiation; ds.
XX
XX Homo sapiens.
XX
XX WO200218632-A2.
XX
XX 07-MAR-2002.
PD
XX
XX 01-SEP-2001; 2001WO-EP10074.
PE
XX
XX 01-SEP-2000; 2000DE-1043826.
PR 05-SEP-2000; 2000DE-1044543.
XX
XX (EPIG-) EPIGENOMICS AG.
PA
XX
XX Olek A, Piepenbrock C, Berlin K, Guetig D;
PI
XX
XX WPI: 2002-371829/40.
DR
XX
XX Determining the degree of cytosine methylation in genomic DNA, useful
PT for diagnosis and prognosis, comprises selective hybridization of
PT amplicons from chemically treated DNA -
XX

PS Claim 12: 56pp + Sequence Listing: 56pp; German.
XX
XX This invention describes a novel method for determining the degree of
CC methylation of a particular cytosine in a motif 5'-CPG-3', present in a
CC genomic sample of DNA. The sample is treated chemically to convert in a
CC cytosine (C) but not methylated C, to uracil, then part of the genomic
CC DNA that contains the target C is amplified to form a labeled amplicon.
CC The amplicon is hybridised to two classes, each with at least one
CC member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers
CC and the degree of hybridisation to both classes is determined from the
CC label on the amplicon. From the ratio of labels hybridised to the two
CC classes of oligomers, the degree of methylation is calculated. The method
CC is used: (i) for diagnosis and/or prognosis of side effects of
CC therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders
CC of the central nervous, cardiovascular, gastrointestinal and respiratory
CC systems etc., particularly by detecting mutations or single nucleotide
CC polymorphisms (SNP/s); and (ii) for differentiation of cell or tissue
CC types and for investigating cell differentiation. The method allows the
CC methylation status of many C residues to be determined simultaneously.
CC ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the
CC method for determining the degree of cytosine methylation described in
CC the disclosure of the invention.
XX
SQ Sequence 542 BP; 6 A; 64 C; 136 G; 336 T; 0 other;
XX
Query Match 0.1%; Score 23; DB 24; Length 542;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 22550 ACGCGAACCCGCAAAAAACG 22572
Db 180 ACGCGAACCCGCAAAAAACG 158
|||||
RESULT 45
ABQ30241
ID ABQ30241 standard; DNA: 542 BP.
XX
XX ABQ30241;
AC
XX
XX 12-JUL-2002 (first entry)
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 16832.
XX
XX Human: cytosine methylation; 5'-CPG-3'; uracil; cytosine; diagnosis;
KW drug; side effect; cancer; central nervous system; cardiovascular;
KW gastrointestinal; respiratory system; single nucleotide polymorphism;
KW SNP; cell differentiation; ds.
XX
XX Homo sapiens.
XX
XX WO200218632-A2.
XX
XX 07-MAR-2002.
PD
XX
XX 01-SEP-2001; 2001WO-EP10074.
PE
XX
XX 01-SEP-2000; 2000DE-1043826.
PR 05-SEP-2000; 2000DE-1044543.
XX
XX (EPIG-) EPIGENOMICS AG.
PA
XX
XX Olek A, Piepenbrock C, Berlin K, Guetig D;
PI
XX
XX WPI: 2002-371829/40.
DR
XX
XX Determining the degree of cytosine methylation in genomic DNA, useful
PT for diagnosis and prognosis, comprises selective hybridization of
PT amplicons from chemically treated DNA -
PS Claim 12: 56pp + Sequence Listing: 56pp; German.
XX
XX This invention describes a novel method for determining the degree of

methylation of a particular cytosine in a motif 5'-CpG-3', present in a genomic sample of DNA. The sample is treated chemically to convert cytosine (C) but not methylated C, to uracil, then part of the genomic DNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the degree of hybridisation to both classes is determined from the label on the amplicon. From the ratio of labels hybridised to the two classes of oligomers, the degree of methylation is calculated. The method is used: (i) for diagnosis and/or prognosis of side effects of therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders of the central nervous, cardiovascular, gastrointestinal and respiratory systems etc., particularly by detecting mutations or single nucleotide polymorphisms (SNPs); and (ii) for differentiation of cell or tissue types and for investigating cell differentiation. The method allows the methylation status of many C residues to be determined simultaneously. ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the method for determining the degree of cytosine methylation described in the disclosure of the invention.

xx
SQ Sequence 542 BP; 336 A; 136 C; 64 G; 6 T; 0 other;

Query Match 0.1%; Score 23; DB 24; Length 542;

Best Local Similarity 100.0%; Pred. No. 62;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 22550 ACGCGAACACCGCAAAAAAAGC 22572

DB 363 ACGCGAACACCGCAAAAAAAGC 385

Search completed: September 29, 2003, 12:41:21
Job time : 7652 secs


```
FT /note="has similarity to KSHV ORF4"
FT CDS 6045..9443
FT /tag= d
FT /product= "ssDNA binding protein"
FT /label= RRV_ORF6
FT /note="has similarity to KSHV ORF6"
FT CDS 9468..11528
FT /tag= e
FT /product= "transport protein"
FT /label= RRV_ORF7
FT /note="has similarity to KSHV ORF7"
FT CDS 11515..14004
FT /tag= f
FT /product= "glycoprotein B"
FT /label= RRV_ORF8
FT /note="has similarity to KSHV ORF8"
FT CDS 14122..17166
FT /tag= g
FT /product= "DNA polymerase protein"
FT /label= RRV_ORF9
FT /note="has similarity to KSHV ORF9"
FT CDS 17261..18511
FT /tag= h
FT /label= RRV_ORF10
FT /note="has similarity to KSHV ORF10"
FT CDS 18520..19749
FT /tag= i
FT /label= RRV_ORF11
FT /note="has similarity to KSHV ORF11"
FT CDS complement (19921..20544)
FT /tag= j
FT /product= "RRV R2"
FT /label= RRV_ORF
FT /note="has similarity to KSHV Interleukin (IL)-6 gene"
FT CDS complement (20777..21778)
FT /tag= k
FT /product= "thymidylate synthase"
FT /label= RRV_ORF70
FT /note="has similarity to KSHV ORF70"
FT CDS complement (22245..22592)
FT /tag= l
FT /product= "RRV R3"
FT /note="has similarity to KSHV K4 viral MIP gene"
FT CDS 26846..27409
FT /tag= m
FT /product= "Bcl2-homologue"
FT /label= RRV_ORF16
FT /note="has similarity to KSHV ORF16"
FT CDS complement (27515..29125)
FT /tag= n
FT /label= RRV_ORF17
FT /note="has similarity to KSHV ORF17"
FT CDS 28998..29897
FT /tag= o
FT /label= RRV_ORF18
FT /note="has similarity to KSHV ORF18"
FT CDS complement (29905..31548)
FT /tag= p
FT /product= "tegument protein"
FT /label= RRV_ORF19
FT /note="has similarity to KSHV ORF19"
FT CDS complement (31043..32095)
FT /tag= q
FT /label= RRV_ORF20
FT /note="has similarity to KSHV ORF20"
FT CDS 32094..33767
FT /tag= r
FT /product= "thymidine kinase"
FT /label= RRV_ORF21
FT /note="has similarity to KSHV ORF21"
FT CDS 33754..35868
FT /tag= s
FT /product= "glycoprotein H"
FT /label= RRV_ORF22
FT /note="has similarity to KSHV ORF22"
FT CDS complement (35865..37073)
FT /tag= t
FT /label= RRV_ORF23
FT /note="has similarity to KSHV ORF23"
FT CDS complement (37123..39321)
FT /tag= u
FT /label= RRV_ORF24
FT /note="has similarity to KSHV ORF24"
FT CDS 39323..43459
FT /tag= v
FT /product= "major capsid protein"
FT /label= RRV_ORF25
FT /note="has similarity to KSHV ORF25"
FT CDS 43491..44408
FT /tag= w
FT /product= "capsid protein"
FT /label= RRV_ORF26
FT /note="has similarity to KSHV ORF26"
FT CDS 44433..45242
FT /tag= x
FT /label= RRV_ORF27
FT /note="has similarity to KSHV ORF27"
FT CDS 45408..45683
FT /tag= y
FT /label= RRV_ORF28
FT /note="has similarity to KSHV ORF28"
FT CDS complement (45733..46779)
FT /tag= z
FT /label= RRV_ORF29b
FT /note="has similarity to KSHV ORF29b"
FT CDS 46905..47135
FT /tag= aa
FT /label= RRV_ORF30
FT /note="has similarity to KSHV ORF30"
FT CDS 47093..47746
FT /tag= ab
FT /label= RRV_ORF31
FT /note="has similarity to KSHV ORF31"
FT CDS 47683..49077
FT /tag= ac
FT /label= RRV_ORF32
FT /note="has similarity to KSHV ORF32"
FT CDS 49049..50059
FT /tag= ad
FT /label= RRV_ORF33
FT /note="has similarity to KSHV ORF33"
FT CDS complement (49977..50960)
FT /tag= ae
FT /label= RRV_ORF29a
FT /note="has similarity to KSHV ORF29a"
FT CDS 50959..51942
FT /tag= af
FT /label= RRV_ORF34
FT /note="has similarity to KSHV ORF34"
FT CDS 51923..52372
FT /tag= ag
FT /label= RRV_ORF35
FT /note="has similarity to KSHV ORF35"
FT CDS 52278..53585
FT /tag= ah
FT /product= "kinase"
FT /label= RRV_ORF36
FT /note="has similarity to KSHV ORF36"
FT CDS 53566..55008
FT /tag= ai
FT /product= "alkaline exonuclease"
FT /label= RRV_ORF37
FT /note="has similarity to KSHV ORF37"
FT CDS 54963..55172
FT /tag= aj
FT /label= RRV_ORF38
```

```
FT /note- "has similarity to KSHV ORF38"
FT complement (55255..56391)
FT /tag- ak
FT /product- "glycoprotein M"
FT /label- RV_ORF39
FT /note- "has similarity to KSHV ORF39"
FT 56526..57932
FT /tag- a1
FT /product- "helicase/primase"
FT /label- RV_ORF40
FT /note- "has similarity to KSHV ORF40"
FT 57917..58528
FT /tag- am
FT /product- "helicase/primase"
FT /label- RV_ORF41
FT /note- "has similarity to KSHV ORF41"
FT complement (58525..59343)
FT CDS
FT /tag- an
FT /label- RV_ORF42
FT /note- "has similarity to KSHV ORF42"
FT complement (59297..61027)
FT CDS
FT /tag- ao
FT /product- "capsid protein"
FT /label- RV_ORF43
FT /note- "has similarity to KSHV ORF43"

Query Match      100.0%; Score 35101; DB 24; Length 128139;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 35101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACACCTAAGGTGGTGTGTAATAATCTTAAGCAAAATGTATATATTACTTAATTACATGTAC 60
DB 29320 ACACCTAAGGTGGTGTGTAATAATCTTAAGCAAAATGTATATATTACTTAATTACATGTAC 29379
QY 61 ACCAATACAGTGAATAATTTACGCTACCAACACATTTAGCGCAATGTATACATG 120
DB 29380 ACCAATACAGTGAATAATTTACGCTACCAACACATTTAGCGCAATGTATACATG 29439
QY 121 TATGAAGTTTAAACAATAATTAATTAAGCTCAGATCTCTGTGTTTATCCGAT 180
DB 29440 TATGAAGTTTAAACAATAATTAATTAAGCTCAGATCTCTGTGTTTATCCGAT 29499
QY 181 ATATGTTACATCATCATGTGTATATATAGAGATATCATATATATATCAATATGCA 240
DB 29500 ATATGTTACATCATCATGTGTATATATAGAGATATCATATATATATCAATATGCA 29559
QY 241 AAGCCGATGACATCATCATATTTCCGGTGTGTTTCCGCTGTTTAAAGTTTAAAGTTT 300
DB 29560 AAGCCGATGACATCATCATATTTCCGGTGTGTTTCCGCTGTTTAAAGTTTAAAGTTT 29619
QY 301 GATTAGATGAACAACAGCTACGATCGAGCACCGAGACGTCACAAAGAACCGGCTCG 360
DB 29620 GATTAGATGAACAACAGCTACGATCGAGCACCGAGACGTCACAAAGAACCGGCTCG 29679
QY 361 GAATGCGACAAAGAGCGCTGTGTTTGGCGGCTGTGTCAGCGTTTCAAGCCAGCGT 420
DB 29680 GAATGCGACAAAGAGCGCTGTGTTTGGCGGCTGTGTCAGCGTTTCAAGCCAGCGT 29739
QY 421 ATTAAGAGTTTTCAGTCATTAATTTGACAGCGTGCATGGAAGCAAGTACCGGCTG 480
DB 29740 ATTAAGAGTTTTCAGTCATTAATTTGACAGCGTGCATGGAAGCAAGTACCGGCTG 29799
QY 481 ATGCGGCTTACGAACATCATCATAGCTACGCTGCGCCCTGATCAAGCTCGGCTT 540
DB 29800 ATGCGGCTTACGAACATCATCATAGCTACGCTGCGCCCTGATCAAGCTCGGCTT 29859
QY 541 TACGAGTTTTCGAGGTTCTTAAACAGCGGATGTTTGTCTGCGCGTTTATCAAAAT 600
DB 29860 TACGAGTTTTCGAGGTTCTTAAACAGCGGATGTTTGTCTGCGCGTTTATCAAAAT 29919
QY 601 TGTTCATTTTAAACGCGCGGTACGCGCTACACATTCGATATGTATTAACCTTTCC 660
DB 29920 TGTTCATTTTAAACGCGCGGTACGCGCTACACATTCGATATGTATTAACCTTTCC 29979
```

```
QY 661 GCCCGAGATAGATGTCGCTGTGATTCGATTTGAGCTATGATGAGAACAG 720
DB 29980 GCCCGAGATAGATGTCGCTGTGATTCGATTTGAGCTATGATGAGAACAG 30039
QY 721 GGACTACAGACATGATGATGTCGAACCCACAGTTCAGCAACCTGTTTCCCG 780
DB 30040 GGACTACAGACATGATGATGTCGAACCCACAGTTCAGCAACCTGTTTCCCG 30099
QY 781 TATTCCTCTTCTTTGACAAACGATTAATTTTCATATCCATATTTGTGTTAATACAC 840
DB 30100 TATTCCTCTTCTTTGACAAACGATTAATTTTCATATCCATATTTGTGTTAATACAC 30159
QY 841 GGTACGCTTGTGAATTCGGGATGTGACAGAGACACGACATGCTATGCAATTA 900
DB 30160 GGTACGCTTGTGAATTCGGGATGTGACAGAGACACGACATGCTATGCAATTA 30219
QY 901 GTATTTCTTTTATTTGACAAATGCTGCTGTATTTTCTGTTTAAAGCTGTTTCCATC 960
DB 30220 GTATTTCTTTTATTTGACAAATGCTGCTGTATTTTCTGTTTAAAGCTGTTTCCATC 30279
QY 961 CTGGCCCTAAACTGTATTAAGCTTAACCTTTAAAGCTTTCCCGTTCCTTTTGG 1020
DB 30280 CTGGCCCTAAACTGTATTAAGCTTAACCTTTAAAGCTTTCCCGTTCCTTTTGG 30339
QY 1021 ATGGTTACGCGGAGCTGAGATTAAGCAACCTCGATAGAGCGTGGCCGTCATATTT 1080
DB 30340 ATGGTTACGCGGAGCTGAGATTAAGCAACCTCGATAGAGCGTGGCCGTCATATTT 30399
QY 1081 GATTCAATCACTCTGTGCGCAACTGAATGCGCAGCTCTCGATTTTGGGAGGAACATTT 1140
DB 30400 GATTCAATCACTCTGTGCGCAACTGAATGCGCAGCTCTCGATTTTGGGAGGAACATTT 30459
QY 1141 AAAAAATTTTGTGCTGCGGCTTAATTAATTCGTCGCGAGCGCCCGGACAAACCTCGAAA 1200
DB 30460 AAAAAATTTTGTGCTGCGGCTTAATTAATTCGTCGCGAGCGCCCGGACAAACCTCGAAA 30519
QY 1201 TCCCTTGAAGAGTGTGAGGACTCTATGAGTTTAAACAAACACATGCTTCCAGCGCG 1260
DB 30520 TCCCTTGAAGAGTGTGAGGACTCTATGAGTTTAAACAAACACATGCTTCCAGCGCG 30579
QY 1261 TGTTTACGCGGAGACATGATGATGAAGTATCTCTGATACGCGGCCCGCCCTTAA 1320
DB 30580 TGTTTACGCGGAGACATGATGATGAAGTATCTCTGATACGCGGCCCGCCCTTAA 30639
QY 1321 CAGCTATTCGGTATGATTTTAAAGTAAAGCAAGATTTTCCAAACCCAAACGCTGC 1380
DB 30640 CAGCTATTCGGTATGATTTTAAAGTAAAGCAAGATTTTCCAAACCCAAACGCTGC 30699
QY 1381 AATAGACAGTGTCTTAAAAAAAGGTGTGATAGCTTTAGTTTAAATTAAGTAAAAAC 1440
DB 30700 AATAGACAGTGTCTTAAAAAAAGGTGTGATAGCTTTAGTTTAAATTAAGTAAAAAC 30759
QY 1441 ATTATAGAGTTTGTGCGCGCTGCATTAATTTGTCACGCTGTTTAAACGCGGTAATGCGGCTC 1500
DB 30760 ATTATAGAGTTTGTGCGCGCTGCATTAATTTGTCACGCTGTTTAAACGCGGTAATGCGGCTC 30819
QY 1501 TCGCCTATTTGTGCTGGCGGAACCATGGCAAAAAATATGTCGCAGTAAACAGTCC 1560
DB 30820 TCGCCTATTTGTGCTGGCGGAACCATGGCAAAAAATATGTCGCAGTAAACAGTCC 30879
QY 1561 GACTGTACATTTGAATGCTGCTGCTGCTGCGGTTGCTTGAAGATGATGCAAGTTTCTTA 1620
DB 30880 GACTGTACATTTGAATGCTGCTGCTGCTGCGGTTGCTTGAAGATGATGCAAGTTTCTTA 30939
QY 1621 TTATCGCGGGAAGCGGCTACATTAAGTGTGCTGCGCATTTGGATGTATTTTGGCTG 1680
DB 30940 TTATCGCGGGAAGCGGCTACATTAAGTGTGCTGCGCATTTGGATGTATTTTGGCTG 30999
QY 1681 GTGTTGCAAGCTGCTTATGAGTATCGTTTGTATTTTGAAGTATACCGGAGGCTC 1740
DB 31000 GTGTTGCAAGCTGCTTATGAGTATCGTTTGTATTTTGAAGTATACCGGAGGCTC 31059
```


6121 ACAACCCGCGGCGCCAAAGAGTTTCAAAACAGAGGCGCTGCAGTTTGACAGAGCGC 6180
|||||
35440 AACACCCCTGGCGCCAAAGAGTTTCAAAACAGAGGCGCTGCAGTTTGACAGAGCGC 35499
6181 GGCCTGGCTCAAGCTGCTGGACAGTCAACGATGGAAATATATCAAGATAGCGCTTGA 6240
|||||
35500 GGCCTGGCTCAAGCTGCTGGACAGTCAACGATGGAAATATATCAAGATAGCGCTTGA 35559
6241 CAGCTGTACCCAGTACTCTGTTATGTCATGCAATGCTCATTCACGAGCAGAGAACAA 6300
|||||
35560 CAGCTGTACCCAGTACTCTGTTATGTCATGCAATGCTCATTCACGAGCAGAGAACAA 35619
6301 ATTTTGATTAATTCCTTTATGTCATTAACCAATGAACTTACTGGAACAAATGCCG 6360
|||||
35620 ATTTTGATTAATTCCTTTATGTCATTAACCAATGAACTTACTGGAACAAATGCCG 35679
6361 AAACTGGCTTATTAACAGCTTCCATGCTGCAATTAATCTGCTACCTGGGCA 6420
|||||
35680 AAACTGGCTTATTAACAGCTTCCATGCTGCAATTAATCTGCTACCTGGGCA 35739
6421 CGGTAGTATTTCTAAGAGCTGTACGCCCATTAACGAAAGTTTGGCAATCGTGT 6480
|||||
35740 CGGTAGTATTTCTAAGAGCTGTACGCCCATTAACGAAAGTTTGGCAATCGTGT 35799
6481 TTTGAGAGAGGCGCTCGAAATGCGGCGCCAGAGGTGGGGCGGCGCGCGCGC 6540
|||||
35800 TTTGAGAGAGGCGCTCGAAATGCGGCGCCAGAGGTGGGGCGGCGCGCGCGC 35859
6541 CGAGTGTATTAATCTCTTCAAGAGCCCAATCTTTGGCGCCCTTGGCTTAACATGAGT 6600
|||||
35860 CGAGTGTATTAATCTCTTCAAGAGCCCAATCTTTGGCGCCCTTGGCTTAACATGAGT 35919
6601 TTTTACCAACTGCTCAGAGAGTCTCGGCGCACCCCATGTTACATAGCGCAGAGG 6660
|||||
35920 TTTTACCAACTGCTCAGAGAGTCTCGGCGCACCCCATGTTACATAGCGCAGAGG 35979
6661 GTACAAACGGAATGACAGAGTACGATCAACATCAGAGTCAAGGAAATGAGAGAGT 6720
|||||
35980 GTACAAACGGAATGACAGAGTACGATCAACATCAGAGTCAAGGAAATGAGAGAGT 36039
6721 AGTCGTGACATGTTAATCATTTACAGACAGAAACAGCGGATCATGAGCGCGCA 6780
|||||
36040 AGTCGTGACATGTTAATCATTTACAGACAGAAACAGCGGATCATGAGCGCGCA 36099
6781 CGTCTTACAGTCCGCTTATATGAAACAGACAGATGCTGTGCTGGAAGT 6840
|||||
36100 CGTCTTACAGTCCGCTTATATGAAACAGACAGATGCTGTGCTGGAAGT 36159
6841 TTTTATACGTTGCTGACAGCTGTACCAACGCTACGCTGCGCATGAGCGTGA 6900
|||||
36160 TTTTATACGTTGCTGACAGCTGTACCAACGCTACGCTGCGCATGAGCGTGA 36219
6901 TTTTACAGCTGCGCTGACAGCTGTACCAACGCGCAGTGTGCTGACAGTGA 6960
|||||
36220 TTTTACAGCTGCGCTGACAGCTGTACCAACGCGCAGTGTGCTGACAGTGA 36279
6961 CCCGACATAGATTTTGGACACCTGGAAGAGCGGACGCTCGCGAGATGCTGAGCG 7020
|||||
36280 CCCGACATAGATTTTGGACACCTGGAAGAGCGGACGCTCGCGAGATGCTGAGCG 36339
7021 TTTGATATACACCCACGTTGACATGATTTGAACCTTTTGAAGTGTTCACCTG 7080
|||||
36340 TTTGATATACACCCACGTTGACATGATTTGAACCTTTTGAAGTGTTCACCTG 36399
7081 CCCGTTTGTACCAAGGCTCCGCTGTGTGACTACGCGGAGCCCGCGCAACTGTGTAC 7140
|||||
36400 CCCGTTTGTACCAAGGCTCCGCTGTGTGACTACGCGGAGCCCGCGCAACTGTGTAC 36459
7141 CACTTCAGACAGCGGAGATACGTGACCAAGTCTCTGTTAAGCGGCTTCGCGGCTT 7200
|||||
36460 CACTTCAGACAGCGGAGATACGTGACCAAGTCTCTGTTAAGCGGCTTCGCGGCTT 36519
7201 TGCTATGCAATAGTGTGCTGAGAGTGTGCGAGACCAATGTTTACCGCGGCTTCAC 7260
|||||
36520 TGCTATGCAATAGTGTGCTGAGAGTGTGCGAGACCAATGTTTACCGCGGCTTCAC 36579
7261 CAAGCTGTACACGATTCCTCTGCTGGCGGACAGCTGCAACCGCTGTGCAATTAAGT 7320
|||||
36580 CAAGCTGTACACGATTCCTCTGCTGGCGGACAGCTGCAACCGCTGTGCAATTAAGT 36639
7321 GACGCGCTCGCGGCGGACAGCGGCTGCGCTTAAAGTCTCCCGGCTCATAGG 7380
|||||
36640 GACGCGCTCGCGGCGGACAGCGGCTGCGCTTAAAGTCTCCCGGCTCATAGG 36699
7381 CGAGTACGAGGATGGGACAACTGTCATGCTGACATGAGAGTGTGCGGCGGCTTAT 7440
|||||
36700 CGAGTACGAGGATGGGACAACTGTCATGCTGACATGAGAGTGTGCGGCGGCTTAT 36759
7441 GCCCAGTGTGACACCTTGGCAGCATGACATGAGAGTGTGCGGCGGCTTAT 7500
|||||
36760 GCCCAGTGTGACACCTTGGCAGCATGACATGAGAGTGTGCGGCGGCTTAT 36819
7501 CTGCAACGCAAGACAAAGATTAACCCGCGCTTGGCATGACCCGCTCCGACCATGA 7560
|||||
36820 CTGCAACGCAAGACAAAGATTAACCCGCGCTTGGCATGACCCGCTCCGACCATGA 36879
7561 GGTGTTGGGGAAGTCTGATTTAGTCCAGGCGCTGACATGATTTTAAAGGCA 7620
|||||
36880 GGTGTTGGGGAAGTCTGATTTAGTCCAGGCGCTGACATGATTTTAAAGGCA 36939
7621 GCCATCGGTTATGCTGCGGGAAGTCAAGGCGGACAGTCAAGTGTGAGTGAATCATGA 7680
|||||
36940 GCCATCGGTTATGCTGCGGGAAGTCAAGGCGGACAGTCAAGTGTGAGTGAATCATGA 36999
7681 GTTGGCATGCTGAGACATGAGCGCTGCTGTTATTTTCCACATACAGCCCGCCAGTTGC 7740
|||||
37000 GTTGGCATGCTGAGACATGAGCGCTGCTGTTATTTTCCACATACAGCCCGCCAGTTGC 37059
7741 GGCATTTACCTGCGCATGAGGCGTTCACATGTCAGAGCAATGTTTTCATGTTTCCGAGGA 7800
|||||
37060 GGCATTTACCTGCGCATGAGGCGTTCACATGTCAGAGCAATGTTTTCATGTTTCCGAGGA 37119
7801 CTGTCAGACGAGACAGGACCTTCAACGACTACGTTTAAACAAAAGCGGATGCAACGATT 7860
|||||
37120 CTGTCAGACGAGACAGGACCTTCAACGACTACGTTTAAACAAAAGCGGATGCAACGATT 37179
7861 CGGTGCTCTGGCCAGATTTGCTGAGACCGCTGCTTACGTTGCGGGGGTCCCGCATGCGGA 7920
|||||
37180 CGGTGCTCTGGCCAGATTTGCTGAGACCGCTGCTTACGTTGCGGGGGTCCCGCATGCGGA 37239
7921 CAACATACCGGCTCTGAGCAGACGCTGACAGCTGAGATGTTTGTGAGCGCGCT 7980
|||||
37240 CAACATACCGGCTCTGAGCAGACGCTGACAGCTGAGATGTTTGTGAGCGCGCT 37299
7981 TACTGACAGCTTACCTATTTTCAAAACCCCAACAGTCCCGGGGACGCGCATCTGCT 8040
|||||
37300 TACTGACAGCTTACCTATTTTCAAAACCCCAACAGTCCCGGGGACGCGCATCTGCT 37359
8041 GATCTGCTGACAGCTGTCACCAACAGAAAGCGGGAAGTGTGCTTGTGACCACTGCAT 8100
|||||
37360 GATCTGCTGACAGCTGTCACCAACAGAAAGCGGGAAGTGTGCTTGTGACCACTGCAT 37419
8101 CCCGATTTCTGCTACGAATACCGACATAGCGGTTAAACCATGAGGCGTGCAGAGGCTC 8160
|||||
37420 CCCGATTTCTGCTACGAATACCGACATAGCGGTTAAACCATGAGGCGTGCAGAGGCTC 37479
8161 CCTGAGAGAGTGTGTAACAACTACCTGCGCGCAAGTGTGCAAGTGTGCAAGGATGTACAG 8220
|||||
37480 CCTGAGAGAGTGTGTAACAACTACCTGCGCGCAAGTGTGCAAGTGTGCAAGGATGTACAG 37539
8221 TCCGTTGCTGCAAGTGTTCACAAAGAGCGCTATTTTGGTAAACAATGCGGCGCTGAAAC 8280
|||||
37540 TCCGTTGCTGCAAGTGTTCACAAAGAGCGCTATTTTGGTAAACAATGCGGCGCTGAAAC 37599
8281 ACTAGTACGGAATACGCGCGGCTGACGGAAGCGCGGACAGCGGAGGAGTACT 8340
|||||

Db 37600 ACTAGTCACGGAATACCGGCGCCCTCACGGGAACCGCGGACACACGCGAGCACT 37659
Qy 8341 GCATACGTGGTGTCAACGGAAGAGATGTTTCTAGAACACCGTGGCCAGTTTCTACA 8400
Db 37660 GCAGTACGTGGTGTCAACGGAAGAGATGTTTCTAGAACACCGTGGCCAGTTTCTACA 37719
Qy 8401 AGAAGCGTTCACGCGTCCGCGCAGTCACAGGTCTCTGTCGACGAATATATGTCGAA 8460
Db 37720 AGAAGCGTTCACGCGTCCGCGCAGTCACAGGTCTCTGTCGACGAATATATGTCGAA 37779
Qy 8461 TAACCTCACGCAACCCCTCTGTCACATGGGACATTTATATGATTTAGAGAAAGGCCCTAT 8520
Db 37780 TAACTCACGCAACCCCTCTGTCACATGGGACATTTATATGATTTAGAGAAAGGCCCTAT 37839
Qy 8521 GAAAGACTATTAAAGATCGGAACAAGTGGCCCTATTAGTTAGTTCAGACGGTCTGGA 8580
Db 37840 GAAAGACTATTAAAGATCGGAACAAGTGGCCCTATTAGTTAGTTCAGACGGTCTGGA 37899
Qy 8581 GCTAACGAGAGATGGCCCTCGATTAAGACATCGTTGTCGCGTGAACGTCTAGATTATTCG 8640
Db 37900 GCTAACGAGAGATGGCCCTCGATTAAGACATCGTTGTCGCGTGAACGTCTAGATTATTCG 37959
Qy 8641 CCGAGAGATAGCAAAATCTTACATCAAAAGATAGATGATTTGGCTCTCAGAACGCC 8700
Db 37960 CCGAGAGATAGCAAAATCTTACATCAAAAGATAGATGATTTGGCTCTCAGAACGCC 38019
Qy 8701 ACCCTCTGACAAATATACAGCGCGTGGGTCTGGGGAACCTGTGCTAGAGATTCCGGG 8760
Db 38020 ACCCTCTGACAAATATACAGCGCGTGGGTCTGGGGAACCTGTGCTAGAGATTCCGGG 38079
Qy 8761 TGGATTTTATTCAGGCAATACATCTATTTTGGACAAATGCATCTCCGCTGTTGGAAGAG 8820
Db 38080 TGGATTTTATTCAGGCAATACATCTATTTTGGACAAATGCATCTCCGCTGTTGGAAGAG 38139
Qy 8821 TCGGTCCCAACAGTTTACGGCTAACGGCATGTGATCCCATGACAAATATATATATATATA 8880
Db 38140 TCGGTCCCAACAGTTTACGGCTAACGGCATGTGATCCCATGACAAATATATATATATATA 38199
Qy 8881 ACAGGTACCAACCGCGCTTCCATTTGGGATTAATCTACTCAGAAATTTGGTATTTACACCGG 8940
Db 38200 ACAGGTACCAACCGCGCTTCCATTTGGGATTAATCTACTCAGAAATTTGGTATTTACACCGG 38259
Qy 8941 TCTTTGGGCGCAAAAGATGCGACCGCTCTCAGTGAAGTCTAACGGGTTTGATGTGTTTCC 9000
Db 38260 TCTTTGGGCGCAAAAGATGCGACCGCTCTCAGTGAAGTCTAACGGGTTTGATGTGTTTCC 38319
Qy 9001 CTGCGGTGGTGGCAAGCACTGGCTCAACAGTGGCTTCAAGACCTGCTGCTATATACA 9060
Db 38320 CTGCGGTGGTGGCAAGCACTGGCTTCAACAGTGGCTTCAAGACCTGCTGCTATATACA 38379
Qy 9061 TATATCTACAGATGGCGAGACGACGCCACGACGTCACCTAGCCGAGGTGAACGCTGT 9120
Db 38380 TATATCTACAGATGGCGAGACGACGCCACGACGTCACCTAGCCGAGGTGAACGCTGT 38439
Qy 9121 ACAGCAACAATATCACTTACATGGGTGCAACTACGCCCTGAGAGTGAACCCGTTGGGT 9180
Db 38440 ACAGCAACAATATCACTTACATGGGTGCAACTACGCCCTGAGAGTGAACCCGTTGGGT 38499
Qy 9181 CGAGCTCAGCTATCGGATGCTGAGACGACCTGCTCATTTACCTGTGGCTTTTGTCCGGT 9240
Db 38500 CGAGCTCAGCTATCGGATGCTGAGACGACCTGCTCATTTACCTGTGGCTTTTGTCCGGT 38559
Qy 9241 TAAATTCGCGGGGTGCTTAAGGCTACTGACCTCATTTGGTGGCGCACAAACACGAT 9300
Db 38560 TAAATTCGCGGGGTGCTTAAGGCTACTGACCTCATTTGGTGGCGCACAAACACGAT 38619
Qy 9301 TAGTCAGATTTTGGAGGGGTGTGCCACCTGAGAGTACAGGCCCTGATCTCAACAACG 9360
Db 38620 TAGTCAGATTTTGGAGGGGTGTGCCACCTGAGAGTACAGGCCCTGATCTCAACAACG 38679
Qy 9361 TAAAGGTGGCGAGACATTAACGCGCATGGGTGCCCTATATACCTATCTACGAAGTCTCA 9420
Db 38680 TAAAGGTGGCGAGACATTAACGCGCATGGGTGCCCTATATACCTATCTACGAAGTCTCA 38739

Qy 9421 GTTCTATATTTAATCTGGGCGCAGATTTTCAGTTTACGGCTTCTCATCGACAGATA 9480
Db 38740 GTTCTATATTTAATCTGGGCGCAGATTTTCAGTTTACGGCTTCTCATCGACAGATA 38799
Qy 9481 CCGCTTCCTGTTGGTGTGCATATATACAGAAAGGGCCCTCCCTGCTTTGACATGTGCA 9540
Db 38800 CCGCTTCCTGTTGGTGTGCATATATACAGAAAGGGCCCTCCCTGCTTTGACATGTGCA 38859
Qy 9541 TCCCAAAATATACAGGTGTCCAGACAAACGAGGGTACGGTGTGGAAGTCCCGGTGG 9600
Db 38860 TCCCAAAATATACAGGTGTCCAGACAAACGAGGGTACGGTGTGGAAGTCCCGGTGG 38919
Qy 9601 ACAAGGACGACACAGAGCCATGATTTATTTACCTTAAGACACCAACTTACAAACGAGC 9660
Db 38920 ACAAGGACGACACAGAGCCATGATTTATTTACCTTAAGACACCAACTTACAAACGAGC 38979
Qy 9661 GCGCGACGTTGTTAAGGACCTTTTGATACGAAACCCAGTGACATTTGTAAGCAAA 9720
Db 38980 GCGCGACGTTGTTAAGGACCTTTTGATACGAAACCCAGTGACATTTGTAAGCAAA 39039
Qy 9721 TTGTTAAGAGGGCTAGCTATATCCAAAAAATTTGGTCCGTTTGGCGTTGATTTAT 9780
Db 39040 TTGTTAAGAGGGCTAGCTATATCCAAAAAATTTGGTCCGTTTGGCGTTGATTTAT 39099
Qy 9781 ATTTTATTTTGCATAGCTGTGCTTGGCTCTGCTCTCTACTTGGCAGTTAAACCGTACA 9840
Db 39100 ATTTTATTTTGCATAGCTGTGCTTGGCTCTGCTCTCTACTTGGCAGTTAAACCGTACA 39159
Qy 9841 TGAACCCACGGGCTGTGTGGGTTTAAACCCATGGTTCACAAACATCTCAGAAAC 9900
Db 39160 TGAACCCACGGGCTGTGTGGGTTTAAACCCATGGTTCACAAACATCTCAGAAAC 39219
Qy 9901 TACCGACCCGGGCTATTTGTCGGTAGGTTTGGGGGACAGCCATCTGTAAAGACGTGA 9960
Db 39220 TACCGACCCGGGCTATTTGTCGGTAGGTTTGGGGGACAGCCATCTGTAAAGACGTGA 39279
Qy 9961 GCGTCCCGCATATCAAAACGAGGCTTGAATGGTTTACACACAGGGGTCTAGCAATTCG 10020
Db 39280 GCGTCCCGCATATCAAAACGAGGCTTGAATGGTTTACACACAGGGGTCTAGCAATTCG 39339
Qy 10021 GTCACGGCGCACATATGGGCTGGCCCTGTTAAAGCGCGCTGCTTCTCATGGAAATG 10080
Db 39340 GTCACGGCGCACATATGGGCTGGCCCTGTTAAAGCGCGCTGCTTCTCATGGAAATG 39399
Qy 10081 TGTGTCCGGAACCACTAGTGGGCAAGGCGTGCATTTCTGTGTCATGGAACGGGACGG 10140
Db 39400 TGTGTCCGGAACCACTAGTGGGCAAGGCGTGCATTTCTGTGTCATGGAACGGGACGG 39459
Qy 10141 AGTGTCCGATTTTAAATCGCAATGGCGCAACCCAGCTTTTGGCGATCCAGAGCGTTC 10200
Db 39460 AGTGTCCGATTTTAAATCGCAATGGCGCAACCCAGCTTTTGGCGATCCAGAGCGTTC 39519
Qy 10201 TGTGTCCGCAATTCATGAAAAAAACCTCTGTCCGCCACCTGGAATGATTAATTAACA 10260
Db 39520 TGTGTCCGCAATTCATGAAAAAAACCTCTGTCCGCCACCTGGAATGATTAATTAACA 39579
Qy 10261 CATCAGTTTAAACAATGAACACCTCTGCAAAATATACCTGTGGTGGCCGAAGGTGA 10320
Db 39580 CATCAGTTTAAACAATGAACACCTCTGCAAAATATACCTGTGGTGGCCGAAGGTGA 39639
Qy 10321 TAGTCCTTAATGCGATGCAATGAGAAACAAATTAAGCTATTTCCACGCACTTCAATGACGT 10380
Db 39640 TAGTCCTTAATGCGATGCAATGAGAAACAAATTAAGCTATTTCCACGCACTTCAATGACGT 39699
Qy 10381 GTTTTATTTGCTGTGTAAGGTATTAACAGTAATGAGAGTTCGCTGGCTCTATTAAG 10440
Db 39700 GTTTTATTTGCTGTGTAAGGTATTAACAGTAATGAGAGTTCGCTGGCTCTATTAAG 39759
Qy 10441 CAAAAGGTCTATAGAGTAAACAAATTTTGATTTGGGGAATAATGCTGTAAATAGTTTATC 10500
Db 39760 CAAAAGGTCTATAGAGTAAACAAATTTTGATTTGGGGAATAATGCTGTAAATAGTTTATC 39819

QY 10501 CGACAGTGTGACGTGACACAGCAATGGGTTTTTAACCCAGACGGGCTTTTCAACAAGTC 10560
| | | | |
Db 39820 CGAACGTAATGACGTGACACAGCAATGGGTTTTTAACCCAGACGGGCTTTTCAACAAGTC 39879
QY 10561 AACCGGAATCGGTTCAAGTTCTCCATTTATGCGGTATTAACAAAACCCCGGTATG 10620
| | | | |
Db 39880 AACCGGAATCGGTTCAAGTTCTCCATTTATGCGGTATTAACAAAACCCCGGTATG 39939
QY 10621 GCTGTTTTTTTTCGCTATGCGGTATGCGGTATGCGGTATGCGGTATGCGGTATG 10680
| | | | |
Db 39940 GCTGTTTTTTTTCGCTATGCGGTATGCGGTATGCGGTATGCGGTATGCGGTATG 39999
QY 10681 TGTGTTGAAGGGGGCGGCTTTGCGGATTCGTGCGACCCCGCTCAACCGCTATG 10740
| | | | |
Db 40000 TGTGTTGAAGGGGGCGGCTTTGCGGATTCGTGCGACCCCGCTCAACCGCTATG 40059
QY 10741 AGATGTTGAATGTTAGTTGCTCCACGGAACCAATGCATAGAGAACTTTCACGTACA 10800
| | | | |
Db 40060 AGATGTTGAATGTTAGTTGCTCCACGGAACCAATGCATAGAGAACTTTCACGTACA 40119
QY 10801 TAGCCAAAGCGACGACGCTGCTCTAGCTGCTTTATCTAGCATTTTAAAAAATTT 10860
| | | | |
Db 40120 TAGCCAAAGCGACGACGCTGCTCTAGCTGCTTTATCTAGCATTTTAAAAAATTT 40179
QY 10861 ATCGTTGTTGCCATGATGCGCATGACGCGGAGACAGACGCTGCTCGACATGCT 10920
| | | | |
Db 40180 ATCGTTGTTGCCATGATGCGCATGACGCGGAGACAGACGCTGCTCGACATGCT 40239
QY 10921 TTTTGTTCGCGAGTACGTGTGACCTCCGCTTTTATGGAATGCAACGATTTGCT 10980
| | | | |
Db 40240 TTTTGTTCGCGAGTACGTGTGACCTCCGCTTTTATGGAATGCAACGATTTGCT 40299
QY 10981 GATTGATCTATTAGATACGCTACGCGGATCAACGATAGCTTAAATGCTGACACAC 11040
| | | | |
Db 40300 GATTGATCTATTAGATACGCTACGCGGATCAACGATAGCTTAAATGCTGACACAC 40359
QY 11041 AATTGGGCTAAGGGCTAAAGCTCCGAGTTCAATGGCTAAATAAAGATCAACGCTT 11100
| | | | |
Db 40360 AATTGGGCTAAGGGCTAAAGCTCCGAGTTCAATGGCTAAATAAAGATCAACGCTT 40419
QY 11101 GGCCTTCTCTGCCCCCAACATGTAAATGGGCGAAGTATAGAGTGTCTTCCACGTG 11160
| | | | |
Db 40420 GGCCTTCTCTGCCCCCAACATGTAAATGGGCGAAGTATAGAGTGTCTTCCACGTG 40479
QY 11161 GGTGTAATAAATCTAAGAGGAGCGGACCAATCTGTTTAAACAGGTTGCTATGCGCATCC 11220
| | | | |
Db 40480 GGTGTAATAAATCTAAGAGGAGCGGACCAATCTGTTTAAACAGGTTGCTATGCGCATCC 40539
QY 11221 GGCATCTTGACGTGCTGTTGCTTCCACGCGGACGTTAACGTGCGTATCTGCGGGTGAAG 11280
| | | | |
Db 40540 GGCATCTTGACGTGCTGTTGCTTCCACGCGGACGTTAACGTGCGTATCTGCGGGTGAAG 40599
QY 11281 GGTACGATCGCTCGAATTTAACGCGGCGGACACATGACGCTATCTGTTACGCGGCTGCC 11340
| | | | |
Db 40600 GGTACGATCGCTCGAATTTAACGCGGCGGACACATGACGCTATCTGTTACGCGGCTGCC 40659
QY 11341 GGTGATGATCTCTTAATAAAAAATGTTCCACGCTTAAATAATGCAATTAATCACTTGTG 11400
| | | | |
Db 40660 GGTGATGATCTCTTAATAAAAAATGTTCCACGCTTAAATAATGCAATTAATCACTTGTG 40719
QY 11401 AATTACCGCAATCACGCGACGATGCGGCTGCGGACGCGTGTGTTGTTGTTGTTGTTGTTG 11460
| | | | |
Db 40720 AATTACCGCAATCACGCGACGATGCGGCTGCGGACGCGTGTGTTGTTGTTGTTGTTGTTG 40779
QY 11461 CGGGCTATGTTAAAGTGGAGACAGGCTTCATCGCGGCTGTATATCTTGTGAGCTGCT 11520
| | | | |
Db 40780 CGGGCTATGTTAAAGTGGAGACAGGCTTCATCGCGGCTGTATATCTTGTGAGCTGCT 40839
QY 11521 CTTTACGGGCGACACATCAATTTGACAGCGAAGAGTCTACAGATTTTATGCAATGCT 11580
| | | | |
Db 40840 CTTTACGGGCGACACATCAATTTGACAGCGAAGAGTCTACAGATTTTATGCAATGCT 40899
QY 11581 TTGACGGAGCGTGGAGGCTGCCCATTAAGTCCGTGGAGATGGGCTTCCAAAAAAG 11640

Db 40900 TTGAGGGAGCGTGGAGGCTGCCCATTTAGCTCCGGGAGAAATGCCCTTTCCAAAAAAG 40959
| | | | |
QY 11641 AATTAGTGTGCTCCGACGCTGCTCATCATGTAATATGAGAGAAATATGACAGCGGTA 11700
| | | | |
Db 40960 AATTAGTGTGCTCCGACGCTGCTCATCATGTAATATGAGAGAAATATGACAGCGGTA 41019
QY 11701 GCACGGGCGACGCCACAGACAGTGTCTGCAAGTTTAAATCATCTTATATGATCCGACATAC 11760
| | | | |
Db 41020 GCACGGGCGACGCCACAGACAGTGTCTGCAAGTTTAAATCATCTTATATGATCCGACATAC 41079
QY 11761 GTAGTTCACACGTTAAGATCTTTTCCGGGCGCTTCAATTAAGTAAAAAATCTACT 11820
| | | | |
Db 41080 GTAGTTCACACGTTAAGATCTTTTCCGGGCGCTTCAATTAAGTAAAAAATCTACT 41139
QY 11821 TGATTTGTCAGATGATTAAGATTAATAAATCATGTTTGGCTCTTTTGAAGCAT 11880
| | | | |
Db 41140 TGATTTGTCAGATGATTAAGATTAATAAATCATGTTTGGCTCTTTTGAAGCAT 41199
QY 11881 AAAACCCAGAAATCGCGGGAGGAGCATCTTTTATGAAGTCCGCTGCTCATATATAG 11940
| | | | |
Db 41200 AAAACCCAGAAATCGCGGGAGGAGCATCTTTTATGAAGTCCGCTGCTCATATATAG 41259
QY 11941 GAGGTGGAACGTCGTGCCCCGAGTGTCTTAAAGGCAAGAAACACAAAGAGTATAG 12000
| | | | |
Db 41260 GAGGTGGAACGTCGTGCCCCGAGTGTCTTAAAGGCAAGAAACACAAAGAGTATAG 41319
QY 12001 CGGATATGAGAGACATACGCTTAAGGACAAATCTCGAAGCTGACTTCAACAGTGTG 12060
| | | | |
Db 41320 CGGATATGAGAGACATACGCTTAAGGACAAATCTCGAAGCTGACTTCAACAGTGTG 41379
QY 12061 AGCGCTTCTTACCGCTCCCATTAAGATCTAATTTATCTGAGAGCTGACGCTTTAAAC 12120
| | | | |
Db 41380 AGCGCTTCTTACCGCTCCCATTAAGATCTAATTTATCTGAGAGCTGACGCTTTAAAC 41439
QY 12121 ACTTTAGCCTATCTGATACAGAGGACGACAAATTTGGAACGAGTGTCTGCTGTTGAC 12180
| | | | |
Db 41440 ACTTTAGCCTATCTGATACAGAGGACGACAAATTTGGAACGAGTGTCTGCTGTTGAC 41499
QY 12181 TGGTGGGAGCAGAAATGCTCTCTTATACACAGATGCTGCAAAAGATGTCAATGACGG 12240
| | | | |
Db 41500 TGGTGGGAGCAGAAATGCTCTCTTATACACAGATGCTGCAAAAGATGTCAATGACGG 41559
QY 12241 CGTCAACAGCCCAATATGCTCATCTTATACAGTCTCTTATACAGTCTTATGAGATTG 12300
| | | | |
Db 41560 CGTCAACAGCCCAATATGCTCATCTTATACAGTCTCTTATACAGTCTTATGAGATTG 41619
QY 12301 TAAGCGCTACGATGAGAGGAGGAGCAAGTGCAGTACGCTACACGCGGAAAA 12360
| | | | |
Db 41620 TAAGCGCTACGATGAGAGGAGGAGCAAGTGCAGTACGCTACACGCGGAAAA 41679
QY 12361 TCTAGTGTGATTTAAGCGGAACGCTGTTTGAATATGTCAGAGCATATGTTCTGTA 12420
| | | | |
Db 41680 TCTAGTGTGATTTAAGCGGAACGCTGTTTGAATATGTCAGAGCATATGTTCTGTA 41739
QY 12421 CGGCTCTCAGAAACCGGCTACCGGACGCTTCAATCGATCGGCTGCTACAGGAC 12480
| | | | |
Db 41740 CGGCTCTCAGAAACCGGCTACCGGACGCTTCAATCGATCGGCTGCTACAGGAC 41799
QY 12481 GAGGAATGCTTTAAAGGAGATATCTGAGTACTTTGAGAGCGTGGGTGAATCTGA 12540
| | | | |
Db 41800 GAGGAATGCTTTAAAGGAGATATCTGAGTACTTTGAGAGCGTGGGTGAATCTGA 41859
QY 12541 GGCATATTTCTACGTTGTCAAGATGACAAATTTGAGCATCATAGTATTAATAGA 12600
| | | | |
Db 41860 GGCATATTTCTACGTTGTCAAGATGACAAATTTGAGCATCATAGTATTAATAGA 41919
QY 12601 CGCTACGTTTAAACAGGCTCTCCGCTAATGAGCGACGCGAAGTGGCAGAGACTGCG 12660
| | | | |
Db 41920 CGCTACGTTTAAACAGGCTCTCCGCTAATGAGCGACGCGAAGTGGCAGAGACTGCG 41979
QY 12661 GCGAGCATTTTACATCCCATATATCTCCATTAATCTCACTAAACGTTATGATTA 12720
| | | | |

Dh 41980 GGGGAGCATTTACATCCATTAATATCTCATATACCTCCATTAACCGGTAATGATAA 42039
Qy 12721 TCTTCTATTTAAATGTACGAAATATAAAATATAGACACACATGTTAAAACTATACAGC 12780
Dh 42040 TCTTCTATTTAAATGTACGAAATATAAAATATAGACACATGTTAAAACTATACAGC 42099
Qy 12781 GCAATGATGCGCATGGTCTCAACCGGCGATCCGTCCGGGTCAGTCCGACGGGGTCTTT 12840
Dh 42100 GCAATGATGCGCATGGTCTCAACCGGCGATCCGTCCGGGTCAGTCCGACGGGGTCTTT 42159
Qy 12841 CAGGTGATCTTCCGCGAGGGTATTATCTCGCAACATATTTACGTGCGGTGAACGGCAG 12900
Dh 42160 CAGGTGATCTTCCGCGAGGGTATTATCTCGCAACATATTTACGTGCGGTGAACGGCAG 42219
Qy 12901 CGGTTTTTTCACACACTTGGTTCCGTGATCTGAGCGACGATTAAGATTTATACGTG 12960
Dh 42220 CGGTTTTTTCACACACTTGGTTCCGTGATCTGAGCGACGATTAAGATTTATACGTG 42279
Qy 12961 TGGGGAACGGGTATTTTCAAAACACGACCCGGGCGCGGGGACGGTCCGGGCGGTG 13020
Dh 42280 TGGGGAACGGGTATTTTCAAAACACGACCCGGGCGCGGGGACGGTCCGGGCGGTG 42339
Qy 13021 TCCGAGCTGGCATTAAGTCTGCTCTGTTTACCAACATGAAAAATTTATCCGTTTGTAT 13080
Dh 42340 TCCGAGCTGGCATTAAGTCTGCTCTGTTTACCAACATGAAAAATTTATCCGTTTGTAT 42399
Qy 13081 GTAGTATTAATCAAGGCGGATGACGCTGACTGTGAAGCTGAGGACGCTGAAGTTTGTG 13140
Dh 42400 GTAGTATTAATCAAGGCGGATGACGCTGACTGTGAAGCTGAGGACGCTGAAGTTTGTG 42459
Qy 13141 TATATGTCAATTAATGCGGCTTACAGAAACGCAATGCGAGTTTAAAAAGTAAAGTTTCG 13200
Dh 42460 TATATGTCAATTAATGCGGCTTACAGAAACGCAATGCGAGTTTAAAAAGTAAAGTTTCG 42519
Qy 13201 CAATGTACCATGCTCCGCGTGTGACGGTTCATCTTAACCGCTTTAAAAAGAACGG 13260
Dh 42520 CAATGTACCATGCTCCGCGTGTGACGGTTCATCTTAACCGCTTTAAAAAGAACGG 42579
Qy 13261 TTGGTATCAACGGGACACTGCTACGCGACCGGTGCGCGCTGCAACCTTACAGATTTG 13320
Dh 42580 TTGGTATCAACGGGACACTGCTACGCGACCGGTGCGCGCTGCAACCTTACAGATTTG 42639
Qy 13321 ACCGAGCTTTACAGTCTAGAGTACGGGACGACTACGTGACACACACCGCTGCGCTTGA 13380
Dh 42640 ACCGAGCTTTACAGTCTAGAGTACGGGACGACTACGTGACACACACCGCTGCGCTTGA 42699
Qy 13381 CGCCCAAGGTATGTGAGGGACAAATATGCCCCGACGGCAGCCAGATGCCAACGGA 13440
Dh 42700 CGCCCAAGGTATGTGAGGGACAAATATGCCCCGACGGCAGCCAGATGCCAACGGA 42759
Qy 13441 TGGCAAGTGTGTAAGGCTTGAATTCGGCTCCGCAACCAAGCAACTATGCCAAGACG 13500
Dh 42760 TGGCAAGTGTGTAAGGCTTGAATTCGGCTCCGCAACCAAGCAACTATGCCAAGACG 42819
Qy 13501 TGGGCGCAGGCGCGTCAAGTTCCTGCTCGCGCATATTAAGTGTGCTATATGATTAAC 13560
Dh 42820 TGGGCGCAGGCGCGTCAAGTTCCTGCTCGCGCATATTAAGTGTGCTATATGATTAAC 42879
Qy 13561 GAAGAACTAGATACCAAGTGTGACGCGCAAGATCCGGCGCTTGGCCGTAGATGTGTC 13620
Dh 42880 GAAGAACTAGATACCAAGTGTGACGCGCAAGATCCGGCGCTTGGCCGTAGATGTGTC 42939
Qy 13621 GATCCGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 13680
Dh 42940 GATCCGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 42999
Qy 13681 GTGATTTCTATAGAAAAAGACGTGAGGTGTAGAACTATTAAGCAATTTTTCGCG 13740
Dh 43000 GTGATTTCTATAGAAAAAGACGTGAGGTGTAGAACTATTAAGCAATTTTTCGCG 43059
Qy 13741 GTTTTGTAAATAGGGAACGAACAGTGTGATTAATTAAGAGCATTTTATAGAGCG 13800
Dh 43060 GTTTTGTAAATAGGGAACGAACAGTGTGATTAATTAAGAGCATTTTATAGAGCG 43119

Qy 13801 TGGTGTGATTTAGAAACAGGTGTGAGAGAGCGCTTGGTTAAAGCGCGCGCTGTTT 13860
Dh 43120 TGGTGTGATTTAGAAACAGGTGTGAGAGAGCGCTTGGTTAAAGCGCGCGCTGTTT 43179
Qy 13861 CGCAAGATATTAACAGTATTTGAGAGATGTTTGGATTTATGAGACATGGGCGCTCAT 13920
Dh 43180 CGCAAGATATTAACAGTATTTGAGAGATGTTTGGATTTATGAGACATGGGCGCTCAT 43239
Qy 13921 AAGTGGGTAGGCTATTAACCACTACCACTGCGAATGCGCAATGCGCACTGCAACTGG 13980
Dh 43240 AAGTGGGTAGGCTATTAACCACTACCACTGCGAATGCGCAATGCGCACTGCAACTGG 43299
Qy 13981 AGCTGGCTCTGTGTGAGAGATATTAACCTGCAATTTAGCGGCGAGTCTACTGTTTGC 14040
Dh 43300 AGCTGGCTCTGTGTGAGAGATATTAACCTGCAATTTAGCGGCGAGTCTACTGTTTGC 43359
Qy 14041 TTAGTTGTCTGCGCTTACCCCTGACCGCGCTGGTGTGCTCCGGGGGCTTTGTTATTTAA 14100
Dh 43360 TTAGTTGTCTGCGCTTACCCCTGACCGCGCTGGTGTGCTCCGGGGGCTTTGTTATTTAA 43419
Qy 14101 GCGCGCTACGACTATCAACCGAGATTTATGTTTGTGGCTTGGAGATATGGCCACCCA 14160
Dh 43420 GCGCGCTACGACTATCAACCGAGATTTATGTTTGTGGCTTGGAGATATGGCCACCCA 43479
Qy 14161 GCGTGTCACTTCTTAAATCGTTTAAACAAGAAATGCAATAGTTTGGACACCCGGG 14220
Dh 43480 GCGTGTCACTTCTTAAATCGTTTAAACAAGAAATGCAATAGTTTGGACACCCGGG 43539
Qy 14221 TACGTCCGCTTTGTTGGGTATTAACACCGGACCACTGCGCATTTGCGCTTTTGAACC 14280
Dh 43540 TACGTCCGCTTTGTTGGGTATTAACACCGGACCACTGCGCATTTGCGCTTTTGAACC 43599
Qy 14281 GCGGTAATCAAGGAAATGCGATGTCTACTTAATTTTAAAGTTTATGATCGTAATCAT 14340
Dh 43600 GCGGTAATCAAGGAAATGCGATGTCTACTTAATTTTAAAGTTTATGATCGTAATCAT 43659
Qy 14341 GAAACCAAAAGATTTGGCCGCTGCTTACCGTGTACATGAATGAGATATTCAGATTT 14400
Dh 43660 GAAACCAAAAGATTTGGCCGCTGCTTACCGTGTACATGAATGAGATATTCAGATTT 43719
Qy 14401 TTGTCCACAGAAATCTGTGCGCATTAAGGAGCTGCTGTGATGGGCGGACTGTGTTTAAT 14460
Dh 43720 TTGTCCACAGAAATCTGTGCGCATTAAGGAGCTGCTGTGATGGGCGGACTGTGTTTAAT 43779
Qy 14461 TCGTTTTGTGATCCCTTTCTAATGCGCGAGAGAGCTTCCGATACCGGGCGCTTGAACC 14520
Dh 43780 TCGTTTTGTGATCCCTTTCTAATGCGCGAGAGAGCTTCCGATACCGGGCGCTTGAACC 43839
Qy 14521 ACATCCGAGAAACCGTGGCGGCTTAACAAACAGAAATTAATATACCTTGCAGAAC 14580
Dh 43840 ACATCCGAGAAACCGTGGCGGCTTAACAAACAGAAATTAATATACCTTGCAGAAC 43899
Qy 14581 AGTGCCAAAGAGAGAGATATACAGATGCCATTAAGGGGAAAGAGTTCCACCAAAATATCC 14640
Dh 43900 AGTGCCAAAGAGAGAGATATACAGATGCCATTAAGGGGAAAGAGTTCCACCAAAATATCC 43959
Qy 14641 GTTTTGTGATTTGATGAGAGAGGCGGCTTTGCAACCTGCTCTGTGATTTATGCT 14700
Dh 43960 GTTTTGTGATTTGATGAGAGAGGCGGCTTTGCAACCTGCTCTGTGATTTATGCT 44019
Qy 14701 GCTCTGCCCCGACTGACACAGTTCCTGCTGCGCAGAGATGTTGGGCTTCTTATACCA 14760
Dh 44020 GCTCTGCCCCGACTGACACAGTTCCTGCTGCGCAGAGATGTTGGGCTTCTTATACCA 44079
Qy 14761 GTGCGATTAAGAGACGTGTAATTTGTACGGGGGCCACGTACACGTTAACCCGATVCG 14820
Dh 44080 GTGCGATTAAGAGACGTGTAATTTGTACGGGGGCCACGTACACGTTAACCCGATVCG 44139
Qy 14821 CGGATACAGCCACCTGACCTGCAAGGAGACTCAACCTGCTGCGCCCTTATCTCGTG 14880
Dh 44140 CGGATACAGCCACCTGACCTGCAAGGAGACTCAACCTGCTGCGCCCTTATCTCGTG 44199

OY	14881	CGGGGCCAGCGCCGGCGATGTCCTGGTTACCGGACACGTTAATCTTTGGCCGTCT	14940
Db	44200	CGGGGCCAGCGCCGGCGGATGTCGGTTACCGGACACGTTAATCTTTGGCCGTCT	44259
OY	14941	CTTTGACCCCAACCTCTCCCAAGAGGACCAAGCTGCGTTTAAAGAAACCAACGCCC	15000
Db	44280	CTTTGACCCCAAGCTCTCCCAAGAGGACCAAGCTGCGTTTAAAGAAACCAACGCCC	44319
OY	15001	GGTACCGATAGAGGACGCATGTGCGGGCGTCACGGCCGAAAGGACCGAGGTGCAACCCAC	15060
Db	44320	GGTACCGATAGAGGACGCATGTGCGGGCGTCACGGCCGAAAGGACCGAGGTGCAACCCAC	44379
OY	15061	TTGCGCTACCGTGGGCCCTCTAATGGCTGCGCGGATTTAGCCAGTCCGCTATGCTACGG	15120
Db	44380	TTTCCCTACCGTGGGCCCTCTAATGGCTGCGCGGATTTAGCCAGTCCGCTATGCTACGG	44439
OY	15121	CTGCACAGACTTAAAGACATCTGCTACGTTCTTTATGTAAGACGCTGCACACATCAGC	15180
Db	44440	CTGCACAGACTTAAAGACATCTGCTACGTTCTTTATGTAAGACGCTGCACACATCAGC	44499
OY	15181	GAACTCGGCGCCGTCGGGGGCTCGCGTACACAGATGTTCCGTTTTCTTCTTAATGTTTC	15240
Db	44500	GAACTCGGCGCCGTCGGGGGCTCGCGTACACAGATGTTCCGTTTTCTTCTTAATGTTTC	44559
OY	15241	AGGTTCTTCCCGGAAACCACTCTGATAGCTGTGGCATATCTCGAGAAACGCGATTTG	15300
Db	44560	AGGTTCTTCCCGGAAACCACTCTGATAGCTGTGGCATATCTCGAGAAACGCGCATTTG	44619
OY	15301	CGCAGCGTTTGTGGGCGAGGTAAACCCACGTGAACGTTTCAACGACGAGAGAAAGA	15360
Db	44620	CGCAGCGTTTGTGGGCGAGGTAAACCCACGTGAACGTTTCAACGACGAGAGAAAGA	44679
OY	15361	ACGCTGATTAATGGCGACACAGATCATGTTTTCCCGCTGCAGACGCGGGATTAACAAACAG	15420
Db	44680	ACGCTGATTAATGGCGACACAGATCATGTTTTCCCGCTGCAGACGCGGGATTAACAAACAG	44739
OY	15421	CTGGCTTCTGCTTAAACGCTCTGTAAACGCTGCTCCGTGGTTTCAATTAACCAAGTGT	15480
Db	44740	CTGGCTTCTGCTTAAACGCTCTGTAAACGCTGCTCCGTGGTTTCAATTAACCAAGTGT	44799
OY	15481	TGCTTAAACGTGGCAATTAACCTGCTGTCGTTTTCGGGTCGTTTATAGCGGATTAANA	15540
Db	44800	TGCTTAAACGTGGCAATTAACCTGCTGTCGTTTTCGGGTCGTTTATAGCGGATTAANA	44859
OY	15541	TAAACGTGTGCATGATTAATGTTGTGAAGGGCTCAAGGCAACAAACCCGGGACAG	15600
Db	44860	TAAACGTGTGCATGATTAATGTTGTGAAGGGCTCAAGGCAACAAACCCGGGACAG	44919
OY	15601	TAACTCCCATTTAAAAATGACGACAGGTTGGCTTAAAAACTGCCGCACTTCTCATTAACG	15660
Db	44920	TAACTCCCATTTAAAAATGACGACAGGTTGGCTTAAAAACTGCCGCACTTCTCATTAACG	44979
OY	15661	GGGCACTCTAGGAAGCTCTGAGGGTCGCTGGGGCGGATTTGGTATTCATGTACTGTCGC	15720
Db	44980	GGGCACTCTAGGAAGCTCTGAGGGTCGCTGGGGCGGATTTGGTATTCATGTACTGTCGC	45039
OY	15721	TTGGCGTTTTCSCAATTTGGAACCCACAAACATGTTTCTTAAAGTAGTTGTGAGTCTCCG	15780
Db	45040	TTGGCGTTTTCSCAATTTGGAACCCACAAACATGTTTCTTAAAGTAGTTGTGAGTCTCCG	45099
OY	15781	GTTAACCGGGGCAACGTAAGCGTGTAGAAATTCGGGGCTTCCACACGTAGGGGCGGCG	15840
Db	45100	GTTAACCGGGGCAACGTAAGCGTGTGTAGAAATTCGGGGCTTCCACACGTAGGGGCGGCG	45159
OY	15841	ATGGGTTCTTGAACCTCTGGGCTACGTTTGAAGTAACTGCTCTTAAACGAGACTATATGCA	15900
Db	45160	ATGGGTTCTTGAACCTCTGGGCTACGTTTGAAGTAACTGCTCTTAAACGAGACTATATGCA	45219
OY	15901	TTAAACCGCGTAATTAACCTCCCAAGCATGGGTGGCCATTCGTTGGCTTTGCGTTTGCC	15960
Db	45220	TTAAACCGCGGTAAATTAACCTCCCAAGCATGGGTGGCCATTCGTTGGCTTTGCGTTTGCC	45279
OY	15961	GATATATAAACGGGGCGGTTGCCAACAAGTTTTCGCAACCAACCGCTGTCAGCCGCGC	16020

Db	45280	GATATAAATAACGGGGGGGTGGCGAAACAGTTTTTCGGACACACCGTCCGAGACACGGC	45335
OY	16021	AAGTTATTGTAAGACGTTCCGATAGCTGTTTAAACAATGTTCCCTTCAGTTTTTTTG	16086
Db	45340	AAGTTATTGTAAGACGTTCCGATAGCTGTTTAAACAATGTTCCCTTCAGTTTTTTTG	45395
OY	16081	AATAACGGGACCCCGGAACGGAAAGCCGCTTCGTTAAAGCGCTTCAGTTAGCTTTAGAC	16140
Db	45400	AATAACGGGACCCCGGAACGGAAAGCCGCTTCGTTAAAGCGCTTCAGTTAGCTTTAGAC	45455
OY	16141	CTGTGTGACAAACCTCCGGGACACTTTTAACTACTTAAACACTCTCTAATACTTTTCTT	16200
Db	45460	CTGTGTGACAAACCTCCGGGACACTTTTAACTACTTAAACACTCTCTAATACTTTTCTT	45519
OY	16201	CTGTATATCCAAAGTTCTCCGGAAATCGCCCGCGTTAGAGACTGTCCGACGCGGAAGG	16266
Db	45520	CTGTATATCCAAAGTTCTCCGGAAATCGCCCGCGTTAGAGACTGTCCGACGCGGAAGG	45575
OY	16261	TTTGACTTTGAACACATTCACCTCCCAAACCTAACACGACATGACGCGTCTCTGGGGCGA	16322
Db	45580	TTTGACTTTGAACACATTCACCTCCCAAACCTAACACGACATGACGCGTCTCTGGGGCGA	45633
OY	16321	TACTCCGACATGTTAACAAAGACGACACGTCGTTAAGCTTAAAGCAATTTCTCTGAAT	16388
Db	45640	TACTCCGACATGTTAACAAAGACGACACGTCGTTAAGCTTAAAGCAATTTCTCTGAAT	45695
OY	16381	TCACAGGGTGCCTGTGTTTATCTCCGATGAGACAGACAAATGAAATGGGCGTCACG	16440
Db	45700	TCACAGGGTGCCTGTGTTTATCTCCGATGAGACAGACAAATGAAATGGGCGTCACG	45755
OY	16441	TTTAAAGAAAGACAGATGGTTTAAATAGGCTGTAGAGGGCTTGTCAAATCCACAGACTCG	16500
Db	45760	TTTAAAGAAAGACAGATGGTTTAAATAGGCTGTAGAGGGCTTGTCAAATCCACAGACTCG	45815
OY	16501	AAAGTTTAAAGCCCGTGGATCTCTTACCGCTCATAGGCTCTGTTTACGGTCTCCGG	16566
Db	45820	AAAGTTTAAAGCCCGTGGATCTCTTACCGCTCATAGGCTCTGTTTACGGTCTCCGG	45875
OY	16561	TGCTTCTCTCGGGAACACAGAGTGCCTATATGAACGCAATTTGGTATGAAGGACCCATA	16620
Db	45880	TGCTTCTCTCGGGAACACAGAGTGCCTATATGAACGCAATTTGGTATGAAGGACCCATA	45933
OY	16621	CTCTTACCGCACATATGATGCCCCCAGAAAGAGCATTAATGACTTTGTCCATCATGTA	16688
Db	45940	CTCTTACCGCACATATGATGCCCCCAGAAAGAGCATTAATGACTTTGTCCATCATGTA	45995
OY	16681	ATTAGTACGTTAAATTTTATAGGTGAACGCGCGTGGGGCTCTGAACGTGAACGCTCC	16744
Db	46000	ATTAGTACGTTAAATTTTATAGGTGAACGCGCGTGGGGCTCTGAACGTGAACGCTCC	46055
OY	16741	CCGCGGTTGAGGCGCTCGCGGTTCCGGGACAGCATGCTGTCTCGGGGACGTGAAGG	16800
Db	46060	CCGCGGTTGAGGCGCTCGCGGTTCCGGGACAGCATGCTGTCTCGGGGACGTGAAGG	46119
OY	16801	GATGACGCAATCTGTCCGCAAAAGTGCATGTTGTCTACCTGTACAAGCAAAAAGATAG	16866
Db	46120	GATGACGCAATCTGTCCGCAAAAGTGCATGTTGTGTCACTGTACAAGCAAAAAGATAG	46179
OY	16861	ATTTCGATTCATGAAACACACAGCTGGGCGAGTCAATGCGATTAGGCGGACAGGTGCGACA	16920
Db	46180	ATTTCGATTCATGAAACACACAGCTGGGCGAGTCAATGCGATTAGGCGGACAGGTGCGACA	46233
OY	16921	TATATAACGCTACTGTTTGGGGCTCAAGCGGTGACAGAGTCTGGGGAATTTGTTTAATC	16980
Db	46240	TATATAACGCTACTGTTTGGGGCTCAAGCGGTGACAGAGTCTGGGGAATTTGTTTAATC	46299
OY	16981	CCCCGTATCAACATTGAAGGGCTGTGAAGCATGATAAGGAACATGGCTCGGACAGAC	17040
Db	46300	CCCCGTATCAACATTGAAGGGCTGTGAAGCATGATAAGGAACATGGCTCGGACAGAC	46355
OY	17041	TAAAAAAATGTTAATAGTTCGACGCTCGAGTGGGAATTCACAAAAAACTGTCACTTC	17100

Db 46360 TAAAAAATGTTAAATGAGAGCTGAGAGTGGAAAAATCAACAAAAAAGTCTCATCTC 46419
Qy 17101 CGATTTGACAGGTTTGGGGCCGACAGTGCCTGTTTAAACGCGAGTATAAGGGAACAG 17160
Db 46420 CGATTTGACAGGTTTGGGGCCGACAGTGCCTGTTTAAACGCGAGTATAAGGGAACAG 46479
Qy 17161 GGAATCGCTGCGGTGATACAAACAGCCCTAAAAAAGAGAGATCTGGCAGCCGTTGTCGG 17220
Db 46480 GGAATCGCTGCGGTGATACAAACAGCCCTAAAAAAGAGAGATCTGGCAGCCGTTGTCGG 46539
Qy 17221 AACGCTAGAAACGTCGCTGCTGAAAAAACAAGCAATTTGGGATTTACTAAAGGGTTTAA 17280
Db 46540 AACCTAGAAACGTCGCTGCTGAAAAAACAAGCAATTTGGGATTTACTAAAGGGTTTAA 46599
Qy 17281 CAGGAAAAAATTTAGAGTTTGAAGCTGTGGCGAGCGGGTTGGCAGCTCAAGAGCA 17340
Db 46600 CAGGAAAAAATTTAGAGTTTGAAGCTGTGGCGAGCGGGTTGGCAGCTCAAGAGCA 46659
Qy 17341 GCTGTACGAGAACTGGAGATTTAGGTAGCGCTTGACAAATGAAATCTGTTCCCGTGAAGA 17400
Db 46660 GCTGTACGAGAACTGGAGATTTAGGTAGCGCTTGACAAATGAAATCTGTTCCCGTGAAGA 46719
Qy 17401 AGAGTCCCCCAAGAGACACATATTATAGTGGAAATTTGGAGCGTCTGCCAGAGTGTCCC 17460
Db 46720 AGAGTCCCCCAAGAGACACATATTATAGTGGAAATTTGGAGCGTCTGCCAGAGTGTCCC 46779
Qy 17461 CAAAAGCCCTTGATCCCATCCCAAGGTTGACACTGACGTGACAGAAACAGCATCGTCCC 17520
Db 46780 CAAAAGCCCTTGATCCCATCCCAAGGTTGACACTGACGTGACAGAAACAGCATCGTCCC 46839
Qy 17521 ATATACCGCTCATTTAAAAACAGTAAGAGATCGGCCAATGAAATACCTAACACATGGG 17580
Db 46840 ATATACCGCTCATTTAAAAACAGTAAGAGATCGGCCAATGAAATACCTAACACATGGG 46899
Qy 17581 GCCAGTGTAGTACACAGGACGACGACGACCGCGCTGTGAGACGGGGCTCGTATGAGTG 17640
Db 46900 GCCAGTGTAGTACACAGGACGACGACGACCGCGCTGTGAGACGGGGCTCGTATGAGTG 46959
Qy 17641 TGGTGAAGTCCATCTCTCGGCGCTGCGCTTAAAGCAATTTTGGAGCGGGCTGAGTTT 17700
Db 46960 TGGTGAAGTCCATCTCTCGGCGCTGCGCTTAAAGCAATTTTGGAGCGGGCTGAGTTT 47019
Qy 17701 TTTTACGAGTCAATTTTAAACGATTAAGTACGCGCGCTCCGAGAAACATCCCTGAAAC 17760
Db 47020 TTTTACGAGTCAATTTTAAACGATTAAGTACGCGCGCTCCGAGAAACATCCCTGAAAC 47079
Qy 17761 GCGGGGGTGAACCGTATCTATGTTTCTTAAAGCCGCTGTAACATGTCGGGCTGATAT 17820
Db 47080 GCGGGGGTGAACCGTATCTATGTTTCTTAAAGCCGCTGTAACATGTCGGGCTGATAT 47139
Qy 17821 TCCCGCAGTTAAACAGGGAATCTGTTAAACGCGGATCTTAAACAGCTGAACCCCTGAAG 17880
Db 47140 TCCCGCAGTTAAACAGGGAATCTGTTAAACGCGGATCTTAAACAGCTGAACCCCTGAAG 47199
Qy 17881 TGGCGGTTGAATCTCTGAGCTGAGGGAAGGCGTTAGTTTCTAAATTAATATATGTGGA 17940
Db 47200 TGGCGGTTGAATCTCTGAGCTGAGGGAAGGCGTTAGTTTCTAAATTAATATATGTGGA 47259
Qy 17941 TCCGTTCACTGTGACATGATCCAGAAATTAATCTGATTAAGGGGAAGTGAACCTGCT 18000
Db 47260 TCCGTTCACTGTGACATGATCCAGAAATTAATCTGATTAAGGGGAAGTGAACCTGCT 47319
Qy 18001 ACAGGACATTTATGATGAGATCTAGAGTCCGCGCTTTTACACAGGGAACCCCTTGA 18060
Db 47320 ACAGGACATTTATGATGAGATCTAGAGTCCGCGCTTTTACACAGGGAACCCCTTGA 47379
Qy 18061 CCGGAGTATGATGACCTCCAAACTCGGGTTCTGTCAGACACACGATCAATTTTAAAGCAC 18120
Db 47380 CCGGAGTATGATGACCTCCAAACTCGGGTTCTGTCAGACACACGATCAATTTTAAAGCAC 47439
Qy 18121 CCGGACATTTATCTGTAAGACATTTACGCGCGCTGTCTCTCTACCGGCTGTCTGC 18180
Db 47440 CCGGACATTTATCTGTAAGACATTTACGCGCGCTGTCTCTCTCTACCGGCTGTCTGC 47499

Qy 18181 TGTCTGCGCGGGGGCCCGAGCGCATATGCTAAATCAAGCCCTTCCAAATCACTCCAC 18240
Db 47500 TGTCTGCGCGGGGGCCCGAGCGCATATGCTAAATCAAGCCCTTCCAAATCACTCCAC 47559
Qy 18241 AACTCGGCTTCACAAATTTGACATATCTGCTCGGTTATATGTTTCTAGCATGCTTAGAGA 18300
Db 47560 AACTCGGCTTCACAAATTTGACATATCTGCTCGGTTATATGTTTCTAGCATGCTTAGAGA 47619
Qy 18301 AATATCTTACGCGCGTACCATTTCCAGAGGGAAGGTTGGCGGACGCTTCCTCCCG 18360
Db 47620 AATATCTTACGCGCGTACCATTTCCAGAGGGAAGGTTGGCGGACGCTTCCTCCCG 47679
Qy 18361 AATCGGCCACCCATTTGTTTATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 18420
Db 47680 AATCGGCCACCCATTTGTTTATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 47739
Qy 18421 TTTTCTGTTGCTTGGGAGCTTCCACTCGATTTAGCCATTTAGCTATCTGCGCAGCGC 18480
Db 47740 TTTTCTGTTGCTTGGGAGCTTCCACTCGATTTAGCCATTTAGCTATCTGCGCAGCGC 47799
Qy 18481 CAGCTATTTCCCTGAGAGGCGTACAGGCGGCTTTTGGCAACAGTATGTTATATTA 18540
Db 47800 CAGCTATTTCCCTGAGAGGCGTACAGGCGGCTTTTGGCAACAGTATGTTATATTA 47859
Qy 18541 GGGCGCAATACAAAGAGGATGCTTAAAGAAACGATCTCGCGCTGTGTAACTCAAAAC 18600
Db 47860 GGGCGCAATACAAAGAGGATGCTTAAAGAAACGATCTCGCGCTGTGTAACTCAAAAC 47919
Qy 18601 TTAATAGTCTTCAGAGCTGTTGCTCAGGACACTATTATGATCTGCGGAAATGCG 18660
Db 47920 TTAATAGTCTTCAGAGCTGTTGCTCAGGACACTATTATGATCTGCGGAAATGCG 47979
Qy 18661 GAGATCATGATTTTCTCAGATGACGCGATGCTGAGGAGATGCGGCTTCGACATC 18720
Db 47980 GAGATCATGATTTTCTCAGATGACGCGATGCTGAGGAGATGCGGCTTCGACATC 48039
Qy 18721 GATGAGCAGCAGCGCTCTCTCGAAATGAGCTTGCCAACTTTTAAACATGAGCA 18780
Db 48040 GATGAGCAGCAGCGCTCTCTCGAAATGAGCTTGCCAACTTTTAAACATGAGCA 48099
Qy 18781 GTAAAGGCGTTTAAACGATTAACAAAGAAATTAAGCATGCGGCTATAGCGTCTG 18840
Db 48100 GTAAAGGCGTTTAAACGATTAACAAAGAAATTAAGCATGCGGCTATAGCGTCTG 48159
Qy 18841 TATATTTTATCTATTCGCAAGTGGGAAATTTTACGCAACCGGATCTAGCAT 18900
Db 48160 TATATTTTATCTATTCGCAAGTGGGAAATTTTACGCAACCGGATCTAGCAT 48219
Qy 18901 TTTTACGTCATCTGCTGTTACAGGGGAGCGCTGACGCGCTGTGGAAGTGTAGAC 18960
Db 48220 TTTTACGTCATCTGCTGTTACAGGGGAGCGCTGACGCGCTGTGGAAGTGTAGAC 48279
Qy 18961 GCGTGCCTAAACATGACACCGCGACGATGACACACGCTGTGTGATTAAGAAAGGTC 19020
Db 48280 GCGTGCCTAAACATGACACCGCGACGATGACACACGCTGTGTGATTAAGAAAGGTC 48339
Qy 19021 ACAGGCGGCAAAACATCAATCTCTGTGGGAGCGCTGTGAGGAGCGGATTAATTCGCG 19080
Db 48340 ACAGGCGGCAAAACATCAATCTCTGTGGGAGCGCTGTGAGGAGCGGATTAATTCGCG 48399
Qy 19081 TCAAAATTTCACTGGGCGCATTAACAAACAGAAATTCGTCAAAAAATTTTAAACCGTGG 19140
Db 48400 TCAAAATTTCACTGGGCGCATTAACAAACAGAAATTCGTCAAAAAATTTTAAACCGTGG 48459
Qy 19141 CTAATAGTCAACAAATCTTTGTAAGCGGCGCTGCTGCTTGGAGTCTGCGAGGAA 19200
Db 48460 CTAATAGTCAACAAATCTTTGTAAGCGGCGCTGCTGCTTGGAGTCTGCGAGGAA 48519
Qy 19201 GTGGTTAAAGAGATGAGGAGCTGCTGATTCAGAGGCGGCACTGTGAACATGAC 19260
Db 48520 GTGGTTAAAGAGATGAGGAGCTGCTGATTCAGAGGCGGCACTGTGAACATGAC 48579

Db 50740 CATAAGTCAGAAATTAACAGTAGTATTTCACCATGACATTAAGATAAAGAGTGCCTCG 50799
Qy 21481 TGAATTTTCATAGTTCAAGAAATCTGCTCGCGGGTGGCTTGGGCAAACTAGCAGTAA 21540
Db 50800 TGAATTTTCATAGTTCAAGAAATCTGCTCGCGGGTGGCTTGGGCAAACTAGCAGTAA 50859
Qy 21541 TCAGCAAGTGGCTTACATGTTACGAGTTTAAATAGGCTCCGCTTTTAAATATCACATTCT 21600
Db 50860 TCAGCAAGTGGCTTACATGTTACGAGTTTAAATAGGCTCCGCTTTTAAATATCACATTCT 50919
Qy 21601 GTGCAAGAGTATGAGCCGACGACACATGAACGCCCGGAGAGTGGCACTACAGGCAATG 21660
Db 50920 GTGCAAGAGTATGAGCCGACGACACATGAACGCCCGGAGAGTGGCACTACAGGCAATG 50979
Qy 21661 TTTTGCACATATCGCTGCATAGACACGACGACGCGGAATTAATTAATCTGCGAGTTC 21720
Db 50980 TTTTGCACATATCGCTGCATAGACACGACGCGGAATTAATTAATCTGCGAGTTC 51039
Qy 21721 ATTTACTGTTATGTCACAAATGCGGAATTCAGGGAGATGCCCATATCTATTGTCACCG 21780
Db 51040 ATTTACTGTTATGTCACAAATGCGGAATTCAGGGAGATGCCCATATCTATTGTCACCG 51099
Qy 21781 AAACATTAAGCAATCTAGTGGGGAATATACGGCGATAAACCGTACAGCAGCTGCA 21840
Db 51100 AAACATTAAGCAATCTAGTGGGGAATATACGGCGATAAACCGTACAGCAGCTGCA 51159
Qy 21841 TAAATGAGCAGCGCGCTAATATATGATGAGTGGGAATCTCGTACTGTTACGGAATCCCA 21900
Db 51160 TAAATGAGCAGCGCGCTAATATATGATGAGTGGGAATCTCGTACTGTTACGGAATCCCA 51219
Qy 21901 TCATTCATTTGTTAAGTCCCAAGCCCGGTGCGGTTAACGTAAAGGCTCAGCGAGCGGAATA 21960
Db 51220 TCATTCATTTGTTAAGTCCCAAGCCCGGTGCGGTTAACGTAAAGGCTCAGCGAGCGGAATA 51279
Qy 21961 TGGTAATGTTGGGGTGGGGAAGAGAGTGGATACCTGCTGTTGGTGGCGGATGAGAG 22020
Db 51280 TGGTAATGTTGGGGTGGGGAAGAGAGTGGATACCTGCTGTTGGTGGCGGATGAGAG 51339
Qy 22021 CCTATCTTCATTTGCGATACCACTATGAGCTTATGTTGATGTTCTGTTGCCAACC 22080
Db 51340 CCTATCTTCATTTGCGATACCACTATGAGCTTATGTTGATGTTCTGTTGCCAACC 51399
Qy 22081 GCGAATTTTGGTCTCAGAGATGTTTCTCAGCTGTTTACGTTTCCAACTTGAAGTTTACC 22140
Db 51400 GCGAATTTTGGTCTCAGAGATGTTTCTCAGCTGTTTACGTTTCCAACTTGAAGTTTACC 51459
Qy 22141 TTAACAAACAGGGGGGTTTATACATATAGGCAATGAGCCAGCAATGCCGAAAGAG 22200
Db 51460 TTAACAAACAGGGGGGTTTATACATATAGGCAATGAGCCAGCAATGCCGAAAGAG 51519
Qy 22201 CGAAAGATGGCGCATTTGGGTATCTTGTATATCTTAAATTTGGGAATCTGTGAATATCAAG 22260
Db 51520 CGAAAGATGGCGCATTTGGGTATCTTGTATATCTTAAATTTGGGAATCTGTGAATATCAAG 51579
Qy 22261 TTGCGGGCAGAGTACACCTTGAATGCGCACCGCAACATTTACGTTCTCTGGGTGG 22320
Db 51580 TTGCGGGCAGAGTACACCTTGAATGCGCACCGCAACATTTACGTTCTCTGGGTGG 51639
Qy 22321 ACGAGGCGTGTATGGAAGAGGGGGCCGCGCGAATTTTAAAGGCGGTGCAATATAGT 22380
Db 51640 ACGAGGCGTGTATGGAAGAGGGGGCCGCGCGAATTTTAAAGGCGGTGCAATATAGT 51699
Qy 22381 TGTTCGGCAGCGGAGAGCGGTAGCGCAAGTTTAACTAGTGTGTCGCGGGGCGACATC 22440
Db 51700 TGTTCGGCAGCGGAGAGCGGTAGCGCAAGTTTAACTAGTGTGTCGCGGGGCGACATC 51759
Qy 22441 CGGAGGAAACCCCTTCCCTCTACTTTTCCGCGTTTCCACACCTCCGCTGTTGTTG 22500
Db 51760 CGGAGGAAACCCCTTCCCTCTACTTTTCCGCGTTTCCACACCTCCGCTGTTGTTG 51819
Qy 22501 GAAAGCCGGAAGGTCGACGTAACCGCGGTCCAGAACTCCCAAAAGCACAATTTGGG 22560
Db 51820 GAAAGCCGGAAGGTCGACGTAACCGCGGTCCAGAACTCCCAAAAGCACAATTTGGG 51879

Qy 22561 TACACTGGCCCCGTTTAAAGATTCATCTTAAAGGGATACAGCTTCTACCTGGCATTT 22620
Db 51880 TACACTGGCCCCGTTTAAAGATTCATCTTAAAGGGATACAGCTTCTACCTGGCATTT 51939
Qy 22621 CACCTTAAAGCCAGTACCGGTTCGTTGCGGCTTTGGGTGAGAGATGTTAACT 22680
Db 51940 CACCTTAAAGCCAGTACCGGTTCGTTGCGGCTTTGGGTGAGAGATGTTAACT 51999
Qy 22681 TGAGTCTGCGAGAGCAGAAAGCGTTGGCCGATAGTGAGCCACATCTTATAGTA 22740
Db 52000 TGAGTCTGCGAGAGCAGAAAGCGTTGGCCGATAGTGAGCCACATCTTATAGTA 52059
Qy 22741 TCATTAATTTTTCATCACTGTTGTCAGCAGCACTTAAATGCGACCGCTGTTTAA 22800
Db 52060 TCATTAATTTTTCATCACTGTTGTCAGCAGCACTTAAATGCGACCGCTGTTTAA 52119
Qy 22801 ATGAGTTGAATATACATACCAACATCTGTCAGGAGCTTCCTTTCATCAAGAG 22860
Db 52120 ATGAGTTGAATATACATACCAACATCTGTCAGGAGCTTCCTTTCATCAAGAG 52179
Qy 22861 AATACACCGGTTCTGCAACATTTTACGTGGCGGCGGAGCGGATATACCTGG 22920
Db 52180 AATACACCGGTTCTGCAACATTTTACGTGGCGGCGGAGCGGATATACCTGG 52239
Qy 22921 CGGCGATTAATTAACACAGTATTCATCAAGGCTCCAGCTCAGCCAGCTGTAAGT 22980
Db 52240 CGGCGATTAATTAACACAGTATTCATCAAGGCTCCAGCTCAGCCAGCTGTAAGT 52299
Qy 22981 GTTTCGCCCATCACTAATATGTTGCGTGAAGAAATGTTACGAGGTTAAATATAC 23040
Db 52300 GTTTCGCCCATCACTAATATGTTGCGTGAAGAAATGTTACGAGGTTAAATATAC 52359
Qy 23041 AGTTCATTTCTTCCACAGGAACAGCAAGGCTGTCAGCCGCTTGAAGGCGCATTTGG 23100
Db 52360 AGTTCATTTCTTCCACAGGAACAGCAAGGCTGTCAGCCGCTTGAAGGCGCATTTGG 52419
Qy 23101 ACTTCCCGTACAGGAACCTTCCACCGCCTGACTGCTGCAAGTGTGAGTCTGCTCCG 23160
Db 52420 ACTTCCCGTACAGGAACCTTCCACCGCCTGACTGCTGCAAGTGTGAGTCTGCTCCG 52479
Qy 23161 GTCCGTGTTTTTAAATATACAGCGGGGTTTTGATGCGGCACTGCGAAGACCCAC 23220
Db 52480 GTCCGTGTTTTTAAATATACAGCGGGGTTTTGATGCGGCACTGCGAAGACCCAC 52539
Qy 23221 CAGGGAACAAACCGGAGCTGCTGCTGAGCTGTATAGAAAGCGGAGCTTGTCT 23280
Db 52540 CAGGGAACAAACCGGAGCTGCTGCTGAGCTGTATAGAAAGCGGAGCTTGTCT 52599
Qy 23281 TAACACTCAGTGTACCGATTTGGGCGCTGGCGGATATCTTACCACCTTTTGGCA 23340
Db 52600 TAACACTCAGTGTACCGATTTGGGCGCTGGCGGATATCTTACCACCTTTTGGCA 52659
Qy 23341 CAGGCGGTGTATATTTTGGCTGCTGCGCACGCGGTGGTAAATGCGGCCCATATG 23400
Db 52660 CAGGCGGTGTATATTTTGGCTGCTGCGCACGCGGTGGTAAATGCGGCCCATATG 52719
Qy 23401 CCTCCCTACCGATGAGTGTGATACGCTGCAAGTTTGTGCGACAAAGCGTGGAC 23460
Db 52720 CCTCCCTACCGATGAGTGTGATACGCTGCAAGTTTGTGCGACAAAGCGTGGAC 52779
Qy 23461 AATCTGCTGTACAAAGAAATGGCGTTACCGGTTGAGCTTGAATTTATGTAATCTACA 23520
Db 52780 AATCTGCTGTACAAAGAAATGGCGTTACCGGTTGAGCTTGAATTTATGTAATCTACA 52839
Qy 23521 GGAGCACTATGTTTTTATGTTGTGTCACAGCGGAGGATACGAGAGTACAGCGGA 23580
Db 52840 GGAGCACTATGTTTTTATGTTGTGTCACAGCGGAGGATACGAGAGTACAGCGGA 52899
Qy 23581 CAATATAGACAAATAGAGAGTTGAAAGGTAATGTTATTTTAAACAGAGTCTG 23640
Db 52900 CAATATAGACAAATAGAGAGTTGAAAGGTAATGTTATTTTAAACAGAGTCTG 52959

23641 TCTGGGATGCTGTAGGCTGGTATTGAAAAATATTTAATACGATCGCTTAGAG 23700
|||||
59960 TCTGGGATGCTGTAGGCTGGTATTGAAAAATATTTAATACGATCGCTTAGAG 53019
23701 GTCTGTGTAATAATGTGCGCAATTAATATTGTAAGATCGCGCGGCGCTTTC 23760
|||||
53020 GTCTGTGTAATAATGTGCGCAATTAATATTGTAAGATCGCGCGGCGCTTTC 53079
23761 TTCTCCAGCTTCTGTGTAGAGGAAAGATTCCTCAATAAATGAGTTTCAGTAAGCCTTT 23820
|||||
53080 TTCTCCAGCTTCTGTGTAGAGGAAAGATTCCTCAATAAATGAGTTTCAGTAAGCCTTT 53139
23821 CATGTGCTGCGCTTTTCGTCACAGCTTATGAGATTTAACCAGCACTAGGGGCGGAC 23880
|||||
53140 CATGTGCTGCGCTTTTCGTCACAGCTTATGAGATTTAACCAGCACTAGGGGCGGAC 53199
23881 GCGCAAAATGCTTGGGGTGGTTTAACCTGTGTAATCGCGCAAGGTGACGCTATAC 23940
|||||
53200 GCGCAAAATGCTTGGGGTGGTTTAACCTGTGTAATCGCGCAAGGTGACGCTATAC 53259
23941 TTGATCCCATTAACAAACGCGGAATCATTAACAGTATACCTCTGATGATACCT 24000
|||||
53260 TTGATCCCATTAACAAACGCGGAATCATTAACAGTATACCTCTGATGATACCT 53319
24001 GCGCCGCTCAGCGCGGACAGATTAATATAGGGGGGCTTATCGTATTTTCAGCAT 24060
|||||
53320 GCGCCGCTCAGCGCGGACAGATTAATATAGGGGGGCTTATCGTATTTTCAGCAT 53379
24061 AGAAATATGACAGAGTCTGTACGCTGCGGCTGCGCGGCTTAAACAGCTGCAGCG 24120
|||||
53380 AGAAATATGACAGAGTCTGTACGCTGCGGCTGCGCGGCTTAAACAGCTGCAGCG 53439
24121 GTCCAGAAAAAGTGGGATATATGTCAGTGGCTGCGATCATCTCTGCTGTCAGCAC 24180
|||||
53440 GTCCAGAAAAAGTGGGATATATGTCAGTGGCTGCGATCATCTCTGCTGTCAGCAC 53499
24181 GCACGAAAGACAAACCCAGTAAACGTTGCGACTGAGCGCTGCGCGCGCGCGCGCGC 24240
|||||
53500 GCACGAAAGACAAACCCAGTAAACGTTGCGACTGAGCGCTGCGCGCGCGCGCGCGC 53559
24241 TAAATCAGGAAGCTTATGTCGTCGTAACACAGCTTATGAGGCTTGGAAACCATGCA 24300
|||||
53560 TAAATCAGGAAGCTTATGTCGTCGTAACACAGCTTATGAGGCTTGGAAACCATGCA 53619
24301 AATGCTATTTTATTTATGTAATCTTCAACATCACTGCGGAAAACTGATATATAGGG 24360
|||||
53620 AATGCTATTTTATTTATGTAATCTTCAACATCACTGCGGAAAACTGATATATAGGG 53679
24361 CCTCTGGAAGACATTCGTTTCAAGCATTAACGCTCAGATCGGCTGCGCTCCGCCAT 24420
|||||
53680 CCTCTGGAAGACATTCGTTTCAAGCATTAACGCTCAGATCGGCTGCGCTCCGCCAT 53739
24421 TAGACGCTCAGTATTTGTCATCGTTTCAGAGCTGAGCTAATTTTGGCAATATTTGT 24480
|||||
53740 TAGACGCTCAGTATTTGTCATCGTTTCAGAGCTGAGCTAATTTTGGCAATATTTGT 53799
24481 GGCCTATGTCATTTATATACACAGACAGCCTGCTGCACATACAGCTGCTGCAATAT 24540
|||||
53800 GGCCTATGTCATTTATATACACAGACAGCCTGCTGCACATACAGCTGCTGCAATAT 53859
24541 CGGTAAACCTTAAGGAAATGAGAGATGATTAATGAGGTCACATGAGTACAGTTTGGCA 24600
|||||
53860 CGGTAAACCTTAAGGAAATGAGAGATGATTAATGAGGTCACATGAGTACAGTTTGGCA 53919
24601 TTATGTACGTAAACGGGCTTAGAGAAATGAAACCTGTCCTGCGATAGGCGATCTCG 24660
|||||
53920 TTATGTACGTAAACGGGCTTAGAGAAATGAAACCTGTCCTGCGATAGGCGATCTCG 53979
24661 TTTCGCTGCGCTGATTTGTCAGACAGGGGTGAGTTGATCGTTTAAACATTTCCCTT 24720
|||||
53980 TTTCGCTGCGCTGATTTGTCAGACAGGGGTGAGTTGATCGTTTAAACATTTCCCTT 54039
24721 CCACAGGCTAGTACTCTTTGAGCATCTCCATTAACGAGGAGCTATTTGAAAAAA 24780

|||||
54040 CCACAGGCTAGTACTCTTTTGAAGCATTCACAAACGAGGAGCTATTGAAAAAA 54099
24781 AGCTGTATTACGAGAGCTGCTTTAGAGATGTAACATTCGATAGTTAATGTTGGGT 24840
|||||
54100 AGCTGTATTACGAGAGCTGCTTTAGAGATGTAACATTCGATAGTTAATGTTGGGT 54159
24841 CCGCGACACCGGATTAACGCTGCAAGCTATTCGAGTACATTAATATCTGCTCG 24900
|||||
54160 CCGCGACACCGGATTAACGCTGCAAGCTATTCGAGTACATTAATATCTGCTCG 54219
24901 GCGTGCCTCCCTGGAACCTGAAACCTGAAACGCTGCTTCAATGCAATGAACTCTTTA 24960
|||||
54220 GCGTGCCTCCCTGGAACCTGAAACCTGAAACGCTGCTTCAATGCAATGAACTCTTTA 54279
24961 CGTAGTCGTCGCTTCTTCTCAAGTTAGAAATGTAACATCTGCTGATGCTGT 25020
|||||
54280 CGTAGTCGTCGCTTCTTCTCAAGTTAGAAATGTAACATCTGCTGATGCTGT 54339
25021 TCGTCAGGCAATTTGAACAGGATTTGAACCTGTTTCGAGACCCCTGGGCTGACTTT 25080
|||||
54340 TCGTCAGGCAATTTGAACAGGATTTGAACCTGTTTCGAGACCCCTGGGCTGACTTT 54399
25081 CCGTACCGGCTCCCAAGAGCTGTTTTTGTCCAAATGTTTGAAGAGCTGTGACGA 25140
|||||
54400 CCGTACCGGCTCCCAAGAGCTGTTTTTGTCCAAATGTTTGAAGAGCTGTGACGA 54459
25141 AATCCATCAACAGCTGTTATGCGCTCAGTCTGTTTGTCTCGGAGCTTATACGA 25200
|||||
54460 AATCCATCAACAGCTGTTATGCGCTCAGTCTGTTTGTCTCGGAGCTTATACGA 54519
25201 AGTTTAGAGCTCCCTCTTGGGGTGGTTTTTGAACATTTCTCTAAGCAGCAATA 25260
|||||
54520 AGTTTAGAGCTCCCTCTTGGGGTGGTTTTTGAACATTTCTCTAAGCAGCAATA 54579
25261 TGCTTTATATCATGTGTTGTCACAGCTGTAACAGAGCTTTTGAAGGCGCGATTTA 25320
|||||
54580 TGCTTTATATCATGTGTTGTCACAGCTGTAACAGAGCTTTTGAAGGCGCGATTTA 54639
25321 GTAAGTACATTAATTTGCTGCTGCGGCTGCTGTAATGTCATTAATGCGGTAATA 25380
|||||
54640 GTAAGTACATTAATTTGCTGCTGCGGCTGCTGTAATGTCATTAATGCGGTAATA 54699
25381 ACCGGTACAGAGGCTATCAAAAGCGAGCTGTCATTTGAATATATAGGCGCGGAACA 25440
|||||
54700 ACCGGTACAGAGGCTATCAAAAGCGAGCTGTCATTTGAATATATAGGCGCGGAACA 54759
25441 CTTCACTGTTATATCTTTTGTCTGAGTGGCGAGATTAAGCAGGCTTATCCGTTAA 25500
|||||
54760 CTTCACTGTTATATCTTTTGTCTGAGTGGCGAGATTAAGCAGGCTTATCCGTTAA 54819
25501 ACTCCACAGACACCTGCGGCTAGTCTGGAATATTAATAGCAGTACATCGGTCATTAATCG 25560
|||||
54820 ACTCCACAGACACCTGCGGCTAGTCTGGAATATTAATAGCAGTACATCGGTCATTAATCG 54879
25561 AGGTAAATCTCTGTCGCAATTTTGTGCACAATCGGCAATATCGTAACGCTCCGGAACCT 25620
|||||
54880 AGGTAAATCTCTGTCGCAATTTTGTGCACAATCGGCAATATCGTAACGCTCCGGAACCT 54939
25621 AGCTTTCTCATCTGTTGACAGTGTGCTGTAATCTGCGGATCGGTGCGGCGG 25680
|||||
54940 AGCTTTCTCATCTGTTGACAGTGTGCTGTAATCTGCGGATCGGTGCGGCGG 54999
25681 TGGCGCTGAACATAGGACCAACCAAGGCGACCAACCAAGTGCAGATCGTTCTAGC 25740
|||||
55000 TGGCGCTGAACATAGGACCAACCAAGGCGACCAACCAAGTGCAGATCGTTCTAGC 55059
25741 ATTAACAGTCTGCTGCTGTAAGTACTGATTAATATGTTTCAAGTATGATGACAG 25800
|||||
55060 ATTAACAGTCTGCTGCTGTAAGTACTGATTAATATGTTTCAAGTATGATGACAG 55119
25801 TTAGAGGAAGGAGTGGCCAGATTCGAAGCTAGACGTTGAATTCGCGGCTGAGGT 25860
|||||

Dh 55120 TTAGACGACGAGTACGTGCCCCAGATTCAAAAGTAGACCGTTTGAAATTCGCGCTCAGGT 55179
Qy 25861 GCTCGACACCGCGCAACGGGGTCTTCAGGGTGGCTGAGTGGTGCAGTCCCTTAAAGA 25920
Dh 55180 GCTCGACACCGCGCGCAACGGGGTCTTCAGGGTGGCTGAGTGGTGCAGTCCCTTAAAGA 55239
Qy 25921 CGTTGTCGATGTGTGACAGCTCCCAATGCGCTTGTATGACAGTGTATGAACAGCTGTTC 25980
Dh 55240 CGTTGTCGATGTGTGACAGCTCCCAATGCGCTTGTATGACAGTGTATGAACAGCTGTTC 55299
Qy 25981 CAAAAGATCCCTGGATTTTCGAAAGACTGAGTGTAGCTTTGACCGCGCAACAGCTGACT 26040
Dh 55300 CAAAAGATCCCTGGATTTTCGAAAGACTGAGTGTAGCTTTGACCGCGCAACAGCTGACT 55359
Qy 26041 TGCCCTGTAGATCTCGAAAAAGGAGATGAGAGTCCGTGCGATGAGCAAAACAGCTGC 26100
Dh 55360 TGCCCTGTAGATCTCGAAAAAGGAGATGAGAGTCCGTGCGATGAGCAAAACAGCTGC 55419
Qy 26101 AACCAAAATCCGGGGTTCATCTTGAACATGACGTCCGATGCCAAAGTCAAGGGGTGCTGC 26160
Dh 55420 AACCAAAATCCGGGGTTCATCTTGAACATGACGTCCGATGCCAAAGTCAAGGGGTGCTGC 55479
Qy 26161 ATACAGTCACTCCGCTCTCAAAATATATCTACACAGCCCAACGGGAATGGGTGGTACAGAC 26220
Dh 55480 ATACAGTCACTCCGCTCTCAAAATATATCTACACAGCCCAACGGGAATGGGTGGTACAGAC 55539
Qy 26221 TGCGCTTCGATCCGGCTGGAAGACTCCGGGCCGTTCTTGCGTTTACCGTTTATCTAATTA 26280
Dh 55540 TGCGCTTCGATCCGGCTGGAAGACTCCGGGCCGTTCTTGCGTTTACCGTTTATCTAATTA 55599
Qy 26281 CGGGAATGCTGTGTGTGGGAAAAATACAGCATATGCGCCGTGTACCAAAATTTAAACT 26340
Dh 55600 CGGGAATGCTGTGTGTGGGAAAAATACAGCATATGCGCCGTGTACCAAAATTTAAACT 55659
Qy 26341 GCGTGAATCAGGGGCGGACCAACCATACCCGACAGAACTATGCGCTGCGCTAAAGACT 26400
Dh 55660 GCGTGAATCAGGGGCGGACCAACCATACCCGACAGAACTATGCGCTGCGCTAAAGACT 55719
Qy 26401 TCTGTCCAGCATCTTACGAGGCTTTTGGCTTTAAGACCGCAGCATCAATATATACCGTCA 26460
Dh 55720 TCTGTCCAGCATCTTACGAGGCTTTTGGCTTTAAGACCGCAGCATCAATATATACCGTCA 55779
Qy 26461 GAAAAGCTCATCAGACCGGAGCGGTATCATAGAGCAAAATTCAGCAACAGAGAGTATCGA 26520
Dh 55780 GAAAAGCTCATCAGACCGGAGCGGTATCATAGAGCAAAATTCAGCAACAGAGAGTATCGA 55839
Qy 26521 AGTATTTGGCGGTATATAGTGGACATTATGAAAAGGTTATGGCGCAAAACCCCAATGCGA 26580
Dh 55840 AGTATTTGGCGGTATATAGTGGACATTATGAAAAGGTTATGGCGCAAAACCCCAATGCGA 55899
Qy 26581 TGTACGGGACTATATCCAGCGCAATTTTGAACCCCTCTCGAGAAATGACCGGACGTTGT 26640
Dh 55900 TGTACGGGACTATATCCAGCGCAATTTTGAACCCCTCTCGAGAAATGACCGGACGTTGT 55959
Qy 26641 TATGACTTCCAAATATATTTATGTAATCGACGAGCGCGGAACCCCTCTTACATATCTCA 26700
Dh 55960 TATGACTTCCAAATATATTTATGTAATCGACGAGCGCGGAACCCCTCTTACATATCTCA 56019
Qy 26701 CCACCGTGTGTCTTTTACTGTCTTAAACAGCTGGCTTAATACCCCTTTTACGGCC 26760
Dh 56020 CCACCGTGTGTCTTTTACTGTCTTAAACAGCTGGCTTAATACCCCTTTTACGGCC 56079
Qy 26761 AGGGGGGGGTTCCGTGATAGTATGCGTGGTGGCCAAAGCAGACAGCTTTCAGT 26820
Dh 56080 AGGGGGGGGTTCCGTGATAGTATGCGTGGTGGCCAAAGCAGACAGCTTTCAGT 56139
Qy 26821 CAACCTTACAAACAGGAGCGCAAAAGAGATATGCGTGGGAGAAACAATCTTAACAT 26880
Dh 56140 CAACCTTACAAACAGGAGCGCAAAAGAGATATGCGTGGGAGAAACAATCTTAACAT 56199
Qy 26881 TCAATGATAGGGAAGAGTGTATCTGATGATGATGATGATGATGATGATGATGATGATGAT 26940
Dh 56200 TCAATGATAGGGAAGAGTGTATCTGATGATGATGATGATGATGATGATGATGATGATGAT 56259

Qy 26941 TTAATAACAAGCGCTGCACCGATCTGAGTTCGGACACCTTCTAAAAATTTTAAAGT 27000
Dh 56260 TTAATAACAAGCGCTGCACCGATCTGAGTTCGGACACCTTCTAAAAATTTTAAAGT 56319
Qy 27001 ATAATCTTCCATTCCTGACGAAGTCATGAGTTACGTAGACAGATTTTGTCTCTTAA 27060
Dh 56320 ATAATCTTCCATTCCTGACGAAGTCATGAGTTACGTAGACAGATTTTGTCTCTTAA 56379
Qy 27061 GTAAAGTTATGATCCCTTTAGAAATACATTTGGCTGGACCCACCTTTTGTCAATAGCG 27120
Dh 56380 GTAAAGTTATGATCCCTTTAGAAATACATTTGGCTGGACCCACCTTTTGTCAATAGCG 56439
Qy 27121 AGGTAAAGCGGTATCTAAACAACCTACACATGTCTAAGCTTAGGGGGGATACAGGG 27180
Dh 56440 AGGTAAAGCGGTATCTAAACAACCTACACATGTCTAAGCTTAGGGGGGATACAGGG 56499
Qy 27181 ACACGAAGCTCTTACCTGTCCGTGTGCGAGTGTGTGAGAGCTTTGAGAGAT 27240
Dh 56500 ACACGAAGCTCTTACCTGTCCGTGTGCGAGTGTGTGAGAGCTTTGAGAGAT 56559
Qy 27241 ACAAGGGGGCGTCAACCTCACCAACCTCACCGGACCGAGTGGTGACAAAAACCTCT 27300
Dh 56560 ACAAGGGGGCGTCAACCTCACCAACCTCACCGGACCGAGTGGTGACAAAAACCTCT 56619
Qy 27301 TTAAGTTAAGTAAATTTTCCAGTTTGTGACAGCAGATGTCCATAGTGCACAGGAAT 27360
Dh 56620 TTAAGTTAAGTAAATTTTCCAGTTTGTGACAGCAGATGTCCATAGTGCACAGGAAT 56679
Qy 27361 CCAGTGAAGCTTGACCCAGGTTACCTTATCACCAAGTGTGTTAAAAACAGCAGCTGT 27420
Dh 56680 CCAGTGAAGCTTGACCCAGGTTACCTTATCACCAAGTGTGTTAAAAACAGCAGCTGT 56739
Qy 27421 CTTTAAATGGAAGAAAAACAAAAATGATGTGGGTTTCAGGGTACGTACTTGAATTC 27480
Dh 56740 CTTTAAATGGAAGAAAAACAAAAATGATGTGGGTTTCAGGGTACGTACTTGAATTC 56799
Qy 27481 AAAGAAATCTAGACAGCGAATCTTCTGTGAGAGCATTTGCAAGACGCTCCGGAATACG 27540
Dh 56800 AAAGAAATCTAGACAGCGAATCTTCTGTGAGAGCATTTGCAAGACGCTCCGGAATACG 56859
Qy 27541 TATACGGTTCCTTAAACACGCTACTGTACAAAGCATATGCTTTTACAGCGCTGAGCGC 27600
Dh 56860 TATACGGTTCCTTAAACACGCTACTGTACAAAGCATATGCTTTTACAGCGCTGAGCGC 56919
Qy 27601 TGACTAGTCAACAGAGAAATATCTGCAAGCATTAATTTGCAACCCCTCCGGCCGCTC 27660
Dh 56920 TGACTAGTCAACAGAGAAATATCTGCAAGCATTAATTTGCAACCCCTCCGGCCGCTC 56979
Qy 27661 TGCAACCGGGCGTGTAGACCTTCAAAACGGTTCGTGAAGATTAAACCTGGAAAGAGCA 27720
Dh 56980 TGCAACCGGGCGTGTAGACCTTCAAAACGGTTCGTGAAGATTAAACCTGGAAAGAGCA 57039
Qy 27721 TCTTCTACACAGTGTGACATCCCGCACCCGCGGTATACCTCCCTCCAGGTTTTGG 27780
Dh 57040 TCTTCTACACAGTGTGACATCCCGCACCCGCGGTATACCTCCCTCCAGGTTTTGG 57099
Qy 27781 TCGACAGTACTGGCGCTTAAAGAGTGTGCGCTCAAGAAATAAAGTGGCGGTGGCT 27840
Dh 57100 TCGACAGTACTGGCGCTTAAAGAGTGTGCGCTCAAGAAATAAAGTGGCGGTGGCT 57159
Qy 27841 GGTTTGGCGGGAATTTGAGAAAGAAAGTTCGCGGTTTACAGTTAACTAGTGTGAA 27900
Dh 57160 GGTTTGGCGGGAATTTGAGAAAGAAAGTTCGCGGTTTACAGTTAACTAGTGTGAA 57219
Qy 27901 GGGACGAGTGTACTTGTCTCCCTTCAGAACTCTCAACGGGCTGTGGCTGTTCAT 27960
Dh 57220 GGGACGAGTGTACTTGTCTCCCTTCAGAACTCTCAACGGGCTGTGGCTGTTCAT 57279
Qy 27961 CGACGTTGGAATGCTATTAATTAAGGGGTACAGTGTTTTACCGGTGACGTTGGTGCT 28020
Dh 57280 CGACGTTGGAATGCTATTAATTAAGGGGTACAGTGTTTTACCGGTGACGTTGGTGCT 57339

28021 GTGAGGGTTGGCAGTCATGATGACCTAGAGAAAGATGCCCTCCCTGCTGTCAGG 28080
|||||
57340 GTGAGGGTTGGCAGTCATGATGACCTAGAGAAAGATGCCCTCCCTGCTGTCAGG 57399
28081 ACTGAGCGGTTTTATCGCGTGTGAGAAATACATCAACAAATTGACCGAAACCATGG 28140
|||||
57400 ACTGAGCGGTTTTATCGCGTGTGAGAAATACATCAACAAATTGACCGAAACCATGG 57459
28141 AGGAGGGAGCGTTTTCCAAAGTGTGCTGTGCGGGGAGCTATGGGGTCAAGCTCAAAATTTAG 28200
|||||
57460 AGGAGGGAGCGTTTTCCAAAGTGTGCTGTGCGGGGAGCTATGGGGTCAAGCTCAAAATTTAG 57519
28201 CCATGACCATCTGTAAGGACAGAGGAATGCTGTGAGCGAGTAGCCCTAGATTTGGGT 28260
|||||
57520 CCATGACCATCTGTAAGGACAGAGGAATGCTGTGAGCGAGTAGCCCTAGATTTGGGT 57579
28261 CCCACAGAGCGTCCGACAGACGACGCTATGTATGACATATCAAGGGGTGTTAACTCA 28320
|||||
57580 CCCACAGAGCGTCCGACAGACGACGCTATGTATGACATATCAAGGGGTGTTAACTCA 57639
28321 ATTTATTTGTCATGAGACGAAACCCCTTTAAACCCCTCCTCAGAGAACCGATGATACA 28380
|||||
57640 ATTTATTTGTCATGAGACGAAACCCCTTTAAACCCCTCCTCAGAGAACCGATGATACA 57699
28381 CCTCGCCGAAGATATAGTCCGCGCTCCGACAAACCCCAACAAACCCCTCATCTACTAA 28440
|||||
57700 CCTCGCCGAAGATATAGTCCGCGCTCCGACAAACCCCAACAAACCCCTCATCTACTAA 57759
28441 TAAATATAAACAAGCAAAATGAAAAATGTTTATTTATTCAGTCCAAACGACGGCCACGG 28500
|||||
57760 TAAATATAAACAAGCAAAATGAAAAATGTTTATTTATTCAGTCCAAACGACGGCCACGG 57819
28501 ATAGTTGTCATTTCCACACACCGGGGGGTGCGCCGATAGTTTGACGACGAAACGCC 28560
|||||
57820 ATAGTTGTCATTTCCACACACCGGGGGGTGCGCCGATAGTTTGACGACGAAACGCC 57879
28561 CGGGGCCCTGTGGTTAGAGATGAGCCCGCCCGCGGTGCGAGGTGATCGTCTGTAGG 28620
|||||
57880 CGGGGCCCTGTGGTTAGAGATGAGCCCGCCCGCGGTGCGAGGTGATCGTCTGTAGG 57939
28621 GCCCTGGGTGTGACCAACATTAATCAACGTCGTCATCACCGTTGACGTCCCTCGTGAGCC 57999
57940 GCCCTGGGTGTGACCAACATTAATCAACGTCGTCATCACCGTTGACGTCCCTCGTGAGCC 57999
28681 GGGCCTTTGCAAGGCGGACGAAACCGCCGCTTGTACGTATGTCATCGTCTGCTG 28740
|||||
58000 GGGCCTTTGCAAGGCGGACGAAACCGCCGCTTGTACGTATGTCATCGTCTGCTG 58059
28741 GTCTAAGATGAACACAGGTCAATCAATCAATGAGGGGCCCGGCTCATGCGGCGTCA 28800
|||||
58060 GTCTAAGATGAACACAGGTCAATCAATCAATGAGGGGCCCGGCTCATGCGGCGTCA 58119
28801 TTCCGTCATGTCATCAACAGAGCGTCTGTCATCACTTCGTCATCTGAATATATAT 28860
|||||
58120 TTCCGTCATGTCATCAACAGAGCGTCTGTCATCACTTCGTCATCTGAATATATAT 58179
28861 GGTCTCTGTCTCTGCAATGATTCACGAAACAGAGTTCTTCTCATGGAAGACCATCC 28920
|||||
58180 GGTCTCTGTCTCTGCAATGATTCACGAAACAGAGTTCTTCTCATGGAAGACCATCC 58239
28921 GCCCTGTGCGGTTGAT 28980
|||||
58240 GCCCTGTGCGGTTGAT 58299
28981 GCCCTGTGCGGTTGAT 29040
|||||
58300 GCCCTGTGCGGTTGAT 58359
29041 TTGCTGTCTGATTCAGATGACTGGGGGTGCGGGGTGTCGCAAGTAAACCGCAACGGG 29100
|||||
58360 TTGCTGTCTGATTCAGATGACTGGGGGTGCGGGGTGTCGCAAGTAAACCGCAACGGG 58419
29101 CCGGAGACACCAACACGGGTCAGTGGCGGGCGCGCTCGGTGTGTGGTGGCACCTGT 29160
|||||
58420 CCGGAGACACCAACACGGGTCAGTGGCGGGCGCGCTCGGTGTGTGGTGGCACCTGT 58479
29161 CGAAGTATGACGGTATGATAGCGGGCGGCTCTGTTAAAGACTACCGTCCGTCGTCG 29220
|||||
58480 CGAAGTATGACGGTATGATAGCGGGCGGCTCTGTTAAAGACTACCGTCCGTCGTCG 58539
29221 CGAATCTATCTAGTGGGAGAGACCGCGGTTCTGCTTCTATCCATCATCATCTGA 29280
|||||
58540 CGAATCTATCTAGTGGGAGAGACCGCGGTTCTGCTTCTATCCATCATCATCTGA 58599
29281 GTGCTGTCTCCGATGAGATCGGTTTCTGCTGCGCTTTTGGAGTGTGAGAGGGA 29340
|||||
58600 GTGCTGTCTCCGATGAGATCGGTTTCTGCTGCGCTTTTGGAGTGTGAGAGGGA 58659
29341 ATCTTGTCAAAAACATCTCAGTGCAGTGCATGTCATCATCTGGGGGCGCTCCGTACCC 29400
|||||
58660 ATCTTGTCAAAAACATCTCAGTGCAGTGCATGTCATCATCTGGGGGCGCTCCGTACCC 58719
58720 GGGCGGTACCGCAACCCCGTACGGGACCGCGCAAAAAACGCTTGTCTGTTTTT 58779
29461 CCTAGGTGCGGGGAGTGGGAGATCCTGGGAGTGGCGGGGCGGCTTGAAGGGTC 29520
|||||
58780 CCTAGGTGCGGGGAGTGGGAGATCCTGGGAGTGGCGGGGCGGCTTGAAGGGTC 58839
29521 GGATTAAGAACATAGCCATGGCGGAAACGTTACCTGTAAAGACGACTGCTATCCCGAT 29580
|||||
58840 GGATTAAGAACATAGCCATGGCGGAAACGTTACCTGTAAAGACGACTGCTATCCCGAT 58899
29581 CAGTTAATATTTCACTCAACGCGACCCCTCCGATTTCTGACATGATGATCATTTCCGAGT 29640
|||||
58900 CAGTTAATATTTCACTCAACGCGACCCCTCCGATTTCTGACATGATGATCATTTCCGAGT 58959
29641 TTAATAATGTTGACGCTTGAAGTACGCGGACGAGGAGAAACGCTTGGCGCGGGTGA 29700
|||||
58960 TTAATAATGTTGACGCTTGAAGTACGCGGACGAGGAGAAACGCTTGGCGCGGGTGA 59019
59020 GCCAGGGGAGAGGATGGCGGCTTGAAGACGAGATGTCGTCTGCTTATACAGCGTC 29760
|||||
29761 GCTTGTCTATAGCCTTTCTTCCCAACAGCATTAATAAAGCAGCAGCTTGAAGCTTGGCAGAA 29820
|||||
59080 GCTTGTCTATAGCCTTTCTTCCCAACAGCATTAATAAAGCAGCAGCTTGAAGCTTGGCAGAA 59139
29821 AGCAGCTTATATGATGAGTGTGTAACCAATCCAGACCAAGGTTGCGGTGACCCCGCC 29880
|||||
59140 AGCAGCTTATATGATGAGTGTGTAACCAATCCAGACCAAGGTTGCGGTGTAACCCCGCC 59199
29881 TTCCCTTTTCCACCGTCAAGATGTTTAAAGCAGAACTCCCGTTTGGCCAAACAG 29940
|||||
59200 TTCCCTTTTCCACCGTCAAGATGTTTAAAGCAGAACTCCCGTTTGGCCAAACAG 59259
29941 TCTAAGCACCCGTGAGAGAGAGCGGTGAACCCAGGTATAGTATGCGTATCTCTTAAAA 30000
|||||
59260 TCTAAGCACCCGTGAGAGAGAGCGGTGAACCCAGGTATAGTATGCGTATCTCTTAAAA 59319
30001 ATATTTTGAAGGCTTGAAGGTATGATGATGTCGGAAGCAACGCTTAAAGGCTAGTCCGGTG 30060
|||||
59320 ATATTTTGAAGGCTTGAAGGTATGATGATGTCGGAAGCAACGCTTAAAGGCTAGTCCGGTG 59379
30061 GCTTGAACCGGATGATGATGATGTCGGAAGCAACGATCAGACCTTATATATCTCTCGGTTTCG 30120
|||||
59380 GCTTGAACCGGATGATGATGATGTCGGAAGCAACGATCAGACCTTATATATCTCTCGGTTTCG 59439
30121 CAACAATGACACCAACATATATCTATCTATGCGTGAATATACAGGTTACGTTGCTC 30180
|||||
59440 CAACAATGACACCAACATATATCTATCTATGCGTGAATATACAGGTTACGTTGCTC 59499
30181 ATATCCATTAACCGGTTGACGAGACCCGAGCTTCTGTTTAAATAATGAGAAAGATTT 30240
|||||

Db	59500	ATATCCATTAACGGCGCTTCAGACAGCCGGAGCTTCTGTTTTAAAAATGGAAGAAAGATT	59559
Oy	30241	AAAAATTCAAGCCATGAGTCGCTAAGTAGCAACGTTTGTGTGAGGGTCTTCTAACA	30300
Db	59560	AAAAATTCAAGCCATGAGTCGCTAAGTAGCAACGTTTGTGTGAGGGTCTTCTAACA	59619
Oy	30301	TCGTGTACACTTTTACTCCAACTATTGTTTTAAGCAACCCCTCAATAATCCCGCGTC	30360
Db	59620	TCGTGTACACTTTTACTCCAACTATTGTTTTAAGCAACCCCTCAATAATCCCGCGTC	59679
Oy	30361	TGGTAATTACCTTACGATATACGTAAGCAACTTTGTACTTCTGTGCGTGGAAATCCACAG	30420
Db	59680	TGGTAATTACCTTACGATATACGTAAGCAACTTTGTACTTCTGTGCGTGGAAATCCACAG	59739
Oy	30421	GTGGCCCGCGATATAAGCAGTTCCGCTTTCACCTACCGTTATGTGAAGTCTTCAACTCG	30480
Db	59740	GTGGCCCGCGATATAAGCAGTTCCGCTTTCACCTACCGTTATGTGAAGTCTTCAACTCG	59799
Oy	30481	CTAAAACTCATCAAGACATATATGCAATATATTCACAATGGAAGCTTCTGTGGGA	30540
Db	59800	CTAAAACTCATCAAGACATATATGCAATATATTCACAATGGAAGCTTCTGTGGGA	59859
Oy	30541	CACGTGAATTTAATCTGTGTCAAAAATCCCTATATAAAAGCCCTCAAGTCAATTCATTTA	30600
Db	59860	CACGTGAATTTAATCTGTGTCAAAAATCCCTATATAAAAGCCCTCAAGTCAATTCATTTA	59919
Oy	30601	CACATATTTCTGTGTGAGCAGATCAGCTTATATGCAATGTGTGTACACAGCCCTG	30660
Db	59920	CACATATTTCTGTGTGAGCAGATCAGCTTATATGCAATGTGTGTACACAGCCCTG	59979
Oy	30661	GACATTAAGCTAAATTTGTTAAATGAAAAGAACATCTCAACGGCTCCGGAATATTA	30720
Db	59980	GACATTAAGCTAAATTTGTTAAATGAAAAGAACATCTCAACGGCTCCGGAATATTA	60039
Oy	30721	AGTACACTAAGTGATATTTTACAACATGATTTACTACAAAGCCCGGTACACAATGTA	30780
Db	60040	AGTACACTAAGTGATATTTTACAACATGATTTACTACAAAGCCCGGTACACAATGTA	60099
Oy	30781	TTAAAAAAATCCACATGTAATTAATAAATTAAGGTATACATATCTTCAATGTTTATA	30840
Db	60100	TTAAAAAAATCCACATGTAATTAATAAATTAAGGTATACATATCTTCAATGTTTATA	60159
Oy	30841	CATTAATATGAAACGCTAATGCTGTACTTATATATATATGATAGAAATATGCCAATACAGTC	30900
Db	60160	CATTAATATGAAACGCTAATGCTGTACTTATATATATATGATAGAAATATGCCAATACAGTC	60219
Oy	30901	ATGTTAGTATATTTTAAAGCATATAATGCAAACTCAAAATATATACCAAAATGACAGC	30960
Db	60220	ATGTTAGTATATTTTAAAGCATATAATGCAAACTCAAAATATATACCAAAATGACAGC	60279
Oy	30961	TTCCGGATATCCGGCCGAGCTGTATACCCGAAATATAGAAATGACTACCAAAACACACT	31020
Db	60280	TTCCGGATATCCGGCCGAGCTGTATACCCGAAATATAGAAATGACTACCAAAACACACT	60339
Oy	31021	GAACCAATTTTATTTCAACATATGCAACAATATTTCAAGGTAAACCCATGTTAATAA	31080
Db	60340	GAACCAATTTTATTTCAACATATGCAACAATATTTCAAGGTAAACCCATGTTAATAA	60399
Oy	31081	ATAGCAGCATGCACATTTTACGTAAAGCTCTCAAGACAAATTTCTCTCAATTTGATG	31140
Db	60400	ATAGCAGCATGCACATTTTACGTAAAGCTCTCAAGACAAATTTCTCTCAATTTGATG	60459
Oy	31141	ACATCATCAACCTGGTTTCCGCTTANTGTCCGAATATATATGATCCAGATATACCTCGT	31200
Db	60460	ACATCATCAACCTGGTTTCCGCTTANTGTCCGAATATATATGATCCAGATATACCTCGT	60519
Oy	31201	CATGCGCACAAAATTAATTCAGAGGCTGTGAAAATATATCATCCAGTGAATCAGCTGTAATG	31260
Db	60520	CATGCGCACAAAATTAATTCAGAGGCTGTGAAAATATATCATCCAGTGAATCAGCTGTAATG	60579
Oy	31261	TCAAGGATGTGTTTCTAATTTTAGCCCATCCAAATGTAAGTGGGTGACACTTTGGGAC	31320
Db	60580	TCAAGGATGTGTTTCTAATTTTAGCCCATCCAAATGTAAGTGGGTGACACTTTGGGAC	60639

QY	31321	AAGACCCCGTAAATTTGCGACGCTGCACACAACGGAAGATGACTTTGATCGTTCCAGA	31380
Db	60640	AAGACCCCGTAAATTTGCGACGCTGCACACAACGGAAGATGACTTTGATCGTTCCAGA	60699
QY	31381	GGGGGAGATATTTTATTTTATTAATCAGGAACCGGACCGCTCAATGACGCACATATGT	31440
Db	60700	GGGGGAGATATTTTATTTTATTAATCAGGAACCGGACCGCTCAATGACGCACATATGT	60759
QY	31441	CCATTAAAGATTGGAGTCGTGACACACTGTTGTAATTCAGCGTGAAAAAATGATTCGTGT	31500
Db	60760	CCATTAAAGATTGGAGTCGTGACACACTGTTGTAATTCAGCGTGAAAAAATGATTCGTGT	60819
QY	31501	CACATGCGTAATATTTTTTAAACACAGAGGGCGGAATAAACGGGTCCCGCGCTAA	31560
Db	60820	CACATGCGTAATATTTTTTAAACACAGAGGGCGGAATAAACGGGTCCCGCGCGCTAA	60879
QY	31561	GGCGCTGAATGGGGCAGGCGACGGCTCATTTGCCATTTCCAGATTTGTTAAATCTGTTCGAA	31620
Db	60880	GGCGCTGAATGGGGCAGGCGACGGCTCATTTGCCATTTCCAGATTTGTTAAATCTGTTCGAA	60939
QY	31621	CATAGAGAGCTTAAATTCAGATTTAACACAGACAGTTCAACAAAGAGCGCACGGCGCTGG	31680
Db	60940	CATAGAGAGCTTAAATTCAGATTTAACACAGACAGTTCAACAAAGAGCGCACGGCGCTGG	60999
QY	31681	TTTCCACCCGCGACATCCCGCGCTCACAAACCCGAACTCTCTAGGAACGCACATCAAAAGCT	31740
Db	61000	TTTCCACCCGCGACATCCCGCGCTCACAAACCCGAACTCTCTAGGAACGCACATCAAAAGCT	61059
QY	31741	TCAGACAAATTTCCGAAACCGAACCCCTATGTTCTGAGCACCATCTGTTATTAACCTGGCG	31800
Db	61060	TCAGACAAATTTCCGAAACCGAACCCCTATGTTCTGAGCACCATCTGTTATTAACCTGGCG	61119
QY	31801	TTAAAGAGAGGCGGCGCACACACTGCTGTTGAGGAATTCAGTTAGTGGGCGCTGACAG	31860
Db	61120	TTAAAGAGAGGCGGCGCACACACTGCTGTTGAGGAATTCAGTTAGTGGGCGCTGACAG	61179
QY	31861	CTTGCTGACAGGCCCGCTAGCTGCTGCGGGCGCTCGCGCACCTTTGACAGCGCACGCCA	31920
Db	61180	CTTGCTGACAGGCCCGCTAGCTGCTGCGGGCGCTCGCGCACCTTTGACAGCGCACGCCA	61239
QY	31921	GTTCCAGAGCGAGGCGAAGAGCGCTCTTTGCACTCGCGCATATCTCGGCCATAGAGATTT	31980
Db	61240	GTTCCAGAGCGAGGCGAAGAGCGCTCTTTGCACTCGCGCATATCTCGGCCATAGAGATTT	61299
QY	31981	CGCTGGCGGATCTTTTAGTGTCATATATATGTTGGGTAACAAACTCACTCCCTGTA	32040
Db	61300	CGCTGGCGGATCTTTTAGTGTCATATATATGTTGGGTAACAAACTCACTCCCTGTA	61359
QY	32041	AAAGGGGATTAAGTCCGCTCTTCTTATACGTTTCTCTGAACTATAGTTACATCTTTAA	32100
Db	61360	AAAGGGGATTAAGTCCGCTCTTCTTATACGTTTCTCTGAACTATAGTTACATCTTTAA	61419
QY	32101	GTAATACCAAGACGCTAAAAACCCAGATGGTGCACACTTTAAAAAATTCGCAAAAGCG	32160
Db	61420	GTAATACCAAGACGCTAAAAACCCAGATGGTGCACACTTTAAAAAATTCGCAAAAGCG	61479
QY	32161	ACCGGATGGCTATATCCGCGCTTTCCATGTCGTTCAAAGTAATGATCAGATGATCTCCCAT	32220
Db	61480	ACCGGATGGCTATATCCGCGCTTTCCATGTCGTTCAAAGTAATGATCAGATGATCTCCCAT	61539
QY	32221	TAGACTGTGTCCTCGTTTAAACACCTTAACGGAATGGAAACAGCATGACACGCTGAA	32280
Db	61540	TAGACTGTGTCCTCGTTTAAACACCTTAACGGAATGGAAACAGCATGACACGCTGAA	61599
QY	32281	CTTCCGTATGTCCTCTAAAACTAACCCCGAAACAGAGCTAAATATCAATGACTGTCACCC	32340
Db	61600	CTTCCGTATGTCCTCTAAAACTAACCCCGAAACAGAGCTAAATATCAATGACTGTCACCC	61659
QY	32341	CTACCCCAAGCAGCGCCCCCGCTACTATTAGACAGGGTGAGTAAACACGCTATCTCTTAA	32400
Db	61660	CTACCCCAAGCAGCGCCCCCGCTACTATTAGACAGGGTGAGTAAACACGCTATCTCTTAA	61719

32401 AACCACATCGTGGATTTGTAAAGTAAACACGCTGCTATATTTACAGAGCCCTGTCATA 32460
|||||
Db 61720 AACCACATCGTGGATTTGTAAAGTAAACACGCTGCTATATTTACAGAGCCCTGTCATA 61779
32461 AATGGATCCGACGACATCAATGATTAATTAATTTTATTTCAAGATTCAGAGAGCG 32520
|||||
Db 61780 AATGGATCCGACGACATCAATGATTAATTAATTTTATTTCAAGATTCAGAGAGCG 61839
32521 TGTTTACAGTGTGTAGTGGAGACATATCTGCCAATGGGAATGGCTGATGAATCCACA 32580
|||||
Db 61840 TGTTTACAGTGTGTAGTGGAGACATATCTGCCAATGGGAATGGCTGATGAATCCACA 61899
32581 CTTAAGCTCGGATGAGTGTCTGTCTTTACTTACTAGTCCGATGAACCTAAATTTGGC 32640
|||||
Db 61900 CTTAAGCTCGGATGAGTGTCTGTCTTTACTTACTAGTCCGATGAACCTAAATTTGGC 61959
32641 GTGTAGGTCTGTACCAACCAAAAACTCGGCTCGCTCTTTTGAAGCTCTATGCAA 32700
|||||
Db 61960 GTGTAGGTCTGTACCAACCAAAAACTCGGCTCGCTCTTTTGAAGCTCTATGCAA 62019
32701 GCTTTAATCGTGTCCAAATGCTTGTCTTTAAAAATGCAACTCTGTGATCTTTATGACA 32760
|||||
Db 62020 GCTTTAATCGTGTCCAAATGCTTGTCTTTAAAAATGCAACTCTGTGATCTTTATGACA 62079
32761 GTGTCCAAAAAACAAGATTTAAAAACAGTTAACTGGGTGCTGCTGATGCTGCTG 32820
|||||
Db 62080 GTGTGTCCAAAAAACAAGATTTAAAAACAGTTAACTGGGTGCTGCTGATGCTGCTG 62139
32821 TATATTAACCTCTCTCAACAAGAAAAATTTTAAACCAACTCGCAGATGATGAAACGAT 32880
62140 TATATTAACCTCTCTCAACAAGAAAAATTTTAAACCAACTCGCAGATGATGAAACGAT 62199
32881 GGTAGGGACAGTGTGAAAAAGTGTCTATCTCTCTTACCTCCCTTTGAAGTTTGG 32940
62200 GGTAGGGACAGTGTGAAAAAGTGTCTATCATCTCTTACCTCCCTTTGAAGTTTGG 62259
32941 GTTACACGACCATGTGATGAGACACGACGCTCAGGGGGAGTGGATCGAGAGGGGT 33000
62260 GTTACACGACCATGTGATGAGACACGACGCTCAGGGGGAGTGGATCGAGAGGGGT 62319
33001 AACCAATCGTGGGCGTGGGGGTACTCCAGTTTATAGATCTCGGAGAGACGCGTACGACT 33060
62320 AACCAATCGTGGGCGTGGGGGTACTCCAGTTTATAGATCTCGGAGAGACGCGTACGACT 62379
33061 TCTTGTCTCAAAATCTACGACGCGCATCTCACCAGGGGAGTACTGATTAATAGTCCC 33120
62380 TCTTGTCTCAAAATCTACGACGCGCATCTCACCAGGGGAGTACTGATTAATAGTCCC 62439
33121 GCAATTTATCTGTGTGATTTTGTGAGCTCTCTTTAGACAGTAAACCATGTTGCTCGCA 33180
62440 GCAATTTATCTGTGTGATTTTGTGAGCTCTCTTTAGACAGTAAACCATGTTGCTCGCA 62499
33181 CACTCGGATGACGATGAACCGCTCTCTGTCTGTGTGTGCATGAGCACTGGATATCTTA 33240
62500 CACTCGGATGACGATGAACCGCTCTCTGTGTGTGTGCATGAGCACTGGATATCTTA 62559
33241 GACAGATTAAGGGCCGTTTCCACTTAAGGGTGGCCGCTTGTGAAGCGGATTTGGGGCA 33300
62560 GACAGATTAAGGGCCGTTTCCACTTAAGGGTGGCCGCTTGTGAAGCGGATTTGGGGCA 62619
33301 TTGAGGCTGAGTGTCTCATTTTACCGACTATCATGCGGAGTGGGGATAGTGAACCTTG 33360
62620 TTGAGGCTGAGTGTCTCATTTTACCGACTATCATGCGGAGTGGGGATAGTGAACCTTG 62679
33361 TACATATGATTTAAAAAGATGTCTTCCGTAATGGCGACTCATGCTGTGTTTTAAGCT 33420
62680 TACATATGATTTAAAAAGATGTCTTCCGTAATGGCGACTCATGCTGTGTTTTAAGCT 62739
33421 TCACAGGGTGTAAAAAACTCAGAAAGTCTGCTGAGACACTTTTGGGACTCTCCGAA 33480
62740 TCACAGGGTGTAAAAAACTCAGAAAGTCTGCTGAGACACTTTTGGGACTCTCCGAA 62799
33481 CCGCTCAGAGATTAACCTGTACACGCGGTGCTTCTTATTAAGCAAGCATACTCTCAAAAA 33540

|||||
Db 62800 CCGCTCAGGATTAAGCTGTACACGCGGTGCTTCTTATTAACGAAGCATACTCTCAAAAA 62859
33541 CATGACCCACGCTACCTAAATAAGCTCACAGAAAGATCTGATGATTTGTAATGAA 33600
62860 CATGACCCACGCTACCTAAATAAGCTCACAGAAAGATCTGATGATTTGTAATGAA 62919
33601 TGTGCTCTCTGTTGCCATCTCCGGGCTCATCGCGGATCTCAATCTCTTTAAGCTGTTG 33660
62920 TGTGCTCTCTGTTGCCATCTCCGGGCTCATCGCGGATCTCAATCTCTTTAAGCTGTTG 62979
33661 TGTGCTCTCTGTTGCCATCTCCGGGCTCAATCGCGGAGTCAATCTCTTTAAGCTGTTG 33720
62980 TGTGCTCTCTGTTGCCATCTCCGGGCTCAATCGCGGAGTCAATCTCTTTAAGCTGTTG 63039
33721 GCAGAAATGCGCCAGGAGATCTGTGAATTTCTACAGAGAGGCGCTTGTGTAACGAA 33780
63040 GCAGAAATGCGCCAGGAGATCTGTGAATTTCTACAGAGAGGCGCTTGTGTAACGAA 63099
33781 AAGATGTTATATGCTGTGCTGTGACAGCGGGGTCTTATACGCCCATGTTGGCAGAGTT 33840
63100 AAGATGTTATATGCTGTGCTGTGACAGCGGGGTCTTATACGCCCATGTTGGCAGAGTT 63159
33841 CTGCACGACGCTTACGCGGAAATGAAGGCGCAAGTGTGGGGGCGTGGCTGCTCATTA 33900
63160 CTGCACGACGCTTACGCGGAAATGAAGGCGCAAGTGTGGGGGCGTGGCTGCTCATTA 63219
33901 TGTTCGAGGCGGCTATCATGAGCTATGCGCATGCGTCTGCTCATTAATACCTG 33960
63220 TGTTCGAGGCGGCTATCATGAGCTATGCGCATGCGTCTGCTCATTAATACCTG 63279
33961 GATGCGGAGGAAATGGAATTAAGTACCAAGCAAGCAAGTGAACCTGTTTTCACCC 34020
63280 GATGCGGAGGAAATGGAATTAAGTACCAAGCAAGTGAACCTGTTTTCACCC 63339
34021 ATCTTCTCTCAAGAATCTTACCCCTATGACGCTACTGACCAAGGAGAGATGCTGCT 34080
63340 ATCTTCTCTCAAGAATCTTACCCCTATGACGCTACTGACCAAGGAGAGATGCTGCT 63399
34081 GACAAATATTTTACATCACCGGATACGCGCGAAGAGGCGCTGTGCTGATGAACT 34140
63400 GACAAATATTTTACATCACCGGATACGCGCGAAGAGGCGCTGTGCTGATGAACT 63459
34141 ACTAGCGGATGACGCTGTCGCGGAGAGAGGCGCTGTCGCTGATGAACTGTCGACGTA 34200
63460 ACTAGCGGATGACGCTGTCGCGGAGAGAGGCGCTGTCGCTGATGAACTGTCGACGTA 63519
34201 TCGGAACGCGGGCTTCTCCGCGACCCCGTGTGACCTGATGAATGTCTTAAAGAAATCCA 34260
63520 TCGGAACGCGGGCTTCTCCGCGACCCCGTGTGACCTGATGAATGTCTTAAAGAAATCCA 63579
34261 GAAATCATCTCAGCGCCCGACCCCTGAGTCAATTTGTATCACAACACGACCCCACT 34320
63580 GAAATCATCTCAGCGCCCGACCCCTGAGTCAATTTGTATCACAACACGACCCCACT 63639
34321 CTGCGCTGCTGATGAGATTTTACGCAACCCAGGGGCTGTTCCGCGCAATGTTT 34380
63640 CTGCGCTGCTGATGAGATTTTACGCAACCCAGGGGCTGTTCCGCGCAATGTTT 63699
34381 ATGACAGCTGGAAGAGCGGTGCACAGAGCATTTACACAGCAGACAGCGCTATTTTG 34440
63700 ATGACAGCTGGAAGAGCGGTGCACAGAGCATTTACACAGCAGACAGCGCTATTTTG 63759
34441 GCGCGCGCACTAACCGGTTTGCATCTGCGGCGCTTGGCGCGCATGCTGTTCCCA 34500
63760 GCGCGCGCACTAACCGGTTTGCATCTGCGGCGCTTGGCGCGCATGCTGTTCCCA 63819
34501 GTTGGCGGACGCTCTCGGAGGTGGAAGGTTCCGGGGCGCTGATGTTGGGGAACACACA 34560
63820 GTTGGCGGACGCTCTCGGAGGTGGAAGGTTCCGGGGCGCTGATGTTGGGGAACACACA 63879
34561 TGCCTTCGAGCGCGGCTTACCGGCCAATGTCGCCGCAAGAGATGAAACGCTATGACA 34620

Db 63880 TGGCTTCGCGACCCCGGCTTACCGCCCAATGTCCCGCCCAAGAGATGGAACGGTAGCA 63939
 QY 34621 CAGTTGGGAAGCCTCCCGTAAAAAGCTCCACATCGAGCGCCGCTATACGCTCACTG 34680
 Db 63940 CAGTTGGGAAGCCTCCCGTAAAAAGCTCCACATCGAGCGCCGCTATACGCTCACTG 63939
 QY 34681 GTTAATATACCAATTAATAGACTTAACGTCCTCCGTCAGGGTCCGGCCAGAGTCCGGCCGAT 34740
 Db 64000 GTTAATATACCAATTAATAGACTTAACGTCCTCCGTCAGGGTCCGGCCAGAGTCCGGCCGAT 64059
 QY 34741 ATGGCCCAACACTCCAGAGTCCCGCATGCGCGCGCTCTCCGCCCTTCCGCCGAACCGCC 34800
 Db 64060 ATGGCCCAACACTCCAGAGTCCCGCATGCGCGCGCTCTCCGCCCTTCCGCCGAACCGCC 64119
 QY 34801 GCAACGTCCTCCGCTTAGAGAGAAAGCAGCCAGCGAGAGCGTGGCAGACAAAGACTGAG 34860
 Db 64120 GCAACGTCCTCCGCTTAGAGAGAAAGCAGCCAGCGAGAGCGTGGCAGACAAAGACTGAG 64179
 QY 34861 GGGGACGTTGGGGCGCGGCAACAGTAACACCCCTTTCGCGGACCGTCCGGGATGCGC 34920
 Db 64180 GGGGACGTTGGGGCGCGGCAACAGTAACACCCCTTTCGCGGACCGTCCGGGATGCGC 64239
 QY 34921 GTTCGCGAGAGGGCTTATTCGATTTATCGAAAGCTCCAGAGTATTAACCGCGCAACGCA 34980
 Db 64240 GTTCGCGAGAGGGCTTATTCGATTTATCGAAAGCTCCAGAGTATTAACCGCGCAACGCA 64299
 QY 34981 TCTGAGACCCAAAAAGCAGCAGCAGCATGCTAGCGGCTTCTCTACAGAGCTGTATGACTA 35040
 Db 64300 TCTGAGACCCAAAAAGCAGCAGCAGCATGCTAGCGGCTTCTCTACAGAGCTGTATGACTA 64359
 QY 35041 CAGTCCCGCCCGGCGCATGATTCCTCCCTCAGCAGCACTCGGACATGAGAGATATTTTCA 35100
 Db 64360 CAGTCCCGCCCGGCGCATGATTCCTCCCTCAGCAGCACTCGGACATGAGAGATATTTTCA 64419
 QY 35101 G 35101
 Db 64420 G 64420

RESULT 2

AAC64754
 ID AAC64754 standard; DNA; 133719 BP.
 AC AAC64754;

XX 28-FEB-2001 (first entry)
 XX

DE Macaca mulatta rhadinovirus 17577 (RRV) genome sequence SEQ ID NO:1.
 XX

XX Macaca mulatta rhadinovirus 17577; RRV; rhesus macaque rhadinovirus;
 KW genome; Kaposi's sarcoma-associated herpesvirus; KSHV; interleukin 6;
 KW IL-6; macrophage inflammatory protein; MIP; diagnosis; vaccine;
 KW cytostatic; anti-HIV; gene therapy; infection; Kaposi's sarcoma;
 KW lymphoproliferative disorder; B-cell hyperplasia; lymphadenopathy;
 KW splenomegaly; hypergammaglobulinemia; autoimmune haemolytic anaemia;
 KW ds.

OS Macaca mulatta rhadinovirus 17577.
 XX

PN W0200028040-A2.
 XX

PD 18-MAY-2000.
 XX

PF 05-NOV-1999; 99WO-US26260.
 XX

PR 06-NOV-1998; 98US-0107507.
 XX

PR 20-NOV-1998; 98US-0109409.
 XX

PA (UYOR-) UNIV OREGON HEALTH SCI.
 XX

PI Wong SM, Axthelm MK, Searles RP;
 XX

DR WPI: 2000-376552/32.
 XX

XX New rhesus rhadino virus for producing non-human primate model useful
 PT for testing potential treatments and efficacy of the candidate vaccine
 PT for conditions associated with RRV infection -
 PS Claim 2; Page 83-122; 141bp; English.

XX The present invention describes a novel rhesus macaque rhadinovirus
 CC called macaca mulatta rhadinovirus 17577 (RRV). AAC64754 represents the
 CC RRV genome sequence, and AAB53123 to AAB53204 represent the proteins
 CC encoded by the genome sequence. The present invention also specifically
 CC claims the individual open reading frame (ORF) nucleotide sequences from
 CC the genome which encode the individual proteins, but these sequences are
 CC not given. A non-human animal infected with RRV can be used for testing
 CC the efficacy of drug in the treatment of condition associated with
 CC infection with RRV such as Kaposi's sarcoma, lymphoproliferative
 CC disorder, B-cell hyperplasia, lymphadenopathy, splenomegaly,
 CC hypergammaglobulinemia or autoimmune hemolytic anaemia, by
 CC administering the drug to an immuno-compromised non-human primate
 CC preferably Rhesus macaque monkey obtained by as a result of infection
 CC by Simian immunodeficiency Virus (SIV). RRV is useful for producing
 CC non-human primate model for testing potential treatments for conditions
 CC associated with RRV infection. It is also useful for testing the
 CC efficacy of the candidate vaccine against RRV infection or conditions
 CC associated with its infection by administering the vaccine to the
 CC subject capable of infection with RRV, inoculating the subject with RRV
 CC and observing the effect of vaccine. AAC64755 to AAC64765 and AAB53205
 CC to AAB53213 represent sequence used in the exemplification of the
 CC present invention.

XX Sequence 133719 BP; 32746 A; 35648 C; 34521 G; 30804 T; 0 other;

Query Match 86.6%; Score 30381; DB 21; Length 133719;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 35101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACACCTAAGGTTGGTGTAATAATCTAAGCAAAATGTATATATTAATTAATACATGTAC 60
 Db 34900 ACACCTAAGGTTGGTGTAATAATCTAAGCAAAATGTATATATTAATTAATACATGTAC 34959
 QY 61 ACCAAATACAGTGAATAATTTACAGCTAACCAACACATTTAGCGGAATGTATGAACATG 120
 Db 34960 ACCAAATACAGTGAATAATTTACAGCTAACCAACACATTTAGCGGAATGTATGAACATG 35019
 QY 121 TATGAAGTTTAAACAAATTAATTAAGCTACAGATTCCTTGTGTTTATCCGTAT 180
 Db 35020 TATGAAGTTTAAACAAATTAATTAAGCTACAGATTCCTTGTGTTTATCCGTAT 35079
 QY 181 ATATTGTTCAATCCATGTGTATATATGTAGAGATATCATATATATGAATTAATCAATAGCA 240
 Db 35080 ATATTGTTCAATCCATGTGTATATATGTAGAGATATCATATATATGAATTAATCAATAGCA 35139
 QY 241 AAGCCCATGACATCACCATATTTCCGCTGTTTCGCCCTGTTTAAAGCTTAAGTTT 300
 Db 35140 AAGCCCATGACATCACCATATTTCCGCTGTTTCGCCCTGTTTAAAGCTTAAGTTT 35199
 QY 301 GATTAGATGAAGAAACAGATACGATCCGAGCAGCAGACAGTCAAAAGAACGGGCTCG 360
 Db 35200 GATTAGATGAAGAAACAGATACGATCCGAGCAGCAGACAGTCAAAAGAACGGGCTCG 35259
 QY 361 GAACGTGACAGAGAGGCTGTGTTTGGCGGCTGTGACACGCTTTCACGCCAGCGCT 420
 Db 35260 GAACGTGACAGAGAGGCTGTGTTTGGCGGCTGTGACACGCTTTCACGCCAGCGCT 35319
 QY 421 ATAACGAGTTTTCAGTCATTAATTTGACAGAGTGGCATGGAAGCAAGTAACCGCGCTG 480
 Db 35320 ATAACGAGTTTTCAGTCATTAATTTGACAGAGTGGCATGGAAGCAAGTAACCGCGCTG 35379
 QY 481 ATGGCGCTTACGAACATCAGTACGTATAGCTCCGTGCGCCCTGATACAGCTCGGCTT 540
 Db 35380 ATGGCGCTTACGAACATCAGTACGTATAGCTCCGTGCGCCCTGATACAGCTCGGCTT 35439
 QY 541 TACGAGGTTTCGAGAGTGTCTTTAACAGCGCGATGTTGTCTCGCGCTTATCAAAAT 600

Db	35440	TACGAGGTTTGGAGGTGTTCTTAACAGCGCATGTTTGTCGGCCGTTTATCCAAAT	35499
OY	601	TGTTCTCAATTTAACACGGCCCGGTAACGCTTACACATTCGGATTTGTAATCACTTTTCC	660
Db	35500	TGTTCTCAATTTTAACCGCCCGCGTAACGCGCTCAACAATTCGGATTTGTAATCACTTTTAC	35559
OY	661	GCCCCGAGGATGAGTATCCGCTGTGTGATTCGATTCGATTTGTTGAGCTATGATGGAACACG	720
Db	35560	GCCCCGAGGATGAGTATCCGCTGTGTGATTCGATTCGATTTGTTGAGCTATGATGGAACACG	35619
OY	721	GGACTACAGACCATGATGTACGTCTCAACCCCAAGTTCAGCCAACTGTTTCCCG	780
Db	35620	GGACTACAGACCATGATGTACGTCTCAACCCCAAGTTCAGCCAACTGTTTCCCG	35679
OY	781	TATTCCTCCTTCTTGTGCAACGATTAATTTTCATATCATTAATTTGTTGTTAATGAACAC	840
Db	35680	TATTCCTCCTTCTTGTGCAACGATTAATTTTCATATCATTAATTTGTTGTTAATGAACAC	35739
OY	841	GGTACCGTGTGAAATTCGGGAGTTGTACAGAAGACAGCACTCAGTCTATTTGCATTA	900
Db	35740	GGTACCGTGTGAAATTCGGGAGTTGTACAGAAGACAGCACTCAGTCTATTTGCATTA	35799
OY	901	GTAATTTGGTTTATTTGGAACAATGTCTGCTGTATTTTGTGTTTAAGCTGTTTTCATC	960
Db	35800	GTAATTTGGTTTATTTGGAACAATGTCTGCTGTATTTTGTGTTTAAGCTGTTTTCATC	35859
OY	961	CTGGCCCTAACTGTTAATAAGCCTAATAACTTTTAAAAAGTTGTTCCCTTCTTTTGG	1020
Db	35860	CTGGCCCTAACTGTTAATAAGCCTAATAACTTTTAAAAAGTTGTTCCCTTCTTTTGG	35919
OY	1021	ATGCTTACGGGGGACGTGAGATTAGCGAACACTCGGATTAGAGGCTGCCGTACATATT	1080
Db	35920	ATGCTTACGGGGGACGTGAGATTAGCGAACACTCGGATTAGAGGCTGCCGTACATATT	35979
OY	1081	GATTCATTCACCTCTGGGCACTGTAATGGGCAAGCTCTCGATTTGGGAGAGAAACATT	1140
Db	35980	GATTCATTCACCTCTGGGCACTGTAATGGGCAAGCTCTCGATTTGGGAGAGAAACATT	36039
OY	1141	AAAAAATATTTGTCGTCGGGTTAATAATCGCTGGCGAGCCCGGACAAAACCTCGAAAA	1200
Db	36040	AAAAAATATTTGTCGTCGGGTTAATAATCGCTGGCGAGCCCGGACAAAACCTCGAAAA	36099
OY	1201	TTCCTTCGAAAGTCGTGGGACTCATGGAAGTTTAAACAAACACATGCTTCCAGGGCC	1260
Db	36100	TTCCTTCGAAAGTCGTGGGACTCATGGAAGTTTAAACAAACACATGCTTCCAGGGCC	36159
OY	1261	TGTTTTCAGCGCGAGACATGATTCGAATATTCTCTGATACGGGCGCCGCGCTTA	1320
Db	36160	TGTTTTCAGCGCGAGACATGATTCGAATATTCTCTGATACGGGCGCCGCGCTTA	36219
OY	1321	CACGATTTCCGCTATAGCATTTTAAAGTGAACAGAAATTTTCCAAACCCAAAGCTGC	1380
Db	36220	CACGATTTCCGCTATAGCATTTTAAAGTGAACAGAAATTTTCCAAACCCAAAGCTGC	36279
OY	1381	AATAGGACGTCGCTTTAAAAAAGTGTTGATATGCGCTTAGTTTAAATTAGTAAAAAC	1440
Db	36280	AATAGGACGTCGCTTTAAAAAAGTGTTGATATGCGCTTAGTTTAAATTAGTAAAAAC	36339
OY	1441	ATTATPAGAGTTGTTGGCGGCTGCATTAATTTGTCACGGTGTAAACGCGGTAATCGGGCTC	1500
Db	36340	ATTATPAGAGTTGTTGGCGGCTGCATTAATTTGTCACGGTGTAAACGCGGTAATCGGGCTC	36399
OY	1501	TTCGCTATTTTGTGGCTGGCGCGAACCATAGCGCAAAAAATATGTCTGCCAGTAAACAGTCC	1560
Db	36400	TTCGCTATTTTGTGGCTGGCGCGAACCATAGCGCAAAAAATATGTCTGCCAGTAAACAGTCC	36459
OY	1561	GACGTACATTTGACTCTGCTGCGCTGGCGGGTTCGTTAGAGATGGATGGAAGTTTTTTA	1620
Db	36460	GACGTACATTTGACTCTGCTGCGCTGGCGGGTTCGTTAGAGATGGATGGAAGTTTTTTA	36519
OY	1621	TTATTCGGCGGAAAGCGGCTACATTAAGTTCGTTGCGCATTTTGATCGTATTTCCGCTG	1680

Db	36520	TTATCCGGCGGAACCGCGCTACAAATTAAGTCGGTGGGCGCAATTTGATCGTAATCTTCCGCG	36537
Qy	1661	GTGTTTGGCACTCGTTTAAGTTAATCGTTTGTATTTGTAAGATTTACCGGTGGGCGC	1740
Db	36580	GTGTTTGCACCTCGTTTAAGTTAATCGTTTGTATTTGTAAGATTTACCGGTGGGCGC	36639
Qy	1741	TTGACGCGTCGCGGGAGCGAAAAATGGCCTCAGTGCAAAAAAGAGATTTACTCGCAATC	1800
Db	36640	TTGACGCGTCGCGGGAGCGAAAAATGGCCTCAGTGCAAAAAAGAGATTTACTCGCAATC	36699
Qy	1801	ACTAATTTTGAAGTTTACGTAATTTGGTGTCTCTCAAAGTCAGAACTTTTAATTTACTGGG	1860
Db	36700	ACTAATTTTGAAGTTTACGTAATTTGGTGTCTCTCAAAGTCAGAACTTTTAATTTACTGGG	36759
Qy	1861	TCTCGAACAATGATATAGCCCTCTCGCCTTCGTCGCGTTCCGACGACAGAGCGTTT	1920
Db	36760	TCTCGAACAATGATATAGCCCTCTCTCGCCTTCGTCGCGTTCCGACGACAGAGCGTTT	36819
Qy	1921	AGCGGTAAGGAGTGGGTGACACCAATTAATTCGACAGCATTTGATTAATTTCCGACGTTTGGG	1980
Db	36820	AGCGGTAAGGAGTGGGTGACACCAATTAATTCGACAGCATTTGATTAATTTCCGACGTTTGGG	36879
Qy	1981	GGCAACAATGGCAATCATGTTTGAATTAATGTCGTCAATTTTAAACAACAGGGGAAGG	2040
Db	36880	GGCAACAATGGCAATCATGTTTGAATTAATGTCGTCAATTTTAAACAACAGGGGAAGG	36939
Qy	2041	GGTAAGCGCGCTCCCGGAAGTCGACACCATTTGCGGCAAGTCCGACAGTACACGACATGA	2100
Db	36940	GGTAAGCGCGCTCCCGGAAGTCGACACCATTTGCGGCAAGTCCGACAGTACACGACATGA	36999
Qy	2101	CAGACGTAATCTGCGCGTTGATAGCTGACACCGCCCCCAACTTAAGGACCTTTAAATCT	2160
Db	37000	CAGACGTAATCTGCGCGTTGATAGCTGACACCGCCCCCAACTTAAGGACCTTTAAATCT	37059
Qy	2161	GAGATTTTATCATTTGATTTCCGTTGCTGATTCAGAAACCGACAGCGCTTGGCTTCG	2220
Db	37060	GAGATTTTATCATTTGATTTCCGTTGCTGATTCAGAAACCGACAGCGCTTGGCTTCG	37119
Qy	2221	CGGTTATATTTTGGTTTATGTCTCCAGTGAAGTCCCAAAAGCTTAATTAAGTGTGCAAT	2280
Db	37120	CGGTTATATTTTGGTTTATGTCTCCAGTGAAGTCCCAAAAGCTTAATTAAGTGTGCAAT	37179
Qy	2281	TACCTGGGGTTTAAAGTTTAAAAAGCGGTGACGGGCGTAAAGCATTAATTAATTT	2340
Db	37180	TACCTGGGGTTTAAAGTTTAAAAAGCGGTGACGGGCGTAAAGCATTAATTAATTT	37239
Qy	2341	GGCGTTGGGTCCTAACTCGCTAACCGTATTTTACTTCGACGATATATCTTTGGAT	2400
Db	37240	GGCGTTGGGTCCTAACTCGCTAACCGTATTTTACTTCGACGATATATCTTTGGAT	37299
Qy	2401	GAGGTTGCAATTTTATATCCCAAGATAGGGCAATTCGTTTGCTTTTGGTGTGACTAAT	2460
Db	37300	GAGGTTGCAATTTTATATCCCAAGATAGGGCAATTCGTTTGCTTTTGGTGTGACTAAT	37359
Qy	2461	GATCGGTTTGAAGTCAAAAGCTACCAAGCGGGGCGGCGTTCAGGGCTCCCAAGATC	2520
Db	37360	GATCGGTTTGAAGTCAAAAGCTACCAAGCGGGGCGGCGTTCAGGGCTCCCAAGATC	37419
Qy	2521	CAAAAGCAAAAGCAACACATTCACCAAAACCTCGATTAACCGCTTGTAGAGTTTG	2580
Db	37420	CAAAAGCAAAAGCAACACATTCACCAAAACCTCGATTAACCGCTTGTAGAGTTTG	37479
Qy	2581	TATTTGGCGTTAATTCCTGTCCAGCGGTGGGAATATTTGGTTTCACTGGTGCAT	2640
Db	37480	TATTTGGCGTTAATTCCTGTCCAGCGGTGGGAATATTTGGTTTCACTGGTGCAT	37539
Qy	2641	TCTAGCAATAGGAAGCGCTTAATTAATGGGTTCAATTCATCCGAAGTTTTTAAAGTAAGG	2700
Db	37540	TCTAGCAATAGGAAGCGCTTAATTAATGGGTTCAATTCATCCGAAGTTTTTAAAGTAAGG	37599
Qy	2701	CCTACCGTATATTTTAAAGTTGTGCGAGTTGCGCGCTTAAACCAAGAAAGCTTGACATCC	2760
Db	37600	CCTACCGTATATTTTAAAGTTGTGCGAGTTGCGCGCTTAAACCAAGAAAGCTTGACATCC	37659

OY	2761	GTCTTTACTGAAACCAACAGAGGAAATTAGTGTGTCGAGAAACCTCTGCGGCCCG	2820
Db	37660	GCTTTTACTGAAACCAACAGAGGAAATTAGTGTGTCGAGAAACCTCTGCGGCCCG	37719
OY	2821	TCCTAACATGATTTGGTTTTCAAGCCCGTGGAGCTGTAACTGAAGATTCCTCAGTGGCAAT	2880
Db	37720	TCCTAACATGATTTGGTTTTCAAGCCCGTGGAGCTGTAACTGAAGATTCCTCAGTGGCAAT	37779
OY	2881	CGAAACCGGGAAAAATGTGCTTCACCGGTAAAAAAGACCTGAGGTTTCCCATAGCAACAT	2940
Db	37780	CGAAACCGGGAAAAATGTGCTTCACCGGTAAAAAAGACCTGAGGTTTCCCATAGCAACAT	37839
OY	2941	AAAGTGGAGATGTCCCCGCTTATGTTAACTGTAATTGCAAGCCCGCTGCACAGGTGTGTC	3000
Db	37840	AAAGTGGAGATGTCCCCGCTTATGTTAACTGTAATTGCAAGCCCGCTGCACAGGTGTGTC	37899
OY	3001	GGAGTACAGACACTACACGCTGATACGCTTCTTCACGAGAAATTTTTCATTACAA	3060
Db	37900	GGAGTACAGACACTACACGCTGATACGCTTCTTCACGAGAAATTTTTCATTACAA	37959
OY	3061	GTTATTAGTAGCCTGGGGATGTTCGATTAATTGACTGAAAGTTCACGGCAGAGACCAACA	3120
Db	37960	GTTATTAGTAGCCTGGGGATGTTCGATTAATTGACTGAAAGTTCACGGCAGAGACCAACA	38019
OY	3121	CGTATTTTGGTATTAATTACCAATTTGGTAATGAAACCTGAGATTTTGAAGTTGGTAA	3180
Db	38020	CGTATTTTGGTATTAATTACCAATTTGGTAATGAAACCTGAGATTTTGAAGTTGGTAA	38079
OY	3181	ACTCATGTGCTTAACTGGATCGAACATGTCTGAGAGAGTTGCGTGTGCTGTCGACG	3240
Db	38080	ACTCATGTGCTTAACTGGATCGAACATGTCTGAGAGAGTTGCGTGTGCTGTCGACG	38139
OY	3241	CGCTGTGTCATATCGATCTGGGTTTTGATGGCGGTTAAAAATTTAAATGTTATCTCTATC	3300
Db	38140	CGCTGTGTCATATCGATCTGGGTTTTGATGGCGGTTAAAAATTTAAATGTTATCTCTATC	38139
OY	3301	TTTTGGTCGATTGAATTCGGCAAAACATGGCCTCTAGAGACCGAGGCTTTCGCCTG	3360
Db	38200	TTTTGGTCGATTGAATTCGGCAAAACATGGCCTCTAGAGACCGAGGCTTTCGCCTG	38259
OY	3361	CCCCAGAAACCTCGGTGTTAGATATACAGCCTGTGGACAGAAATGGCACACGTTCCGCCAC	3420
Db	38260	CCCCAGAAACCTCGGTGTTAGATATACAGCCTGTGGACAGAAATGGCACACGTTCCGCCAC	38319
OY	3421	AGACATCCACATTTGCGACGCGGAAATTTGGTACTCTGGGCGGCAACGTTAGATAGACT	3480
Db	38320	AGACATCCACATTTGCGACGCGGAAATTTGGTACTCTGGGCGGCAACGTTAGATAGACT	38379
OY	3481	TGACTTTGGCGTCACAACAACATACCTGTACGCTTTTTCGCGGATCCCTTTTGTAAAT	3540
Db	38380	TGACTTTGGCGTCACAACAACATACCTGTACGCTTTTTCGCGGATCCCTTTTGTAAAT	38439
OY	3541	TTTTACCTGATGATTTTACGTCAAGCGATGATTTACTATGTTTGGTACTGATGATTTAA	3600
Db	38440	TTTTACCTGATGATTTTACGTCAAGCGATTTGATTTACTATGTTTGGTACTGATGATTTAA	38499
OY	3601	TTTCGTCGCCACTTGTGATGTCGTGAATAATTTGTTTCTTTGAGAGGTTTTTTAAAAAGTAC	3660
Db	38500	TTTCGTCGCCACTTGTGATGTCGTGAATAATTTGTTTCTTTGAGAGGTTTTTTAAAAAGTAC	38559
OY	3661	CGGATTTGGATTCGATGTTTGCAATTAATTACCGTTTGGACGCCATGCAATTCGGGATGGCA	3720
Db	38560	CGGATTTGGATTCGATGTTTGCAATTAATTACCGTTTGGACGCCATGCAATTCGGGATGGCA	38619
OY	3721	AATTCATTCGGAAGTAAAAACCAAAATGTTAAATTTTAAAGTAAATTCAGATGCAAGTTTGC	3780
Db	38620	AATTCATTCGGAAGTAAAAACCAAAATGTTAAATTTTAAAGTAAATTCAGATGCAAGTTTGC	38679
OY	3781	ACACGGGGGCGGACACCCGAGCTAGCGCTGAGAGATTTTGAATGCTCTTAAAAAGTTTAAAGTA	3840
Db	38680	ACACGGGGGCGGACACCCGAGCTAGCGCTGAGAGATTTTGAATGCTCTTAAAAAGTTTAAAGTA	38739

QY	3841	ATTGCGATTAACACGTCGCCGATCAGATGTTCGCCGAGTGTGCCGCTAAAGCAGCAAAAGCA	3900
.Db	38740	ATTTCGATTAACACGTCGCCGATCAGATGTTCGCCGAGTGTGCCGCTAAAGCAGCAAAAGCA	3879
QY	3901	TTCCGCGAATTCGCCATTTGTAAGGTAAAGCAGAGGGATTCGGAACAATGCTTCATATTT	3960
Db	38800	TTCTCGAATTCGCCATTTGTAAGGTAAAGCAGAGGGATTCGGAACAATGCTTCATATTT	3885
QY	3961	TACGCCACATACCAATTAATGGCGAACAAGCAGACGACCTAGATTTGCGTTCGCTTTTG	4020
Db	38860	TACGCCACATACCAATTAATGGCGAACAAGCAGACGACCTAGATTTGCGTTCGCTTTTG	3891
QY	4021	AACCAAAACCGCTGTCGACGACTGTCTAGGTGAAACGGTGGGTAAAAAGTATCCGCTTC	4080
Db	38920	AACCAAAACCGCTGTCGACGACTGTCTAGGTGAAACGGTGGGTAAAAAGTATCCGCTTC	3897
QY	4081	GATATGGGAAATGTACATCCGATACATGCAATTAATTAACCCGGTCCGGGTACTC	4140
Db	38980	GATATGGGAAATGTACATCCGATACATGCAATTAATTAACCCGGTCCGGGTACTC	3903
QY	4141	GTTACCGGCTTTGGCCAAACGATACCACTTTGACGGGTGTAATAAGGGTATAGTCTTCCTCC	4200
Db	39040	GTTACCGGCTTTGGCCAAACGATACCACTTTGACGGGTGTAATAAGGGTATAGTCTTCCTCC	3909
QY	4201	CAATACACAGACGCGGAGCGCAGCGACGCGTAAAGGGTGTCTGTTGCATAGCCCT	4260
Db	39100	CAATACACAGACGCGGAGCGCAGCGACGCGTAAAGGGTGTCTGTTGCATAGCCCT	3915
QY	4261	GTCCAAAGGCGCTGTAGCGAGCGTTCGAAAGAACTCATTTGGTGGCCAGGCAAGCAAA	4320
Db	39160	GTCCAAAGGCGCTGTAGCGAGCGTTCGAAAGAACTCATTTGGTGGCCAGGCAAGCAAA	3921
QY	4321	AATTCGCAAGTTGAGTTTTAAATCGGAATTTGGCGGTACCGGGCGTTCGCTGCACCGT	4380
Db	39220	AATTCGCAAGTTGAGTTTTAAATCGGAATTTGGCGGTACCGGGCGTTCGCTGCACCGT	3927
QY	4381	AGCAGGACACGCGGGCAGAGAACAAGGCCCTCGACAACGATTAATGAGCGCGCTTGGA	4440
Db	39280	AGCAGGACACGCGGGCAGAGAACAAGGCCCTCGACAACGATTAATGAGCGCGCTTGGA	3933
QY	4441	GGTACGACCCCTTCCATATATGGCCAGGAGGCAATCGTTCGTGCAATGAAGAAGTC	4500
Db	39340	GGTACGACCCCTTCCATATATGGCCAGGAGGCAATCGTTCGTGCAATGAAGAAGTC	3939
QY	4501	GCGACCCAGCGGACTTTTTAAAGTTTTCAACTGCTGTTGGGAAAGAAGCGCAGGAGGG	4560
Db	39400	GCGACCCAGCGGACTTTTTAAAGTTTTCAACTGCTGTTGGGAAAGAAGCGCAGGAGGG	3945
QY	4561	AGGAGTTCAATTTGAGGGCTCTTTGGCGGTATACCAACGTAATTCAGTTTGTGAAGTT	4620
Db	39460	AGGAGTTCAATTTGAGGGCTCTTTGGCGGTATACCAACGTAATTCAGTTTGTGAAGTT	3951
QY	4621	TCTGGAACGTCGCTAGCGGTTGGCTGGCTTAACACGGAATTTAAGACCTCAACGAAT	4680
Db	39520	TCTGGAACGTCGCTAGCGGTTGGCTGGCTTAACACGGAATTTAAGACCTCAACGAAT	3957
QY	4681	GACCGATGGAAAAATTCAGTTTAAGGTTCTGTACCGGACCAATCGCGGTATGGGGAGCGGAG	4740
Db	39580	GACCGATGGAAAAATTCAGTTTAAGGTTCTGTACCGGACCAATCGCGGTATGGGGAGCGGAG	3963
QY	4741	GCGGCGCCAAACAAACAAACAATACATTATCATGAAGGCTGCAATAGCATCAATTTGG	4800
Db	39640	GCGGCGCCAAACAAACAAACAATACATTATCATGAAGGCTGCAATAGCATCAATTTGG	3969
QY	4801	TGCGGAGATAGAGCTGTGACTGATGATGACATGAGAGCTGTATTCAATTGACAGAGAAACCC	4860
Db	39700	TGCGGAGATAGAGCTGTGACTGATGATGACATGAGAGCTGTATTCAATTGACAGAGAAACCC	3975
QY	4861	ACTGATTTACACAGAATACGCGCGGGGCGGTAAACAGATTTACCGGCTCTCCAGGTTTGG	4920
Db	39760	ACTGATTTACACAGAATACGCGCGGGGCGGTAAACAGATTTACCGGCTCTCCAGGTTTGG	3981
QY	4921	CGTGAGCGCGGTGAGAGAGGGGCTGAGTGATACGCTATTGAATTTTAAAGTTAGTCCGC	4980

```

39820 CGTGGACGCTGGAGAGGGGCTGGTAGTACCGATTGAAAGTTAAGCTTAGGCTCCG 39879
QY 4981 CCCGCCGATGTTTATTTCTAAAAAACTATCAGACCCTGCTACACCGAAACGGGGGTAA 5040
Db 39880 CCCGCCGATGTTTATTTCTAAAAAACTATCAGACCCTGCTACACCGAAACGGGGGTAA 39939
QY 5041 GAAGCTGTTAACTCAGACATGGTGTGCATGTTTCAAAAGCTACCTTATGATTAACGCTT 5100
Db 39940 GAAGCTGTTAACTCAGACATGGTGTGCATGTTTCAAAAGCTACCTTATGATTAACGCTT 39999
QY 5101 TTTCCGCAAAATCAGACATGGCCGCTCAAGGGAAGCAAGTACGTCGTCGCTGCTC 5160
Db 40000 TTTCCGCAAAATCAGACATGGCCGCTCAAGGGAAGCAAGTACGTCGTCGCTGCTC 40059
QY 5161 CGACATGTTGGGGGCGGTGTGCACGAAACGGTTTTAAAGGGAGCAATACGATCTGTC 5220
Db 40060 CGACATGTTGGGGGCGGTGTGCACGAAACGGTTTTAAAGGGAGCAATACGATCTGTC 40119
QY 5221 TGCATGGGAGAGCAATTCGCGAGTCAATGAGACCCAGAAACGTAATGCGAAACT 5280
Db 40120 TGCATGGGAGAGCAATTCGCGAGTCAATGAGACCCAGAAACGTAATGCGAAACT 40179
QY 5281 GTTAAACATGCTAGTCAAGTTGACGGGGGCAATGTCGGTCCGGCTTACGCCAATTA 5340
Db 40180 GTTAAACATGCTAGTCAAGTTGACGGGGGCAATGTCGGTCCGGCTTACGCCAATTA 40239
QY 5341 CGTTGTCAAGGGGGAATAATCTGCTAACCCGCTGACGTACGGTCCGCTATGCGAAGTT 5400
Db 40240 CGTTGTCAAGGGGGAATAATCTGCTAACCCGCTGACGTACGGTCCGCTATGCGAAGTT 40299
QY 5401 TGACCAATGCTATGAAGCAACGATAGTGCACCTCCCAACGGCAGCCAGCTGACGATGA 5460
Db 40300 TGACCAATGCTATGAAGCAACGATAGTGCACCTCCCAACGGCAGCCAGCTGACGATGA 40359
QY 5461 TCGGGACGGGGTGGGGGAGGAGGACCTCCCTGCGCAAAACACGATGCGGGGCGCTGT 5520
Db 40360 TCGGGACGGGGTGGGGGAGGAGGACCTCCCTGCGCAAAACACGATGCGGGGCGCTGT 40419
QY 5521 TATCCAGATTGGAGATAAAGTGGCTTTGGAAATTTACAGCGAATGTACAAACAGAC 5580
Db 40420 TATCCAGATTGGAGATAAAGTGGCTTTGGAAATTTACAGCGAATGTACAAACAGAC 40479
QY 5581 CCAGTTTCCCTTCCGCTTAAACAGGCTATGCACATTAATTTTTTCCCATTTGGCTT 5640
Db 40480 CCAGTTTCCCTTCCGCTTAAACAGGCTATGCACATTAATTTTTTCCCATTTGGCTT 40539
QY 5641 GCACATGCGCCGCTCCTCAATTTCCACGTCGGCCAAATTAAGGGGTGAGACCCAGC 5700
Db 40540 GCACATGCGCCGCTCCTCCTCAATTTCCACGTCGGCCAAATTAAGGGGTGAGACCCAGC 40599
QY 5701 GGAACAAATCCGTCGAAACGTGATTTGTAATAAAAAACAAGTACTGCTAGTTTCAATTA 5760
Db 40600 GGAACAAATCCGTCGAAACGTGATTTGTAATAAAAAACAAGTACTGCTAGTTTCAATTA 40659
QY 5761 TCAAAAACGGCTCAAGTCAATCTGTCATCCGCGCATGCAAAACCGATCCGTTGGCA 5820
Db 40660 TCAAAAACGGCTCAAGTCAATCTGTCATCCGCGCATGCAAAACCGATCCGTTGGCA 40719
QY 5821 AGCTTTGGGTACAGGGGTTCCAGATCCGAGACAGTTCACAGGTACGGCAAAAGATCTGA 5880
Db 40720 AGCTTTGGGTACAGGGGTTCCAGATCCGAGACAGTTCACAGGTACGGCAAAAGATCTGA 40779
QY 5881 GCACCCCGCGAATGAACCTATAGGGGCTGGTGTACAACTATTACAGGGCAAAAACGT 5940
Db 40780 GCACCCCGCGAATGAACCTATAGGGGCTGGTGTACAACTATTACAGGGCAAAAACGT 40839
QY 5941 GGCACACGTTCCGGATGTCGCCCTAAAGGCGACGATGACACAGATGAGTGTCTGCACCC 6000
Db 40840 GGCACACGTTCCGGATGTCGCCCTAAAGGCGACGATGACACAGATGAGTGTCTGCACCC 40899
QY 6001 AACCTGACGAGAGGCTTGTGGAGGTTCACCCGATGTTGATTTTTTGTTCATCA 6060
Db 6060 AACCTGACGAGAGGCTTGTGGAGGTTCACCCGATGTTGATTTTTTGTTCATCA 6060

```


[illegible]

Db	44200	TAGTCGAGATTTCGAGGGGGTGCGCACCTGAGGTACAGGGCCCTCGAATCTCCAAACG	44259
OY	9361	TAACCGTGGCCGACGACATATACGGCGATGGGTGCGCTCATACCTATCTACGAGTCTCA	9420
Db	44260	TAAACGTGGCCGACGACATATACGGCGATGGGTGCGCTCATACCTATCTACGAGTCTCA	44319
OY	9421	GTTCATATTTAAATCTGGCGCGAGATTTACGTTTACGGTTCATCGACACGACAAATA	9480
Db	44320	GTTCATATTTAAATCTGGCGCGAGATTTACGTTTACGGTTCATCGACACGACAAATA	44379
OY	9481	CCGCTTCCTGTGGGTGTGCATATTACTAGAAACGGGCTCCCTGTGCTTTGACATGTGCA	9540
Db	44380	CCGCTTCCTGTGGGTGTGCATATTACTAGAAACGGGCTCCCTGTGCTTTGACATGTGCA	44439
OY	9541	TCCCAAAATTTATAGCGGTGTCCAGAGACAGACGAGGTACGGTGTGTGAAGTCGGGGTGG	9600
Db	44440	TCCCAAAATTTATAGCGGTGTCCAGAGACAGACGAGGTACGGTGTGTGAAGTCGGGGTGG	44499
OY	9601	ACAAAGGAGACACAGAGCGATGATTTATACCTTAAGACACACCACTTAGCAAAAGAC	9660
Db	44500	ACAAAGGAGACACAGAGCGATGATTTATACCTTAAGACACACCACTTAGCAAAAGAC	44559
OY	9661	GGCGGACGTTGTTAAAGAGCTTTGATTTCCGAAACCCGACGTGACATTTGAAGCAAA	9720
Db	44560	GGCGGACGTTGTTAAAGAGCTTTGATTTCCGAAACCCGACGTGACATTTGAAGCAAA	44619
OY	9721	TTGTTAAAGAGGCGCTAGCTATATTCGAAAAAAATTTGCGTTCGGTTCGGCTGTATTTAT	9780
Db	44620	TTGTTAAAGAGGCGCTAGCTATATTCGAAAAAAATTTGCGTTCGGTTCGGCTGTATTTAT	44679
OY	9781	ATTTTATTTGAGTACGT	9840
Db	44680	ATTTTATTTGAGTACGT	44739
OY	9841	TGACCCACACCGGGTCTGCGTGTGTTGCGGGTTAAACCCATGGGTCCAAACATGTACAGAAAC	9900
Db	44740	TGACCCACACCGGGTCTGCGTGTGTTGCGGGTTAAACCCATGGGTCCAAACATGTACAGAAAC	44799
OY	9901	TACCGCACCCGGCTATTTGTTGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	9960
Db	44800	TACCGCACCCGGCTATTTGTTGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	44859
OY	9961	GCGTCCCGCATATTCAAAAACGAGACTTTGGAATGGTTTACGACAAACGGGTGTACGATTCG	10020
Db	44860	GCGTCCCGCATATTCAAAAACGAGACTTTGGAATGGTTTACGACAAACGGGTGTACGATTCG	44919
OY	10021	GTCAGCGCGCACATATGGGCTGTGGCCCTGTTAAAGCGGCGTGGCTTGTATGGAAGATG	10080
Db	44920	GTCAGCGCGCACATATGGGCTGTGGCCCTGTTAAAGCGGCGTGGCTTGTATGGAAGATG	44979
OY	10081	TGTGTCGCGAACAGATAGTGGCGGCAAGGGGCGTCATTACTGTGTCATGTGAACCGGACGG	10140
Db	44980	TGTGTCGCGAACAGATAGTGGCGGCAAGGGGCGTCATTACTGTGTCATGTGAACCGGACGG	45039
OY	10141	AGTGTGCGAATTTTAAATCGGCAATGGCGCAACCAAGTTTGTGGGATCCAAAGCGCTTC	10200
Db	45040	AGTGTGCGAATTTTAAATCGGCAATGGCGCAACCAAGTTTGTGGGATCCAAAGCGCTTC	45099
OY	10201	TGTGTTCACCGATTCATGAAAAAACCTCTGTGCGCCCACTGTGAATGTTAATTAA	10260
Db	45100	TGTGTTCACCGATTCATGAAAAAACCTCTGTGCGCCCACTGTGAATGTTAATTAA	45159
OY	10261	CATCAGTTTTTACAAATGAAATCACTGTGTCCAAATTTACTGTGGGCGCCGCAAGATGTA	10320
Db	45160	CATCAGTTTTTACAAATGAAATCACTGTGTCCAAATTTACTGTGGGCGCCGCAAGATGTA	45219
OY	10321	TAGTGTCTTAATGTGTGATGATGAGAACAAATTAACGTAATCCACGACATCTTATGACGTT	10380
Db	45220	TAGTGTCTTAATGTGTGATGATGAGAACAAATTAACGTAATCCACGACATCTTATGACGTT	45279
OY	10381	GTTTTTATTTGTGTGTGAAGGATTTTAACGTAATGGAGGTTCCGCTGTGCTTTAAAG	10440

Dp	45280	GGTTTTTATTTGGCTGTGTAAGTATTAAACGTAATGGAGGTTCCGGTGGCTATTAAAG	45339
Qy	10441	CAAAACGGTCATAGAGTAAACCATATTGTGTAATGGGAAAAATAGTCTGTAAATAGTTATC	10500
Dp	45340	CAAAACGGTCATAGAGTAAACCATATTGTGTAATGGGAAAAATAGTCTGTAAATAGTTATC	45399
Qy	10501	CGAACAGTATGACTGCACACACGAATGGGGTTTTTAACCAAGACGAGGGCTTTTCAACAATC	10560
Dp	45400	CGAACAGTATGACTGCACACAGAAATGGGGTTTTTAACCAAGACGAGGGCTTTTCAACAATC	45459
Qy	10561	AGCCGGATCGGTCAAGTTTCCATTTTATCGGTAAATACAAAACCTCCGTTATGG	10620
Dp	45460	AGCCGGAAATCGGTCAAGTTTCCATTTTATCGGTAAATACAAAACCTCCGTTATGG	45519
Qy	10621	GCTTATTTTTTGGCGGCTATGTGGGTATATCGCGTTGGTATAGTACGATACGGAGGG	10680
Dp	45520	GCTTATTTTTTGGCGGCTATGTGGGTATATCGCGTTGGTATAGTACGATACGGAGGG	45579
Qy	10681	TGTGTTGTAAGGGGGCGGTTGTTGCCGATTCGTGCGACCCCGCTCAACCCGCTATG	10740
Dp	45580	TGTGTTGTAAGGGGGCGGTTGTTGCCGATTCGTGCGACCCCGCTCAACCCGCTATG	45639
Qy	10741	AGATGTGAATTTAGTGTGGCTGCCGCCACGGAAACCAATCATAGAACACTTCACGTACA	10800
Dp	45640	AGATGTGAATTTAGTGTGGCTGCCGCCACGGAAACCAATCATAGAACACTTCACGTACA	45699
Qy	10801	TAGCCAAAGCGCACACGCTGCTCTAGCTCGTTTATTTCTAGCGATTTAAAAACAATTT	10860
Dp	45700	TAGCCAAAGCGCACACGCTGCTCTAGCTCGTTTATTTCTAGCGATTTAAAAACAATTT	45759
Qy	10861	ATCGTTGGTGGCAGTACTAGTGGGCCATGACGGCGGCGAACAACAGTCTGTCGACATGGT	10920
Dp	45760	ATCGTTGGTGGCAGTACTAGTGGGCCATGACGGCGGCGAACAACAGTCTGTCGACATGGT	45819
Qy	10921	TTTTTGTTTGGCGAGTACGTGTGACCTCCGCTCTTTAGTGGAAATGCAACGATTTGCCCTT	10980
Dp	45820	TTTTTGTTTGGCGAGTACGTGTGACCTCCGCTCTTTAGTGGAAATGCAACGATTTGCCCTT	45879
Qy	10981	GATTGGATCTATTAAATACGCTACGCGGATCAAAACGATAGCTTAATAGTGTGAGACCCAC	11040
Dp	45880	GATTGGATCTATTAAATACGCTACGCGGATCAAAACGATAGCTTAATAGTGTGAGACCCAC	45939
Qy	11041	AGTTGGCTAGCGCTAAACGTTCCCGAGTTCATCGTAAATAAAAAGATTCAACCCCTT	11100
Dp	45940	AGTTGGCTAGCGCTAAACGTTCCCGAGTTCATCGTAAATAAAAAGATTCAACCCCTT	45999
Qy	11101	GCGTTTCTCTGGCCCCCAACATGTAAATGGCGGACGATTAAGAGTCTTCTGCCACGTG	11160
Dp	46000	GCGTTTCTCTGGCCCCCAACATGTAAATGGCGGACGATTAAGAGTCTTCTGCCACGTG	46059
Qy	11161	GTTGTAATAAACTAAAGGAGCCGACCAATCTCGTTTAAACAGGGTTGGTATGGCCATCC	11220
Dp	46060	GTTGTAATAAACTAAAGGAGCCGACCAATCTCGTTTAAACAGGGTTGGTATGGCCATCC	46119
Qy	11221	GGCATCTTGACTGCTGTTGCCCTTCCACGGCGACGTTAAAGTCCGTATCGCGGGTGAAG	11280
Dp	46120	GGCATCTTGACTGCTGTTGCCCTTCCACGGCGACGTTAAAGTCCGTATCGCGGGTGAAG	46179
Qy	11281	GGTAAACGATCGCTCGAATTAACGGCGGCGACATAGACGTATCTGTACGCGCGGTGCC	11340
Dp	46180	GGTAAACGATCGCTCGAATTAACGGCGGCGACATAGACGTATCTGTGTAGCGGCGGTGCC	46239
Qy	11341	GTTTGAATCTCTTAAAAAAAAATGTTCCACGGCTTAATAAATGCAATTAATACCTGTG	11400
Dp	46240	GTTTGAATCTCTTAAAAAAAAATGTTCCACGGCTTAATAAATGCAATTAATACCTGTG	46299
Qy	11401	ATTTAACGCCAATCACCGCACCGATGCCGGTCCGACGCGCTGTGTGTGTGTGTGACGC	11460
Dp	46300	ATTTAACGCCAATCACCGCACCGATGCCGGTCCGACGCGCTGTGTGTGTGTGTGACGC	46359
Qy	11461	CGGGCTCTATGTAACAGTGGAGACACAGGCTTATTCGCGGCTTATATCTGTGACGTGCT	11520
Dp	46360	CGGGCTCTATGTAACAGTGGAGACACAGGCTTATTCGCGGCTTATATCTGTGACGTGCT	46419

QY 11521 CTTTACGCGACAGATCCAAATTTGTACAGGAGAGTCCGTAACGATTTTATGCAATGCT 11580
|||||
Db 46420 CTTTACGCGACAGATCCAAATTTGTACAGGAGAGTCCGTAACGATTTTATGCAATGCT 46479
QY 11581 TTGAGCGGAGAGTGGCAGCGTCCCATTTAGCTCCGTGAGAAATCGCTTCCAAAANAAG 11640
|||||
Db 46480 TTGAGCGGAGAGTGGCAGCGTCCCATTTAGCTCCGTGAGAAATCGCTTCCAAAANAAG 46539
QY 11641 ATTAGTGTGCTCGTACCGTCTCATCATGTAATATATAGCAGGAATATGACAGCGGTA 11700
|||||
Db 46540 ATTAGTGTGCTCGTACCGTCTCATCATGTAATATATAGCAGGAATATGACAGCGGTA 46599
QY 11701 GCACGGGACGCGCACAGAGTGTCTTCAAGTTAAATCATCTTTATGATCCGACATATC 11760
46600 GCACGGGACGCGCACAGAGTGTCTTCAAGTTAAATCATCTTTATGATCCGACATATC 46659
QY 11761 GTAGTTACCAACGTTAAGCATCTTTTGTGGGCGTCTTCAATTAAGTAAAAACTAGT 11820
|||||
Db 46660 GTAGTTACCAACGTTAAGCATCTTTTGTGGGCGTCTTCAATTAAGTAAAAACTAGT 46719
QY 11821 TGATTTGTACAGATGATTTACTTGAGATATAAAAATAGTTTGTGCTCCCTTTGAGCAT 11880
|||||
Db 46720 TGATTTGTACAGATGATTTACTTGAGATATAAAAATAGTTTGTGCTCCCTTTGAGCAT 46779
QY 11881 AAAACCCAGATCCGCGGGGAGGGGCACTTTTTTATGAAAGTTCCGCTCGTGCATATATAG 11940
46780 AAAACCCAGATCCGCGGGGAGGGGCACTTTTTTATGAAAGTTCCGCTCGTGCATATATAG 46839
QY 11941 GAGTGGAGAGCTGTCTCCCGGAGTGTCTTAAAGCAAGAAACAAAACGAGTTACG 12000
46840 GAGTGGAGAGCTGTCTCCCGGAGTGTCTTAAAGCAAGAAACAAAACGAGTTACG 46899
QY 12001 CGGGTATGAGAAAGATACGGCTTAAGGACAAATCTGGAGAGTGCATCTTCAACAGTGC 12060
46900 CGGGTATGAGAAAGATACGGCTTAAGGACAAATCTGGAGAGTGCATCTTCAACAGTGC 46959
QY 12061 AGGGGTTCTTTACACCGTCCCATTAAGAGATCTAATTTTATCTGAGCTGCACCTTTAAAC 12120
46960 AGGGGTTCTTTACACCGTCCCATTAAGAGATCTAATTTTATCTGAGCTGCACCTTTAAAC 47019
QY 12121 ACTTTACCTATCTGATTCAGACGAGCATAAATTGGAAGGATTTGTTCTTCTGTTAGC 12180
47020 ACTTTACCTATCTGATTCAGACGAGCATAAATTGGAAGGATTTGTTCTTCTGTTAGC 47079
QY 12181 TGGTGGGAGAGATGTCTCTCTTATACAGATCGGTGCAAAAGATGTCAAAATGACGCG 12240
47080 TGGTGGGAGAGATGTCTCTCTTATACAGATCGGTGCAAAAGATGTCAAAATGACGCG 47139
QY 12241 CGTCAACAGCCCAATATGTGATTTTCAATACGTCCTAATCTTATACAGTGTGTTGATTTG 12300
47140 CGTCAACAGCCCAATATGTGATTTTCAATACGTCCTAATCTTATACAGTGTGTTGATTTG 47199
QY 12301 TAAAGCTATACGATATGCGACGCGGAGCAGCACTCGGTGATCTGTAACCTCCGAAATA 12360
47200 TAAAGCTATACGATATGCGACGCGGAGCAGCACTCGGTGATCTGTAACCTCCGAAATA 47259
QY 12361 TCTAGTGTGATTTTAAAGGAACTGGTTTGGATATATGTGAGAGCGTATGTGTA 12420
47260 TCTAGTGTGATTTTAAAGGAACTGGTTTGGATATATGTGAGAGCGTATGTGTA 47319
QY 12421 CGGTCTCTCAGAAAGCGCGGTACCCGAGCGCTTCATGATCCGCTGTCTGTCACACGCGAC 12480
47320 CGGTCTCTCAGAAAGCGCGGTACCCGAGCGCTTCATGATCCGCTGTCTGTCACACGCGAC 47379
QY 12481 GAGGGAATGTCTTAAAGCGATATACAGAGTACTTTGAGACGCTCGGTGTGAATCTGA 12540
47380 GAGGGAATGTCTTAAAGCGATATACAGAGTACTTTGAGACGCTCGGTGTGAATCTGA 47399
QY 12541 GGCATATTTACCGTTGTCAAGAAATGACAAATTAAGGATAGTATAGTAAATAGA 12600
47440 GGCATATTTACCGTTGTCAAGAAATGACAAATTAAGGATAGTATAGTAAATAGA 47499

QY 12601 CGTTACGTTTAAAGATGCTCTTCCGTAATGAGGACGCGAAGTGGCAGAGACTTCGC 12660
|||||
Db 47500 CGTTACGTTTAAAGATGCTCTTCCGTAATGAGGACGCGAAGTGGCAGAGACTTCGC 47559
QY 12661 GCGGAGCATTTACATCCACATAAATTTATCTCCATATCTCCACTAAAGGATATATGATA 12720
|||||
Db 47560 GCGGAGCATTTACATCCACATAAATTTATCTCCATATCTCCACTAAAGGATATATGATA 47619
QY 12721 TCTTCTATTTTAAAGTACGAAATAAAAAATATAGACACATTTGTAATAATATACAGAC 12780
47620 TCTTCTATTTTAAAGTACGAAATAAAAAATATAGACACATTTGTAATAATATACAGAC 47679
QY 12781 GCAATGATGCGCATGCTTCAACCGCGGATCCGTCCGGGTCACTGCGAGCGGTTGTT 12840
47680 GCAATGATGCGCATGCTTCAACCGCGGATCCGTCCGGGTCACTGCGAGCGGTTGTT 47739
QY 12841 CACGTGATCTTCCGCGAGGTTATCTCTCCGAAACATATTTAGTGGGTTGAACGCGAG 12900
47740 CACGTGATCTTCCGCGAGGTTATCTCTCCGAAACATATTTAGTGGGTTGAACGCGAG 47799
QY 12901 CGGTTTTTTTGCACACACTTGTGCTCATCTGAGACGACGTCATAAGACTTTATACGTG 12960
47800 CGGTTTTTTTGCACACACTTGTGCTCATCTGAGACGACGTCATAAGACTTTATACGTG 47859
QY 12961 TGGGAGCGGATTTTCAAAACACCGACCCCGGGGAGCGGTCCGCGGCGGTG 13020
47860 TGGGAGCGGATTTTCAAAACACCGACCCCGGGGAGCGGTCCGCGGCGGTG 47919
QY 13021 TCCGAGCTGGCGATTTAGTCTGCTCTGTTTACACAAATGGAATAATTTTATCCGTTGAT 13080
47920 TCCGAGCTGGCGATTTAGTCTGCTCTGTTTACACAAATGGAATAATTTTATCCGTTGAT 47979
QY 13081 GTAGTTATACCAAGGCGGATACGCTCATCTGTGAACTGTGGAGCCGTGAAGTCTTG 13140
47980 GTAGTTATACCAAGGCGGATACGCTCATCTGTGAACTGTGGAGCCGTGAAGTCTTG 48039
QY 13141 TATATGTCATTAATTTGGCGCTTACAGAAACCAATGCGAGTTTAAAGATAAATTTGCG 13200
48040 TATATGTCATTAATTTGGCGCTTACAGAAACCAATGCGAGTTTAAAGATAAATTTGCG 48099
QY 13201 CAATGTACCGGATGCGCGCTTACGAGTACGCTGTAAGTATCTCTTAAACGCTTAAAGAACCG 13260
48100 CAATGTACCGGATGCGCGCTTACGAGTACGCTGTAAGTATCTCTTAAACGCTTAAAGAACCG 48159
QY 13261 TTGATATACCGGACACTGTACGAGACCCGTGTCGCGGTCAACCCCTACAGATGTTG 13320
48160 TTGATATACCGGACACTGTGTACGAGACCCGTGTCGCGGTCAACCCCTACAGATGTTG 48219
QY 13321 ACCGACTCTTACAGTCTAGGGTACGGGACGATACGTGACACACACACCGTCCGTA 13380
48220 ACCGACTCTTACAGTCTAGGGTACGGGACGATACGTGACACACACCGTCCGTA 48279
QY 13381 CGCCGAGGTATGTGAGGGGACAAAGTATCCGCCGACGCGCACCCGAGATATCCAAACGGA 13440
48280 CGCCGAGGTATGTGAGGGGACAAAGTATCCGCCGACGCGCACCCGAGATATCCAAACGGA 48339
QY 13441 TCCGCAAGTCTGTAAAGGCTTGAATTCGCCCTCCCAAAACGCAACCTATCCAAAGAGC 13500
48340 TCCGCAAGTCTGTAAAGGCTTGAATTCGCCCTCCCAAAACGCAACCTATCCAAAGAGC 48399
QY 13501 TGGGCGAGGCGCTCAAGTTTCTGTTGCGCATATTAACGTGTGCGTATATGATTAAC 13560
48400 TGGGCGAGGCGCTCAAGTTTCTGTTGCGCATATTAACGTGTGCGTATATGATTAAC 48459
QY 13561 GAAGAACTAGATACCAAGTGTGACAGCGGACAGATCCGCGCGCTTGTGATTTGCTC 13620
48460 GAAGAACTAGATACCAAGTGTGACAGCGGACAGATCCGCGCGCTTGTGATTTGCTC 48519
QY 13621 GATCCGCGCGCTCTGTTAAGAGGAGATTTGTTTTAGAGGCAAGCAATGCGGTTT 13680
48520 GATCCGCGCGCTCTGTTAAGAGGAGATTTGTTTTAGAGGCAAGCAATGCGGTTT 48579
QY 13681 GTGATTTCTATAGAAAGAGCTGACAGTGTCAAGAACTATACCAATTAAGCAATTTTTCG 13740

Db 48580 GTGATTCATAGAAAGACGTGCAGTGTGCAGAACTATACATTAAAGCAATTTTTCG 48639
OY 13741 GTTTTGATTAATAGGACAAACGAAACGTCGACTTAATTAAGGACATTTTATAGAGCG 13800
Db 48640 GTTTTGATTAATAGGACAAACGAAACGTCGACTTAATTAAGGACATTTTATAGAGCG 48699
OY 13801 TCGTTCGTATTAGAAACAGGTGTGAGAGAGAGCGCTTGGTAAAGCGCGCTGTT 13860
Db 48700 TCGTTCGTATTAGAAACAGGTGTGAGAGAGAGCGCTTGGTAAAGCGCGCTGTT 48759
OY 13861 CGCAACGATAGTAACGATTTGGAGAGAGTGTGGATTAATGGAGATGGGCTCAT 13920
Db 48760 CGCAACGATAGTAACGATTTGGAGAGAGTGTGGATTAATGGAGATGGGCTCAT 48819
OY 13921 AAGCTGGGTAGGCTATTAACATACCAATGCGAAGCTTGCATGCGGACGCAAACTCG 13980
Db 48820 AAGCTGGGTAGGCTATTAACATACCAATGCGAAGCTTGCATGCGGACGCAAACTCG 48879
OY 13981 AAGCTGGCTCTGTGTGAGAGAGATTAACCTCGGTCAATTAAGCGGACGTCTACTGTTGC 14040
Db 48880 AAGCTGGCTCTGTGTGAGAGAGATTAACCTCGGTCAATTAAGCGGACGTCTACTGTTGC 48939
OY 14041 TTAGTTGTCGCGCTACCGCTGACCGCGCTGGCTGTGCTCCGCGGCGCTTGTATTAA 14100
Db 48940 TTAGTTGTCGCGCTACCGCTGACCGCGCTGGCTGTGCTCCGCGGCGCTTGTATTAA 48999
OY 14101 GGCCTGTACGACCTATCAAGCAGAGATTAATGTTTGTGGCTTCGAGATATGGCCACCA 14160
Db 49000 GGCCTGTACGACCTATCAAGCAGAGATTAATGTTTGTGGCTTCGAGATATGGCCACCA 49059
OY 14161 GGGTGTCACTTCTTAATTCGTTTTTAACAAGAGATGATGTTGCGACACCCGG 14220
Db 49060 GGGTGTCACTTCTTAATTCGTTTTTAACAAGAGATGATGTTGCGACACCCGG 49119
OY 14221 TACGTCCGCTTGTGTGAGAGATTAACCGCGACCACTGCGCATTCGCGCTTGTGACC 14280
Db 49120 TACGTCCGCTTGTGTGAGAGATTAACCGCGACCACTGCGCATTCGCGCTTGTGACC 49179
OY 14281 GCCGGTAAGTGAATGCGATGTCATTAATTTTAAATGTTATGATGTAATCAT 14340
Db 49180 GCCGGTAAGTGAATGCGATGTCATTAATTTTAAATGTTATGATGTAATCAT 49239
OY 14341 GAAACCAAAAGATTTGGCCGCTTACCGGTATACGATGATGATGATTTTATGATTT 14400
Db 49240 GAAACCAAAAGATTTGGCCGCTTACCGGTATACGATGATGATGATTTTATGATTT 49299
OY 14401 TTGTGCAAGATGTCGCGCATTAAGGAGCGCTGTAGGGGAGCTGTGTTAAT 14460
Db 49300 TTGTGCAAGATGTCGCGCATTAAGGAGCGCTGTAGGGGAGCTGTGTTAAT 49359
OY 14461 TCGTTTTGTACCTTTCTTAATGCGCGAGAGAGCTTCCGATACCCGGCGCTTGAACCC 14520
Db 49360 TCGTTTTGTACCTTTCTTAATGCGCGAGAGAGCTTCCGATACCCGGCGCTTGAACCC 49419
OY 14521 ACATCCGCGAAGAACCGTCCCGGCTTAACAAACAGAAATTAATACACTTCCGAAC 14580
Db 49420 ACATCCGCGAAGAACCGTCCCGGCTTAACAAACAGAAATTAATACACTTCCGAAC 49479
OY 14581 ACTGCCAAGAGACAGATACAGATGCGCATTAAGGAGGAAAGTCCACCAATAAATCC 14640
Db 49480 ACTGCCAAGAGACAGATACAGATGCGCATTAAGGAGGAAAGTCCACCAATAAATCC 49539
OY 14641 GTTTTGTGTTTGAAGAGGCGCTTTTGGCAACTGTTCTCTGTGATTTTATGCT 14700
Db 49540 GTTTTGTGTTTGAAGAGGCGCTTTTGGCAACTGTTCTCTGTGATTTTATGCT 49599
OY 14701 GCTCTGTCCCGCACTGACACAGTTCCGCTTGGCGAGAACTGTTGGCTTCTTACACA 14760
Db 49600 GCTCTGTCCCGCACTGACACAGTTCCGCTTGGCGAGAACTGTTGGCTTCTTACACA 49659
OY 14761 GTGCGATAGAGCAGGTGTAATTTGTACGGGGGCCCGACGATACCGTTAACCCGATCG 14820
Db 49660 GTGCGATAGAGCAGGTGTAATTTGTACGGGGGCCCGACGATACCGTTAACCCGATCG 14979
OY 14821 CGGATACACGCCACCTGACTCGCAAGGAGCCTACCTGTGCTGCTGCTTATCTGCTG 14880
Db 49720 CGGATACACGCCACCTGACTCGCAAGGAGCCTACCTGTGCTGCTGCTTATCTGCTG 49779
OY 14881 CGGGGCGAGCGCGCGGAGATGCTGCTGTACCGGACAGTTAATCTTTGGGCTGCT 14940
Db 49780 CGGGGCGAGCGCGCGGAGATGCTGCTGTACCGGACAGTTAATCTTTGGGCTGCT 49839
OY 14941 CTTTGACCCCAAGCCCTCCCAAGTGAACAAAGTGCCTTTTAAAGAAAGAACCCAGCC 15000
Db 49840 CTTTGACCCCAAGCCCTCCCAAGTGAACAAAGTGCCTTTTAAAGAAAGAACCCAGCC 49899
OY 15001 GGTACCGATAGAGAGCAGCATGTGCGGCTGACAGGCGGAAGGAGCCGAGGTGCAACCCAC 15060
Db 49900 GGTACCGATAGAGAGCAGCATGTGCGGCGTACAGGCGGAAGGAGCCGAGGTGCAACCCAC 49959
OY 15061 TTGCTACCGTGGGCTCTATTCGCTGCTGCGGATTTAGCCAGTCCGCTGATGCTATACG 15120
Db 49960 TTGCTACCGTGGGCTCTATTCGCTGCTGCGGATTTAGCCAGTCCGCTGATGCTATACG 50019
OY 15121 CTGCGCAACTTAAAGACATGCTTACGTTCTTTTGAAGACGTCGACACATCAGC 15180
Db 50020 CTGCGCAACTTAAAGACATGCTTACGTTCTTTTGAAGACGTCGACACATCAGC 50079
OY 15181 GAACCTGGCCGCGCTCGGCGCTGCGTACAGAGTTCCTTTCTTTATGTTTC 15240
Db 50080 GAACCTGGCCGCGCTCGGCGCTGCGTACAGAGTTCCTTTCTTTATGTTTC 50139
OY 15241 AGGTTCTTGGCGGAACCACTGATGATGATGATGATGATGATGATGATGATGATG 15300
Db 50140 AGGTTCTTGGCGGAACCACTGATGATGATGATGATGATGATGATGATGATGATG 50199
OY 15301 GCGACGTGTTTTGTGTGGGCGCAAGTACACCACTGATGATGATGATGATGATGATG 15360
Db 50200 GCGACGTGTTTTGTGTGGGCGCAAGTACACCACTGATGATGATGATGATGATGATG 50259
OY 15361 AGCTGATTAATGCGCAGCAGATCATGTTTCCGTGACAGCGCGGATTAACAAACAG 15420
Db 50260 AGCTGATTAATGCGCAGCAGATCATGTTTCCGTGACAGCGCGGATTAACAAACAG 50319
OY 15421 CTGGCTTCTGCTTAAGCTGATGATGATGATGATGATGATGATGATGATGATG 15480
Db 50320 CTGGCTTCTGCTTAAGCTGATGATGATGATGATGATGATGATGATGATGATG 50379
OY 15481 TCGTTAAAGTGAGCAATTAAGTGTGCTTCTTGGGCTGCTTGAATGACCGGATTA 15540
Db 50380 TCGTTAAAGTGAGCAATTAAGTGTGCTTCTTGGGCTGCTTGAATGACCGGATTA 50439
OY 15541 TAAACGTGTGATGATTAATGTTGTTGAAGGCTCAAGGCAACAAACCCCGGACAG 15600
Db 50440 TAAACGTGTGATGATTAATGTTGTTGAAGGCTCAAGGCAACAAACCCCGGACAG 50499
OY 15601 TAACTTCCATTTAAATTAATACACAGGTGCTTAAACATGCGCGAGTCTGATTAAG 15660
Db 50500 TAACTTCCATTTAAATTAATACACAGGTGCTTAAACATGCGCGAGTCTGATTAAG 50559
OY 15661 GGGCACTTAGGAAAGCTTCGCGGCTTGGGCGGATGATGATGATGATGATGATGATG 15720
Db 50560 GGGCACTTAGGAAAGCTTCGCGGCTTGGGCGGATGATGATGATGATGATGATGATG 50619
OY 15721 TTGGCGTTTGCAATTTGACCCGCAACATGTTTGTAAAGTAGTTTGTGAGTTCG 15780
Db 50620 TTGGCGTTTGCAATTTGACCCGCAACATGTTTGTAAAGTAGTTTGTGAGTTCG 50679
OY 15781 GTTAACCGGCGAGGATGATGATGATGATGATGATGATGATGATGATGATGATG 15840
Db 50680 GTTAACCGGCGAGGATGATGATGATGATGATGATGATGATGATGATGATGATG 50739
OY 15841 ATGGGTTTGAAGTCTGCGGATGATGATGATGATGATGATGATGATGATGATGATG 15900
Db 50740 ATGGGTTTGAAGTCTGCGGATGATGATGATGATGATGATGATGATGATGATGATG 50799

QY	15801	TTAACGCGTGAATTAACCTCCCAAGCATGGGTGGGCCAATTCGTTGGCTCTTGCTGTGCC	15960
Db	50800	TTAACGCGCGAATTAACCTCCCAAGCATGGGTGGGCCATCTGTTGGCTCTTGCTGTGCC	50859
QY	15961	GATATTAATACGGGGGGTGGCCGAACACAGTTTGTGGCAACACACGCGTCGTACACAGGGC	16020
Db	50860	GATATTAATACGGGGGGTGGCCGAACACAGTTTGTGGCAACACACGCGTCGTACACAGGGC	50919
QY	16021	AAGTTATTTGAAGAGCTTCGCGATAGCTGTGTAAACACATCTTCCCTTCAAGTTTGTG	16080
Db	50920	AAGTTATTTGAAGAGCTTCGCGATAGCTGTGTAAACACATCTTCCCTTCAAGTTTGTG	50979
QY	16081	AATTAACGGGACACCCCGGAACGGAAGCCGCTTCGTTAAAGCGCTTCAGTTAGCTTAAAC	16140
Db	50980	AATTAACGGGACACCCCGGAACGGAAGCCGCTTCGTTAAAGCGCTTCAGTTAGCTTAAAC	51039
QY	16141	CTGTGTACACACATCCGGGACAGTTTAAACTAGTTGAACACACCTTAAATAGTTTCTT	16200
Db	51040	CTGTGTACACACATCCGGGACAGTTTAAACTAGTTGAACACACCTTAAATAGTTTCTT	51099
QY	16201	CTGTGTACACAGTTTCTGCCGATTCGGCGATCGCGCCCGTTAGAGACTTCCGACGCGGAAGG	16260
Db	51100	CTGTGTACACAGTTTCTGCCGATTCGGCGATTCGGCGATTCGGCGCGGAAGG	51159
QY	16261	TTTGTACTTGAACACATCCACCTCCGAAAACCTAACCGCATGACAGTGTCTCTGGGGGA	16320
Db	51160	TTTGTACTTGAACACATCCACCTCCGAAAACCTAACCGCATGACAGTGTCTCTGGGGGA	51219
QY	16321	TACTGCGACCATGTTAAACAACGACGACAGTGCCTTAAAGCAAGTTCCTCGAAT	16380
Db	51220	TACTGCGACCATGTTAAACAACGACGACAGTGCCTTAAAGCAAGTTCCTCGAAT	51279
QY	16381	TCACAGGTGCTCTTGTTTATCTCGCCGTATGACACAGACGAATGGAATTTGGCGCTCACG	16440
Db	51280	TCACAGGTGCTCTTGTTTATCTCGCCGTATGACACAGACGAATGGAATTTGGCGCTCACG	51339
QY	16441	TTAAGGAAGACAAAGTTGGTTAAATAAGGCTGTAGAGGCTTGTCAAAATCCACGACCTGG	16500
Db	51340	TTAAGGAAGACAAAGTTGGTTAAATAAGGCTGTAGAGGCTTGTCAAAATCCACGACCTGG	51399
QY	16501	AAAGGTTTAGAGCCCGGTGGATCTTTAACGCGCTCATATGCGCTTCTGTTTACGGTTCGGG	16560
Db	51400	AAAGGTTTAGAGCCCGGTGGATCTTTAACGCGCTCATATGCGCTTCTGTTTACGGTTCGGG	51459
QY	16561	TCGTTCTGTGGGAACACAGAGTGCCTATATGAACGCAATTTGGATGAAGGAGCCCATTA	16620
Db	51460	TCGTTCTGTGGGAACACAGAGTGCCTATATGAACGCAATTTGGATGAAGGAGCCCATTA	51519
QY	16621	CTCTTACCGGCACATATGATGCGCCGCCCAAAAGACGTAATGACTTTGTCCATCATGTA	16680
Db	51520	CTCTTACCGGCACATATGATGCGCCGCCCAAAAGACGTAATGACTTTGTCCATCATGTA	51579
QY	16681	ATTAAGTAAGCTTAAATTTTTTATACGGAACGCGCGTGGGGGCTTGAACATCAACCGTCC	16740
Db	51580	ATTAAGTAAGCTTAAATTTTTTATACGGAACGCGCGTGGGGGCTTGAACATCAACCGTCC	51639
QY	16741	CCGCGCTTTCAGAGCCTTCGCGTGGCGCGACAGCCATGCTCTGCTCGGGGACCTGGAAGCG	16800
Db	51640	CCGCGCTTTCAGAGCCTTCGCGTGGCGCGACAGCCATGCTCTGCTCGGGGACCTGGAAGCG	51699
QY	16801	GATGACGCATACCTGTTCGGAAGTGCATGTTGTCTACCTGTACACGAAAAACGATACG	16860
Db	51700	GATGACGCATACCTGTTCGGAAGTGCATGTTGTCTACCTGTACACGAAAAACGATACG	51759
QY	16861	ATTTCGATTCATGAACACACACGCGGGGAGTATGCAATTAGCGCGAGACGCTGCGAGA	51819
Db	51760	ATTTCGATTCATGAACACACACGCGGGGAGTATGCAATTAGCGCGAGACGCTGCGAGA	51879
QY	16921	TATATTAACGCTCTAGTGTTCGGGCTCAACGGTGCAGAGTTCGGGAGATTTTGTTAAATC	16980
Db	51820	TATATTAACGCTCTAGTGTTCGGGCTCAACGGTGCAGAGTTCGGGAGATTTTGTTAAATC	51879

QY	16961	CCCCGTACAACTTTGAAGGGCTCGTAAGCATGATTAAGGAACATGGCCTGGCGACAGC	17040
Db	51880	CCCCGTACAACTTTGAAGGGCTCGTAAGCATGATTAAGGAACATGGCCTGGCGACAGC	51939
QY	17041	TAATAAAATGTAATTAAGTCGGAGCTCGAGTCGGAAATTCAAACAAAATGTCATCTC	17100
Db	51940	TAATAAAATGTAATTAAGTCGGAGCTCGAGTCGGAAATTCAAACAAAATGTCATCTC	51999
QY	17101	CGTATTTGACAGTTTTGGGGCCGACAGTGCCTGTTTTAACGGCGAGTAATAAGGAACAG	17160
Db	52000	CGTATTTGACAGTTTTGGGGCCGACAGTGCCTGTTTTAACGGCGAGTAATAAGGAACAG	52059
QY	17161	GGATTCGTCGGCTGTCACAAAGCCTTAATAAAGAGACGATTCGGACCGTTGTCGG	17220
Db	52060	GGATTCGTCGGCTGTCACAAAGCCTTAATAAAGAGACGATTCGGACCGTTGTCGG	52119
QY	17221	AACGGTAACAAAGTCGTCGGTGGMAAAACAAGCGAATTTGGGATTAATAAGGGGTTTA	17280
Db	52120	AACGGTAACAAAGTCGTCGGTGGMAAAACAAGCGAATTTGGGATTAATAAGGGGTTTA	52179
QY	17281	CAGGAAAAAATTTGAAAGATTTGACGCTGTGGCGACCGGTTCCGACCTCAAGACGA	17340
Db	52180	CAGGAAAAAATTTGAAAGATTTGACGCTGTGGCGACCGGTTCCGACCTCAAGACGA	52239
QY	17341	GCTGTACGGAACTGAGATTTCTAAGTACCTTGACAAATGATCTTTCCCGTGAAGA	17400
Db	52240	GCTGTACGGAACTGAGATTTCTAAGTACCTTGACAAATGATCTTTCCCGTGAAGA	52299
QY	17401	AGAGTCCCCCAAGGACGACATTTATAGTGGMAATTTGAAGGTCGTCGCCAAGTGTGCC	17460
Db	52300	AGAGTCCCCCAAGGACGACATTTATAGTGGMAATTTGAAGGTCGTCGCCAAGTGTGCC	52359
QY	17461	CAAAAGCCCTTGATCCATTCCTCCAAAGTTCAAGACTGACGTGCAGACAGATGTCCTC	17520
Db	52360	CAAAAGCCCTTGATCCATTCCTCCAAAGTTCAAGACTGACGTGCAGACAGATGTCCTC	52419
QY	17521	ATATACCGCTATTAAAAACAGTAAAGACGATCGCCCAACTGAAGATACCTAAACACTGGG	17580
Db	52420	ATATACCGCTATTAAAAACAGTAAAGACGATCGCCCAACTGAAGATACCTAAACACTGGG	52479
QY	17581	GCCAGTGTATACACGAGCGAGACGTCGACCCGCTCTCGSAGCGGGCTGTATGGTG	17640
Db	52480	GCCAGTGTATACACGAGCGAGACGTCGACCCGCTCTCGSAGCGGGCTGTATGGTG	52539
QY	17641	TGTTAGAGTCCATGTCCTCGGCGCCTCGCTTAACCATTTTTGGCAGCGGCTGAGATTTT	17700
Db	52540	TGTTAGAGTCCATGTCCTCGGCGCCTCGCTTAACCATTTTTGGCAGCGGCTGAGATTTT	52599
QY	17701	TTTACGATGCAATTTTAAACGATATATAGTACGGCCTGCGCGGAGAAACATCCCTGAAC	17760
Db	52600	TTTACGATGCAATTTTAAACGATATATAGTACGGCCTGCGCGGAGAAACATCCCTGAAC	52659
QY	17761	GGGGGGGTGACCGTATACTATGTTTTCTTAAGACCGTGGGTACATGTGGCGGCTGAATAT	17820
Db	52660	GGGGGGGTGACCGTATACTATGTTTTCTTAAGACCGTGGGTACATGTGGCGGCTGAATAT	52719
QY	17821	TCGCCACATTAACAGGAATCGCTAAACCGGGAATCTTAACACGTGAACCTGAAACGGC	17880
Db	52720	TCGCCACATTAACAGGAATCGCTAAACCGGGAATCTTAACACGTGAACCTGAAACGGC	52779
QY	17881	TGGCGCTTGAATTTCTCTGAGCTGAGGAGAGGCGTTAGTTTTCTTAATATATATGTGCA	17940
Db	52780	TGGCGCTTGAATTTCTCTGAGCTGAGGAGAGGCGTTAGTTTTCTTAATATATATGTGCA	52839
QY	17941	TGCTTCACTGTGACATCAAGTCCAGAAAATATATCTATAAAGGGGAACTGACACTGCGT	18000
Db	52840	TGCTTCACTGTGACATCAAGTCCAGAAAATATATCTATAAAGGGGAACTGACACTGCGT	52899
QY	18001	ACGGAGACTATATGATGGAGATCTAAGGTCGCGCTCTTTACACAGGGAACCCCTTGA	18060
Db	52900	ACGGAGACTATATGATGGAGATCTAAGGTCGCGCTCTTTACACAGGGAACCCCTTGA	52959
QY	18061	CCGAGTATGATGATCTCCAAACTCGGGGTTTCGTCACACACGTAACATTTTAAGGCAC	18120

Db	52960	CCGAGTATGATGCTACCTCCAAATCGGGTTCGTGACGACACACTACCATTTTAAGGCAC	53019
Qy	18121	CGGGCAGATTTATCTGTAGACACATTTACGGCCGTGTGTCTCTCTACCGGTGTCTGC	18180
Db	53020	CGGGCAGATTTATCTGTAGACACATTTACGGCCGTGTGTCTCTCTACCGGTGTCTGC	53079
Qy	18181	TGTGTGGCGGGGGGGCCGACGAGCGCATATGTAATACAGCCGTTTCCAAATCACTCCAC	18240
Db	53080	TGTGTGGCGGGGGGGCCGACGAGCGCATATGTAATACAGCCGTTTCCAAATCACTCCAC	53139
Qy	18241	AACCTGGTCTCACAATTGACATATTCGTCCTGGGTATAGTTTGTAGCATGCTCTAGAGA	18300
Db	53140	AACCTGGTCTCACAATTGACATATTCGTCCTGGGTATAGTTTGTAGCATGCTCTAGAGA	53199
Qy	18301	AATATCTTCACGACGTGACCATTTGCTCCAGCGAGGGAGTTGGGAGAGCTTCCCTCCG	18360
Db	53200	AATATCTTCACGACGTGACCATTTGCTCCAGCGAGGGAGGGTGGGAGAGCTTCCCTCCG	53259
Qy	18361	AATCGCCGCCACCATTTGTTCTATTTTGGTTGCATGATGCCAAGATGATCGCCGAGA	18420
Db	53260	AATCGCCGCCACCATTTGTTCTATTTTGGTTGCATGATGCCAAGATGATCGCCGAGA	53319
Qy	18421	TTTTTTCGTGGCTGGGAGCGTTCCACTCCATTTAGCATTTGACTCATCTGGCAGCGC	18480
Db	53320	TTTTTTCGTGGCTGGGAGCGTTCCACTCCATTTAGCATTTGACTCATCTGGCAGCGC	53379
Qy	18481	CAGCTATTTCCCTGAGAGAAAGCTGACAGCGGTTTTTGGCAACCACTGATGTTTATATA	18540
Db	53380	CAGCTATTTCCCTGAGAGAAAGCTGACAGCGGTTTTTGGCAACCACTGATGTTTATATA	53439
Qy	18541	GGGGCGCAATACAAAGAGATGCGTTAGAAAAGCATCTCGCGCTGTGTACTCAAAAC	18600
Db	53440	GGGGCGCAATACAAAGAGATGCGTTAGAAAAGCATCTCGCGCTGTGTACTCAAAAC	53499
Qy	18601	TTTAACAGTCTCTCAGAAAGCTGTGGTCAAGGAGCTATTAGTCATTTGGGGAACGCG	18660
Db	53500	TTTAACAGTCTCTCAGAAAGCTGTGGTCAAGGAGCTATTAGTCATTTGGGGAACGCG	53559
Qy	18661	GAGATCATGATTTTTTCTCGATGAGCCGATGTTTCAGAGATGGCGCTTCTGCATC	18720
Db	53560	GAGATCATGATTTTTTCTCGATGAGCCGATGTTTCAGAGATGGCGCTTCTGCATC	53619
Qy	18721	GATGAGACAGAGGGCTCTCTCGAATAATGAGCTGGCCAACTTTTAAACATGAGCGCA	18780
Db	53620	GATGAGACAGAGGGCTCTCTCGAATAATGAGCTGGCCAACTTTTAAACATGAGCGCA	53679
Qy	18781	GTAAGGCGTTTTTTTACGATTAACAAAAGAAATTAAGCATGGCGCTATACGTTCTGT	18840
Db	53680	GTAAGGCGTTTTTTTACGATTAACAAAAGAAATTAAGCATGGCGCTATACGTTCTGT	53739
Qy	18841	TATATATTTTATCATTTCCGCCAAGGTGGAGATTTTATCGGCAACACCGAGTGTACAT	18900
Db	53740	TATATATTTTATCATTTCCGCCAAGGTGGAGATTTTATCGGCAACACCGAGTGTACAT	53799
Qy	18901	TTTTACGTCACCTTGCCTGTCAGGGGAGCGCTGACGCGCTGTGCGGAAGTGTACGAC	18960
Db	53800	TTTTACGTCACCTTGCCTGTCAGGGGAGCGCTGACGCGCTGTGCGGAAGTGTACGAC	53859
Qy	18961	GGCTGCTTAACATGACACCCGACGATGACACACAGCTGTGTGCATTTGATAGAAGGTC	19020
Db	53860	GGCTGCTTAACATGACACCCGACGATGACACACAGCTGTGTGCATTTGATAGAAGGTC	53919
Qy	19021	ACGGGGGCCAAAACATCATCTCTGTGTGGAGCGTCTGAGGACGCGCATATTTGTGTG	19080
Db	53920	ACGGGGGCCAAAACATCATCTCTGTGTGGAGCGTCTGAGGACGCGCATATTTGTGTG	53979
Qy	19081	TCAAAATTTTCACTGGCGCATATAAACAAGATTGCTCCAAAATAATTTTAAACCGGTG	19140
Db	53980	TCAAAATTTTCACTGGCGCATATAAACAAGATTGCTCCAAAATAATTTTAAACCGGTG	54039
Qy	19141	CTATATGTCACACATCATCTTTGTAGCGGGCCGCTGCGCTTTGGAGCTGGCTTGCAGGAA	19200
Db	54040	CTATATGTCACACATCATCTTTGTAGCGGGCCGCTGCGCTTTGGAGCTGGCTTGCAGGAA	54099
Qy	19201	GTGGTTAAAAAAGTACTGGCGACGTTGCTGTCATCCAGGCGAGCGCACGTGTAACATC	19260
Db	54100	GTGGTTAAAAAAGTACTGGCGACGTTGCTGTCATCCAGGCGAGCGCACGTGTAACATC	54159
Qy	19261	GCATTCATGACAGAGTCTCTCAACAGGGGTTTTTGGCTGTCCTGTGATTTTGAATTAAC	19320
Db	54160	GCATTCATGACAGAGTCTCTCAACAGGGGTTTTTGGCTGTCCTGTGATTTTGAATTAAC	54219
Qy	19321	GTCAGGTCGACCCAAAAGACGTTTGGAGTTTCAACCAGACTGCAAAATCTATGAATA	19380
Db	54220	GTCAGGTCGACCCAAAAGACGTTTGGAGTTTCAACCAGACTGCAAAATCTATGAATA	54279
Qy	19381	AAATGCGGGTTTAAAGTACATTTTTCAGATGAGAGTGTGACCCGATTTAGCTCGAT	19440
Db	54280	AAATGCGGGTTTAAAGTACATTTTTCAGATGAGAGTGTGACCCGATTTAGCTCGAT	54339
Qy	19441	GCTAAACTTATTCAGAAAGCCACGATGACAGCGCTTAAAGGGTTTTTGTACTCATATCT	19500
Db	54340	GCTAAACTTATTCAGAAAGCCACGATGACAGCGCTTAAAGGGTTTTTGTACTCATATCT	54399
Qy	19501	AAACCGGCGATGAGTTTGTGGAAGAGACAGGCTCCCAAGTAATCGACATATCTTGTG	19560
Db	54400	AAACCGGCGATGAGTTTGTGGAAGAGACAGGCTCCCAAGTAATCGACATATCTTGTG	54459
Qy	19561	GCATATGACAAAAGAAATGGAGGTGTGTCCGCGGAAAAGAGAGCGTTAACTGCACTAC	19620
Db	54460	GCATATGACAAAAGAAATGGAGGTGTGTCCGCGGAAAAGAGAGCGTTAACTGCACTAC	54519
Qy	19621	CATCTAGTTTAAAAAGTGCATGATTTACAACTCTACGCGCTTCTGTGATGTATATTTG	19680
Db	54520	CATCTAGTTTAAAAAGTGCATGATTTACAACTCTACGCGCTTCTGTGATGTATATTTG	54579
Qy	19681	TCAGATCCGACAGAAACCGAGGCCAAATATTAATAAGCTCATCTGAGCGCCAACTA	19740
Db	54580	TCAGATCCGACAGAAACCGAGGCCAAATATTAATAAGCTCATCTGAGCGCCAACTA	54639
Qy	19741	TTTTTAAACGTGAGGCATCCGTAATTAATTAATCAAGTGTGCTCACTCTCGTTTACAG	19800
Db	54640	TTTTTAAACGTGAGGCATCCGTAATTAATTAATCAAGTGTGCTCACTCTCGTTTACAG	54699
Qy	19801	GAGTACATGATCTCCCAAGGAGACTAAAAATTTGGGAACCCACAAAACCTTTATACG	19860
Db	54700	GAGTACATGATCTCCCAAGGAGACTAAAAATTTGGGAACCCACAAAACCTTTATACG	54759
Qy	19861	ACTGGCTTTTAAAGAAAGGCAAGTTTCAAGACCCGAGCTGCTGCAGCATGCGTAATTT	19920
Db	54760	ACTGGCTTTTAAAGAAAGGCAAGTTTCAAGACCCGAGCTGCTGCAGCATGCGTAATTT	54819
Qy	19921	GGCCGCTTGGATCCACAGTAAAGATACCAGACCTTTTAACTGTGACACCGGTATTTT	19980
Db	54820	GGCCGCTTGGATCCAC	

OY	20281	TATCTTATATGAGCTGGGGGTGATGCTGTGGGGTTGGGAAGGAATGGATTTGAGGGAG	20340
Db	55180	TATCTTTATATGAGATGGGGGTGGATGGTGTGGGGTTGGGAAGGAATGGATTTGAGGGAG	55239
OY	20341	GATCAAAATGCTAGAAATCATATATGTAATTTTGGATATGCAATCCCTGTAATGGCTCAGCTCTTC	20400
Db	55240	GATGAAATGCTAGAAATCATATATGTAATTTTGGATATGCAATCCCTGTAATGGCTCAGCTCTTC	55299
OY	20401	TTCTGTTTCAATATAACGGCTTCAGTTCCGGGGAGACTTAACCTTTTGTGCTTCTCTTT	20460
Db	55300	TTCTGTTTCAATATAACGGCTTCAGTTCCGGGGAGACTTAACCTTTTGTGCTTCTCTTT	55359
OY	20461	AGGGCTTTGAGGAAGGGGTGCTATTTGGGGCGACTTTTGGCAGCAATTTCCAAATGCTTTC	20520
Db	55360	AGGGCTTTGAGGAAGGGGTGCTATTTGGGGCGACTTTTGGCAGCAATTTCCAAATGCTTTC	55419
OY	20521	GATAATTTCTTAAGATGATGGCTAGGATGCAATGTATGCGAATCATAGAGATGTTCAAGGC	20580
Db	55420	GATAATTTCTTAAGATGATGGCTAGGATGCAATGTATGCGAATCATAGAGATGTTCAAGGC	55479
OY	20581	TATGACTTTTGTGACAGGCTGGCAGATATGAAATACCTTGTGCTATGCAAGCAGCAGGGAAGAG	20640
Db	55480	TATGACTTTTGTGACAGGCTGGCAGATATGAAATACCTTGTGCTATGCAAGCAGCAGGGAAGAG	55539
OY	20641	CAGAAATCAGGTACTGACAAAAAGCCCAAGCTAGAAATCCGATCTGTGCTTTAGTACTT	20700
Db	55540	CAGAAATCAGGTACTGACAAAAAGCCCAAGCTAGAAATCCGATCTGTGCTTTAGTACTT	55599
OY	20701	TACTAGAAATAGTTCTGTGTGATATACCAAGCTATTGTAAGCAAAAAACAAGTTAT	20760
Db	55600	TACTAGAAATAGTTCTGTGTGATATACCAAGCTATTGTAAGCAAAAAACAAGTTAT	55659
OY	20761	TGAACCAAAACAATATCGAAGAGAGCATATAGAACTGTTTCCAAATAGCCATCATCGT	20820
Db	55660	TGAACCAAAACAATATCGAAGAGAGCATATAGAACTGTTTCCAAATAGCCATCATCGT	55719
OY	20821	TCCGGGGAGAAATCTAATCATCTCCATGGCTATTAAAGCAAGATTAACATTTGGCCCAAT	20880
Db	55720	TCCGGGGAGAAATCTAATCATCTCCATGGCTATTAAAGCAAGATTAACATTTGGCCCAAT	55779
OY	20881	CGGTTTTCCGTAAACGCAACAGGGGTGCTAGCAAGCTATTTCAGGAATCTCCTGCTCTAA	20940
Db	55780	CGGTTTTCCGTAAACGCAACAGGGGTGCTAGCAAGCTATTTCAGGAATCTCCTGCTCTAA	55839
OY	20941	GACCGGTAGAGACCAGGTGGCCGAATTGCAAGATATTCATAGCCTGGACGTGGCTAAACGA	21000
Db	55840	GACCGGTAGAGACCAGGTGGCCGAATTGCAAGATATTCATAGCCTGGACGTGGCTAAACGA	55899
OY	21001	TAGGCAAAAATGTAATACGTAATACAAACAGAGGCTAAAGTATATGTTGTACGACAGAAC	21060
Db	55900	TAGGCAAAAATGTAATACGTAATACAAACAGAGGCTAAAGTATATGTTGTACGACAGAAC	55959
OY	21061	GTAATTAATTAAGTGAATGATGCTCCACAGCCTCAAAATTAACATTAATAACTGTGGGA	21120
Db	55960	GTAATTAATTAAGTGAATGATGCTCCACAGCCTCAAAATTAACATTAATAACTGTGGGA	56019
OY	21121	GCCTATGAGCAGACATCATGCTGTGAGGCTGCTCATTTGTGTGCTGACAGCGCTTGGC	21180
Db	56020	GCCTATGAGCAGACATCATGCTGTGAGGCTGCTCATTTGTGTGCTGACAGCGCTTGGC	56079
OY	21181	CTTGAAATTTGGCCAGAGATGGGCCCAACGATTAACACACAGCATATCCGTCCACCAAAA	21240
Db	56080	CTTGAAATTTGGCCAGAGATGGGCCCAACGATTAACACACAGCATATCCGTCCACCAAAA	56139
OY	21241	CGCCACAGAGATGTAGACAAACATTTCTGTGCTTCCAAAAACAAGTCGGCGTCAGATG	21300
Db	56140	CGCCACAGAGATGTAGACAAACATTTCTGTGCTTCCAAAAACAAGTCGGCGTCAGATG	56199
OY	21301	TTTACAGAACTTCTGACCGTTAGGTTTAAACGCGCTGTAGTTGACCAACGTTTAAAGTA	21360
Db	56200	TTTACAGAACTTCTGACCGTTAGGTTTAAACGCGCTGTAGTTGACCAACGTTTAAAGTA	56259

QY	21361	GCACGGAAATTC	CAAGTCCCGGGAAAT	GTGGGGGTCACT	GGCCTACCGCGTACATTTATAA	21440			
Db	56260	GCACGGAAATTC	CAAGTCCCGGGAAAT	GTGGGGGTCACT	GGCCTACCGCGTACATTTATAA	56319			
QY	21421	CATTAAGTCC	AAAGATTAAC	CGATGTTTTAC	CCATGTGACGATTAAGATTAAC	GAAGTCTCGC	21480		
Db	56320	CATTAAGTCC	AAAGATTAAC	CGATGTTTTAC	CCATGTGACGATTAAGATTAAC	GAAGTCTCGC	56379		
QY	21481	TGAATTTTCAT	ATAGTTC	CAAGAAATCT	GTCTCGCGGGTGC	TCGTGGCAAACT	AGTATAAA	21540	
Db	56380	TGAATTTTCAT	ATAGTTC	CAAGAAATCT	GTCTCGCGGGTGC	TCGTGGCAAACT	AGTATAAA	56439	
QY	21541	TCACCAAGTGG	CTTACCTGTT	TACCGGATTTAA	TAGCCTCGCTTTTAAAT	FATCACATTC	21600		
Db	56440	TCACCAAGTGG	CTTACCTGTT	TACCGGATTTAA	TAGCCTCGCTTTTAAAT	FATCACATTC	56499		
QY	21601	GTGCAAAAGG	ATTAGCCACG	GGACCACTGAA	AGCCCGGGAGG	GGGACACACGGGACATG	21660		
Db	56500	GTGCAAAAGG	ATTAGCCACG	GGACCACTGAA	AGCCCGGGAGG	GGGACACACGGGACATG	56559		
QY	21661	TTTTGCACAT	ATCGCTGCAT	AGCACG	CACAGCGCAGAAATTAAT	TAATCTGGCAGTTTC	21720		
Db	56560	TTTTGCACAT	ATCGCTGCAT	AGCACG	CACAGCGCAGAAATTAAT	TAATCTGGCAGTTTC	56619		
QY	21721	ATTACTTGT	ATGTCAACAAT	TGCGGAAT	TAGGGAATG	CCGCATATCTATTTGTCACCG	21780		
Db	56620	ATTACTTGT	ATGTCAACAAT	TGCGGAAT	TAGGGAATG	CCGCATATCTATTTGTCACCG	56679		
QY	21781	AAACATTTA	AGCAATAC	AGTACGTGGG	AAATATAC	CGGCGATTAAC	CGTCAACGCACTGCA	21840	
Db	56680	AAACATTTA	AGCAATAC	AGTACGTGGG	AAATATAC	CGGCGATTAAC	CGTCAACGCACTGCA	56739	
QY	21841	TAAATGAG	CACAGCGCGCT	TAATTAAT	GTACAGTGGG	AACTCCGTACTCGTTAC	GGAAATCCCA	21900	
Db	56740	TAAATGAG	CACAGCGCGCT	TAATTAAT	GTACAGTGGG	AACTCCGTACTCGTTAC	GGAAATCCCA	56799	
QY	21901	TCATTTCAAT	TTGTTAAGT	CTGCCAC	CCCGTGGTTA	ACGTAAAGGCTAC	AGACGCGGAAT	21960	
Db	56800	TCATTTCAAT	TTGTTAAGT	CTGCCAC	CCCGTGGTTA	ACGTAAAGGCTAC	AGACGCGCGAAT	56859	
QY	21961	TGCTAATTA	ATGATGGG	CTGGCAAG	CAAGCGTTGGAT	ATACATCGTGGTGGCG	ACGTGAG	22020	
Db	56860	TGCTAATTA	ATGATGGG	CTGGCAAG	CAAGCGTTGGAT	ATACATCGTGGTGGCG	ACGTGAG	56919	
QY	22021	CCATATCT	TCATTTGCGAT	TACACAT	ATGAGCATTTAG	TTGATCTGTTGTGCCA	ACCC	22080	
Db	56920	CCATATCT	TCATTTGCGAT	TACACAT	ATGAGCATTTAG	TTGATCTGTTGTGTGCCA	ACCC	56979	
QY	22081	CGCAATTT	TTGGTTCT	CAGAGATG	TTTTCTCTAC	CTGTTAGTTTCAAC	ATTTGAAGTTTACC	22140	
Db	56980	CGCAATTT	TTGGTTCT	CAGAGATG	TTTTCTCTAC	CTGTTAGTTTCAAC	ATTTGAAGTTTACC	57039	
QY	22141	TTTAAACA	ACAGGGGGG	TTTATAC	ATATGGGCAT	TCGAGTGCAC	GAACGCCGAA	AAAGG	22200
Db	57040	TTTAAACA	ACAGGGGGG	TTTATAC	ATATGGGCAT	TCGAGTGCAC	GAACGCCGAA	AAAGG	57099
QY	22201	CGAAAGAT	GTGCGCAT	TTGGGAT	ATTTCTTGAT	TTTAAATTCG	ATTCGATTCGAAG	22260	
Db	57100	CGAAAGAT	GTGCGCAT	TTGGGAT	ATTTCTTGAT	TTTAAATTCG	ATTCGATTCGAAG	57159	
QY	22261	TTTGCGGG	CAGAGTAC	ACTTGTAG	TATCGCCAC	CGCAACATTTCA	CACTTCTGGGTGG	22320	
Db	57160	TTTGCGGG	CAGAGTAC	ACTTGTAG	TATCGCCAC	CGCAACATTTCA	CACTTCTGGGTGG	57219	
QY	22321	ACGAGGCG	GTATGTGA	AGGGGGC	CTGGCCGAAT	TTTTTATAG	GGGGCTGCACAA	TAAGT	22380
Db	57220	ACGAGGCG	GTATGTGA	AGGGGGC	CTGGCCGAAT	TTTTTATAG	GGGGCTGCACAA	TAAGT	57279
QY	22381	TGTTTCGG	GAGACGGG	AGGCGTAT	AGCGCCCA	CGTTAAACGTAT	CTCGGGGGCCACATC	22440	
Db	57280	TGTTTCGG	GAGACGGG	AGGCGTAT	AGCGCCCA	CGTTAAACGTAT	CTCGGGGGCCACATC	57339	
QY	22441	CGAGGGG	AACCCCTT	CCCCCTT	ACTTCTTCC	CGCTTTCC	ACACACTCCG	CGCTGTGTTG	22500


```
|||||
Db 57340 CGAGAGAACCCCTTCCCCCTTCTTTTCGGCTTCCACACCTCCCGCTGCTTTGG 57399
OY 22501 GAAGACCGGGAAGGCTCGACGTAAACCGCGCTCCAGAACTCCCAAAAGCAAAATTCGG 22560
Db 57400 GAAGACCGGGAAGGCTCGACGTAAACCGCGCTCCAGAACTCCCAAAAGCAAAATTCGG 57459
OY 22561 TACACTGCCCCCGTTTAAAGATTCATTTAGGGGATCAGCTTCTCATACCTGGCATTT 22620
Db 57460 TACACTGCCCCCGTTTAAAGATTCATTTAGGGGATCAGCTTCTCATACCTGGCATTT 57519
OY 22621 CACCTAAAAAGCAGGTACCGTACCCGTTGGCGCTGGGGGAGGATGTAACT 22680
Db 57520 CACCTAAAAAGCAGGTACCGTACCCGTTGGCGCTGGGGGAGGATGTAACT 57579
OY 22681 TGAAGTCTCGAGAGACGACAGAAAGGTTGCCGCACTAGTCACACCACATTTCTATAGTAA 22740
Db 57580 TGAAGTCTCGAGAGACGACAGAAAGGTTGCCGCACTAGTCACACCACATTTCTATAGTAA 57639
OY 22741 TCATATAATTTTCTATCTGTTGTGCGACACCTATAAATGCAACGCTGCTTTGTTAAA 22800
Db 57640 TCATATAATTTTCTATCTGTTGTGCGACACCTATAAATGCAACGCTGCTTTGTTAAA 57699
OY 22801 ATGAGTTAGATATACATAGCAACATCTGTTCAGAGGACCTGGCTTCATCCAGAGAG 22860
Db 57700 ATGAGTTAGATATACATAGCAACATCTGTTCAGAGGACCTGGCTTCATCCAGAGAG 57759
OY 22861 AATACAAACCGGTTACTTGGCACCATTTTTCAGTGGCGCGGCGAGACGGGTTATACCTGGC 22920
Db 57760 AATACAAACCGGTTACTTGGCACCATTTTTCAGTGGCGCGGCGAGACGGGTTATACCTGGC 57819
OY 22921 CGGCCATTTGATATAAACACAGATTTTCATATAAGGCTCCCAAGCTCAGCGACGTCTATAGTG 22980
Db 57820 CGGCCATTTGATATAAACACAGATTTTCATATAAGGCTCCCAAGCTCAGCGACGTCTATAGTG 57879
OY 22981 GTTTCGCCATCAGTAAATAGTTGGCGAGGAAACAAATGTATACGAAGTTTAAATAATAC 23040
Db 57880 GTTTCGCCATCAGTAAATAGTTGGCGAGGAAACAAATGTATACGAAGTTTAAATAATAC 57939
OY 23041 ACTTCATTTCTTTTACAGAGAAACAGCAAAAGTCTGACCCGCTTTGAGGCGCATTTTGGG 23100
Db 57940 ACTTCATTTCTTTTACAGAGAAACAGCAAAAGTCTGACCCGCTTTGAGGCGCATTTTGGG 57999
OY 23101 ACTTCGCCATCAGGAACTTCCACCCGCTCAGTACGCTCAAGTGTGAGTCTGCTCCGC 23160
Db 58000 ACTTCGCCATCAGGAACTTCCACCCGCTCAGTACGCTCAAGTGTGAGTCTGCTCCGC 58059
OY 23161 GTCCGTGTTTTTAAATAATACAGCGGGGTTTTGTATGCGGAGCTCGCAAGAGACCCAC 23220
Db 58060 GTCCGTGTTTTTAAATAATACAGCGGGGTTTTGTATGCGGAGCTCGCAAGAGACCCAC 58119
OY 23221 CAGGGAAGCAAAACGGGACTGCTGCTGAGCTGTCTAGTAGAAGCGCGACGTTGTGCT 23280
Db 58120 CAGGGAAGCAAAACGGGACTGCTGCTGAGCTGTCTAGTAGAAGCGCGACGTTGTGCT 58179
OY 23281 TAAACAATCAGTGTACGATGGGGGCTGGCGGGATCTTACCACACCTTTTGGCAA 23340
Db 58180 TAAACAATCAGTGTACGATGGGGGCTGGCGGGATCTTACCACACCTTTTGGCAA 58239
OY 23341 CAGGGGTGTGTTAAATTTTGGCTGCTGCAAGCGCGTGGGTAAATGCGGCCCATATG 23400
Db 58240 CAGGGGTGTGTTAAATTTTGGCTGCTGCAAGCGCGTGGGTAAATGCGGCCCATATG 58299
OY 23401 CCCTCCCTACCGATTTGACTGTGTTAAGCTTCACAGTTTGTGCTGACAAAGCGTGGACC 23460
Db 58300 CCCTCCCTACCGATTTGACTGTGTTAAGCTTCACAGTTTGTGCTGACAAAGCGTGGACC 58359
OY 23461 AATCGTGTGTTAAGGAATGAGAGGTGTTATAGAGTCCATGAGTCTTATGTTGGCGA 24500
Db 58360 AATCGTGTGTTAAGGAATGAGAGGTGTTATAGAGTCCATGAGTCTTATGTTGGCGA 58419
OY 23521 GGAGGCACTATGTTTTAGTGTGTCTCAAGGGGAGGTACGAGAGTCAAGCGGA 23580
|||||

Db 58420 GGAGGCACTATGTTTTAGTGTGTGTCTCAAGGGGAGGTACGAGAGTCAAGCGGA 58479
OY 23581 CAATATACGACAATATAGAGAGTTTGAAGAGTACTATGTTTATTTTAAACAGAGTCTG 23640
Db 58480 CAATATACGACAATATAGAGAGTTTGAAGAGTACTATGTTTATTTTAAACAGAGTCTG 58539
OY 23641 TCTGGGATGCTGTGATAGCTGTTTATTTGAAAATTTTAAATACCGATGCGTTATGAG 23700
Db 58540 TCTGGGATGCTGTGATAGCTGTTTATTTGAAAATTTTAAATACCGATGCGTTATGAG 58599
OY 23701 GTGTGTGTTAAAAATTTGTCGCGCAATATAATATGTAAAGTCTCCGCTGGCCCTTC 23760
Db 58600 GTGTGTGTTAAAAATTTGTCGCGCAATATAATATGTAAAGTCTCCGCTGGCCCTTC 58659
OY 23761 TTCTCCAACTTCTCTGTTTAGACGAAAGATTCCAAATTAATGGTTTCAATAGGCTTT 23820
Db 58660 TTCTCCAACTTCTCTGTTTAGACGAAAGATTCCAAATTAATGGTTTCAATAGGCTTT 58719
OY 23821 CATGTGCTGCGTTTTCGTCACACGCTTATGAGATTTGAAACCGCACTAGGGGCGGAA 23880
Db 58720 CATGTGCTGCGTTTTCGTCACACGCTTATGAGATTTGAAACCGCACTAGGGGCGGAA 58779
OY 23881 GCGCAAAATGCTTGGGGTGGGTTTAACTCGTGTATGCGCCCAAGGTGAGCTATCAC 23940
Db 58780 GCGCAAAATGCTTGGGGTGGGTTTAACTCGTGTATGCGCCCAAGGTGAGCTATCAC 58839
OY 23941 TTGATCCCATCAATATACAAACGCGGAATCATTTACAGTATACCTCTGCTGATAGTACT 24000
Db 58840 TTGATCCCATCAATATACAAACGCGGAATCATTTACAGTATACCTCTGCTGATAGTACT 58899
OY 24001 GGCCCGGTAAACGCGGACAGATTAATATAGGGGGGCTATGCTATTTTCCAGCAT 24060
Db 58900 GGCCCGGTAAACGCGGACAGATTAATATAGGGGGGCTATGCTATTTTCCAGCAT 58959
OY 24061 AGAAGAAATGACAGAGAGTCTGTTACGCTCGCGCTCGCGGCTTAAACAGCTGACGCG 24120
Db 58960 AGAAGAAATGACAGAGAGTCTGTTACGCTCGCGCTCGCGGCTTAAACAGCTGACGCG 59019
OY 24121 GTACAAAAAAGCTGCGATATATGTCCAGTGCCTGATCATGCTCTGTTTCCAGCAC 24180
Db 59020 GTACAAAAAAGCTGCGATATATGTCCAGTGCCTGATCATGCTCTGTTTCCAGCAC 59079
OY 24181 GCACGCAAAAGCAAAACCGATTAAGTTTCCGACAGTACCGGTGGCGACGTGACGCGC 24240
Db 59080 GCACGCAAAAGCAAAACCGATTAAGTTTCCGACAGTACCGGTGGCGACGTGACGCGC 59139
OY 24241 TAAATCAGGAAGCTTTAGTCTGCTCGAACAACAGCTTAGGCGTATTTGGAAGCATGCA 24300
Db 59140 TAAATCAGGAAGCTTTAGTCTGCTCGAACAACAGCTTAGGCGTATTTGGAAGCATGCA 59199
OY 24301 AATGCTATTTTTTATATGCTTCCACATCATCACTGCGGAAAAAAGCTGATATATAGGG 24360
Db 59200 AATGCTATTTTTTATATGCTTCCACATCATCACTGCGGAAAAAAGCTGATATATAGGG 59259
OY 24361 CCCTCTGACGAGCAATCTGTTCAAGCAATTCACGCTCAGATGCGTGTCTCCCCAT 24420
Db 59260 CCCTCTGACGAGCAATCTGTTCAAGCAATTCACGCTCAGATGCGTGTCTCCCCAT 59319
OY 24421 TAGACGCTTCAATTTTGGTTCATGCTGTTCAAGGCTGGCTAAATTTGTTGCAATATTTGT 24480
Db 59320 TAGACGCTTCAATTTTGGTTCATGCTGTTCAAGGCTGGCTAAATTTGTTGCAATATTTGT 59379
OY 24481 GGCTATGCTATTTATATACAGACAGCTCTCTCCACATACAGCTGTGTGCAAAAT 24540
Db 59380 GGCTATGCTATTTATATACAGACAGCTCTCTCTCCACATACAGCTGTGTGCAAAAT 59439
OY 24541 CGTGTAACTTAAAGGAATGAGAGGTGTTATAGAGTCCATGAGTCTTATTTGGCGA 24600
Db 59440 CGTGTAACTTAAAGGAATGAGAGGTGTTATAGAGTCCATGAGTCTTATTTGGCGA 59499
OY 24601 TTATGTAGCTAAACGGGCTTAAAGAAATGAAACCGTGTCTGCAAGTAGGCGATGCTCG 24660
Db 59500 TTATGTAGCTAAACGGGCTTAAAGAAATGAAACCGTGTCTGCAAGTAGGCGATGCTCG 59559
|||||
```

QY 24661 TTGCGTCCCCGTGATTGTGACACGAGGTGTGAGTTGTACGTTTGAACATTTCCCTT 24720
|||||
Db 59560 TTGCGTCCCCGTGATTGTGACACGAGGTGTGAGTTGTACGTTTGAACATTTCCCTT 59619
QY 24721 CCCACAGGCTAGTTAGCTCTTTGAGCATCTCCATTAAGAGGACGATTTGTAAAAA 24780
|||||
Db 59620 CCCACAGGCTAGTTAGCTCTTTGAGCATCTCCATTAAGAGGACGATTTGTAAAAA 59679
QY 24781 AGCGTTTACTAGGAGCTGCTTTAGGGATGTACATTTGGATAGGTTAATGGTGGGT 24840
|||||
Db 59680 AGCTGTTTACTAGGAGCTGCTTTAGGGATGTACATTTGGATAGGTTAATGGTGGGT 59739
QY 24841 CGCGACAGCCGATTAAGCCCTGCAACGATTTCTGAGTATTAATATCTGTCTGG 24900
|||||
Db 59740 CGCGACAGCCGATTAAGCCCTGCAACGATTTCTGAGTATTAATATCTGTCTGG 59799
QY 24901 GCCTGCCTCCCTCTGCTGTAACCTGGAAGCACTCGCTTCAATGCAATTTCTTTA 24960
|||||
Db 59800 GCCTGCCTCCCTCTGCTGTAACCTGGAAGCACTCGCTTCAATGCAATTTCTTTA 59859
QY 24961 CGTAGTGTCTGCTTTCTTTCTCAAGTTAGAAATTTGATGACAGTGGCTGTGATCTGGT 25020
|||||
Db 59860 CGTAGTGTCTGCTTTCTTTCTCAAGTTAGAAATTTGATGACAGTGGCTGTGATCTGGT 59919
QY 25021 TCGTCAGGCAATTTGACACGCGTATTTGAAACCTGTTCCGAGACCCCTGGGTCTACTTT 25080
|||||
Db 59920 TCGTCAGGCAATTTGACACGCGTATTTGAAACCTGTTCCGAGACCCCTGGGTCTACTTT 59979
QY 25081 CCGTACGGGTCCCAAGAGCTGTTTGTGTCACAAATGTTTGAGAGACGCTGTGACGA 25140
|||||
Db 59980 CCGTACGGGTCCCAAGAGCTGTTTGTGTCACAAATGTTTGAGAGACGCTGTGACGA 60039
QY 25141 AATCTCAACAAAGCTGTTTGTGCGGCTCACTGTTTGTGTCGCGGAGCTTTATACGA 25200
|||||
Db 60040 AATCTCAACAAAGCTGTTTGTGCGGCTCACTGTTTGTGTCGCGGAGCTTTATACGA 60099
QY 25201 AGTTAGAGAGCTCCCTCTTGGGGTGGTTTTTTTGAAGAGATGCTTAAGCGACCAATA 25260
|||||
Db 60100 AGTTAGAGAGCTCCCTCTTGGGGTGGTTTTTTTGAAGAGATGCTTAAGCGACCAATA 60159
QY 25261 TGTCTTATACATGTCGTTGACAGTGTCTACGACAGCGCTTTTGAAGCGCGGTATTTA 25320
|||||
Db 60160 TGTCTTATACATGTCGTTGACAGTGTCTACGACAGCGCTTTTGAAGCGCGGTATTTA 60219
QY 25321 GTAACTGACATAACTTTGGCGTCCGGGGTCTGTGATGATGATATGCGGGTAATA 25380
|||||
Db 60220 GTAACTGACATAACTTTGGCGTCCGGGGTCTGTGATGATGATATGCGGGTAATA 60279
QY 25381 ACCGCTACAGAGGCTATCAAAAGCGAGCGCTCCATTGTAATTAAGCGGTGAACAA 25440
|||||
Db 60280 ACCGCTACAGAGGCTATCAAAAGCGAGCGCTCCATTGTAATTAAGCGGTGAACAA 60339
QY 25441 CTTCAACTGTTATATCTTTTGTCTGATGAGTCCGAGATTAAGACGCTTATCTCCGTTAA 25500
|||||
Db 60340 CTTCAACTGTTATATCTTTTGTCTGATGAGTCCGAGATTAAGACGCTTATCTCCGTTAA 60399
QY 25501 ACTCCAGAGACCTCGGGCGTAGTCTGGAATATAAATAGACGATCGGTCAATTATCG 25560
|||||
Db 60400 ACTCCAGAGACCTCGGGCGTAGTCTGGAATATAAATAGACGATCGGTCAATTATCG 60459
QY 25561 AGGTAACTCTCTGTGCGAGTTTGTGACAAATCCGCGATATGTAACGTCCTCGGAAGGT 25620
|||||
Db 60460 AGGTAACTCTCTGTGCGAGTTTGTGACAAATCCGCGATATGTAACGTCCTCGGAAGGT 60519
QY 25621 ACCTTTTCTCTATCTGTTGACAGTGTCTGTATCTGCGGATGCTGCTGCGGGGG 25680
|||||
Db 60520 ACCTTTTCTCTATCTGTTGACAGTGTCTGTATCTGCGGATGCTGCTGCGGGGG 60579
QY 25681 TGGCGCTGACAAATAGGACCAACCAAGGGGACACCCATGCAACGATATGCTTCGTA 25740
|||||
Db 60580 TGGCGCTGACAAATAGGACCAACCAAGGGGACACCCATGCAACGATATGCTTCGTA 60639

QY 25741 ATAAACAGTCTGCTGTGTGTAGTACCTGATTAAATAGTGTTCAGTAACAGTTGATGACTG 25800
|||||
Db 60640 ATAAACAGTCTGCTGTGTGTGTAGTACCTGATTAAATAGTGTTCAGTAACAGTTGATGACTG 60699
QY 25801 TTACACGACGCTACGTCGCCACAGATTCAAAAGCTGTTGAATTTCCGGCTCAGGT 25860
|||||
Db 60700 TTACACGACGCTACGTCGCCACAGATTCAAAAGCTGTTGAATTTCCGGCTCAGGT 60759
QY 25861 GCTGACACCGCGCAACGGGTCTTTCAGGGGGGTCTGGAAGTTGGTCCAGTCTTTTAA 25920
|||||
Db 60760 GCTGACACCGCGCAACGGGTCTTTCAGGGGGGTCTGGAAGTTGGTCCAGTCTTTTAA 60819
QY 25921 CGTTGTGTATGTACAGCTCCCAATGCGCTCTTGTACAGGTGTATGAACAGTCTCTTC 25980
|||||
Db 60820 CGTTGTGTATGTACAGCTCCCAATGCGCTCTTGTACAGGTGTATGAACAGTCTCTTC 60879
QY 25981 CAAAGATCCCTGATTTTCGAAAGACTGGAGTATAGCTTTGACCGCGAAGCTACGCTACT 26040
|||||
Db 60880 CAAAGATCCCTGATTTTCGAAAGACTGGAGTATAGCTTTGACCGCGAAGCTACGCTACT 60939
QY 26041 TGCCCTGATAGATCTCGAAAAAGCGATGGAGATCTCGTGGATGGACCAACACGTCG 26100
|||||
Db 60940 TGCCCTGATAGATCTCGAAAAAGCGATGGAGATCTCGTGGATGGACCAACACGTCG 60999
QY 26101 AACCAATCCGGGGTTCATCTTGAACATGACGTCGATGCCAAAGTCAGGGGTCTGTGG 26160
|||||
Db 61000 AACCAATCCGGGGTTCATCTTGAACATGACGTCGATGCCAAAGTCAGGGGTCTGTGG 61059
QY 26161 ATCACTGACGTCGCTGCTCAAAATATTAATACACGCCACCGGAAATGGGTGTGACGCC 26220
|||||
Db 61060 ATCACTGACGTCGCTGCTCAAAATATTAATACACGCCACCGGAAATGGGTGTGACGCC 61119
QY 26221 TGGCCTTCGATCCGGCTGAAGACTCCGGGGCTCTTCCGCTTAAACGTTTATCAATTA 26280
|||||
Db 61120 TGGCCTTCGATCCGGCTGAAGACTCCGGGGCTCTTCCGCTTAAACGTTTATCAATTA 61179
QY 26281 CGGGAACGCTGTGTGTGGAAGATACACAGCATATGCGCCCTGTACCAAAATTTAACT 26340
|||||
Db 61180 CGGGAACGCTGTGTGTGGAAGATACACAGCATATGCGCCCTGTACCAAAATTTAACT 61239
QY 26341 GCCGTGATCAGGGGGCGGACACCATAGCCGCACAGAACCTATCGCGTGGCTTAAAGAGCT 26400
|||||
Db 61240 GCCGTGATCAGGGGGCGGACACCATAGCCGCACAGAACCTATCGCGTGGCTTAAAGAGCT 61299
QY 26401 TCTGTCCACGATCTGACGCTTTTGGCTTTTGAAGCGGACACATCAATPATAGCCGCA 26460
|||||
Db 61300 TCTGTCCACGATCTGACGCTTTTGGCTTTTGAAGCGGACACATCAATPATAGCCGCA 61359
QY 26461 GAAAAGCTCATCAGACCGGACCGGTATCATAGACAAATTCAGCAACGAGAGCTATCGA 26520
|||||
Db 61360 GAAAAGCTCATCAGACCGGACCGGTATCATAGACAAATTCAGCAACGAGAGCTATCGA 61419
QY 26521 AGTATTTGGCGGTTATAGTGAACATTTAAGAAAGAGTTATGGCGAAAAACCAATGCGCA 26580
|||||
Db 61420 AGTATTTGGCGGTTATAGTGAACATTTAAGAAAGAGTTATGGCGAAAAACCAATGCGCA 61479
QY 26581 TGTGAGGAGCTATATCCAAAGCGAATTTTGAACCCCTGAGAGATGACCGGACGCTT 26640
|||||
Db 61480 TGTGAGGAGCTATATCCAAAGCGAATTTTGAACCCCTGAGAGATGACCGGACGCTT 61539
QY 26641 TATGACTTCCAAATATTAATGTAATCGACGAGGGCGGAACCTGTCTTACATATCA 26700
|||||
Db 61540 TATGACTTCCAAATATTAATGTAATCGACGAGGGCGGAACCTGTCTTACATATCA 61599
QY 26701 CCACCGTCTGTCTCTTTTACTGTGTTTCTTAACACGTGGCTTAATATCCCTCTTTACGCC 26760
|||||
Db 61600 CCACCGTCTGTCTCTTTTACTGTGTTTCTTAACACGTGGCTTAATATCCCTCTTTACGCC 61659
QY 26761 AGGGGGGGGTTCCGGGATATATGCGGTGGTGGCCAAAGCAGCAAAAGCGTTTCAGT 26820
|||||
Db 61660 AGGGGGGGGTTCCGGGATATATGCGGTGGTGGCCAAAGCAGCAAAAGCGTTTCAGT 61719
QY 26821 CAACTTACAAACACGAGGACGCAAAAGACGAGATATGCTCGTGGAGAACATCTTAACAT 26880


```
Db 61720 CAACCTTACACACGCGGACGCAAAAGACGAGATATCGTCGCGGAACATCTTAACAT 61779
Oy 26881 TCATGATAGGAAGAAGTGTATCTGATCTAGCTACTTGAGAGAAATGGGCGCTGT 26940
Db 61780 TCATGATAGGAAGAAGTGTATCTGATCTAGCTACTTGAGAGAAATGGGCGCTGT 61839
Oy 26941 TTATTAACAACAAGCGCTCCACCGATCTCAGTTCGGACACCTCTTAAAAATTTAGAT 27000
Db 61840 TTATTAACAACAAGCGCTCCACCGATCTCAGTTCGGACACCTCTTAAAAATTTAGAT 61899
Oy 27001 ATAACTTCCCAATTCCTGACGAAGTATAGTTAGCTAGACAGATTTGCTCCCTAAA 27060
Db 61900 ATAACTTCCCAATTCCTGACGAAGTATAGTTAGCTAGACAGATTTGCTCCCTAAA 61959
Oy 27061 GTAGATTTAGATCTTATAGATATACATTGGCTGAGCCGACCTTTTGTCCATAGCG 27120
Db 61960 GTAGATTTAGATCTTATAGATATACATTGGCTGAGCCGACCTTTTGTCCATAGCG 62019
Oy 27121 AGGTAAAGCGGTATCTTAACAAACCTACACATGTCTTAACGCTAAGGGCGCATACG 27180
Db 62020 AGGTAAAGCGGTATCTTAACAAACCTACACATGTCTTAACGCTAAGGGCGCATACG 62079
Oy 27181 AACGAAGCTCTTTACCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 27240
Db 62080 AACGAAGCTCTTTACCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 62139
Oy 27241 AACAGGGGCGGTCAACCTACACACCTACACCTGACCGGTGACCGGTGACAAAAACCT 27300
Db 62140 AACAGGGGCGGTCAACCTACACACCTACACCTGACCGGTGACCGGTGACAAAAACCT 62199
Oy 27301 TTAAGTTAAGTAAATTTTGGCAGTTTGTGACAGGACATGTCCATAGTCCACGGA 27360
Db 62200 TTAAGTTAAGTAAATTTTGGCAGTTTGTGACAGGACATGTCCATAGTCCACGGA 62259
Oy 27361 CCAGTGAAGCTTCGACCCGAGTTTACCTTATCCAGCAAGTTTGTAAAAACAGCCAGCT 27420
Db 62260 CCAGTGAAGCTTCGACCCGAGTTTACCTTATCCAGCAAGTTTGTAAAAACAGCCAGCT 62319
Oy 27421 CTTTAAATGGAACAAAAAATGATATGTGGGTTTCAGGGTACGACTTTGAGATTCA 27480
Db 62320 CTTTAAATGGAACAAAAAATGATATGTGGGTTTCAGGGTACGACTTTGAGATTCA 62379
Oy 27481 AAGAGATCTTACACAGCGACCTTCTGAGAGACGATTCGCAAGCCGTCGGGATACG 27540
Db 62380 AAGAGATCTTACACAGCGACCTTCTGAGAGACGATTCGCAAGCCGTCGGGATACG 62439
Oy 27541 TATAGGTTTCTTAAACAGCTACTGTACACGCCATGTACGCTTTCAGCGGTACGGG 27600
Db 62440 TATAGGTTTCTTAAACAGCTACTGTACACGCCATGTACGCTTTCAGCGGTACGGG 62499
Oy 27601 TGACTAGGTACACAGGAAATATCTGCAAGACCTAAATTTGCACCCCTCCGCGCGCT 27660
Db 62500 TGACTAGGTACACAGGAAATATCTGCAAGACCTAAATTTGCACCCCTCCGCGCGCT 62559
Oy 27661 TGGCAACCGGCGGTGTAGACCTTCAACCGCTTCGTGAGAGATTAAACCTGGAAGAC 27720
Db 62560 TGGCAACCGGCGGTGTAGACCTTCAACCGCTTCGTGAGAGATTAAACCTGGAAGAC 62619
Oy 27721 TCTTTCACAGGTGTGACGTCCCGCGCACCGCGGGGTATCACTCCCTCCAGGTTTGG 27780
Db 62620 TCTTTCACAGGTGTGACGTCCCGCGCACCGCGGGGTATCACTCCCTCCAGGTTTGG 62679
Oy 27781 TCGACACGTACTGCGCCCTAAAGAGAGTGTGCGCTCCAGAAATTAAGGTGGGCTGCGCT 27840
Db 62680 TCGACACGTACTGCGCCCTAAAGAGAGTGTGCGCTCCAGAAATTAAGGTGGGCTGCGCT 62739
Oy 27841 GGTTCGGCGGGAGTTTGAAGAAGAAAGCTTTTCCGCGTTTACGCTTAAACATGTCTAA 27900
Db 62740 GGTTCGGCGGGAGTTTGAAGAAGAAAGCTTTTCCGCGTTTACGCTTAAACATGTCTAA 62799
Oy 27901 GGGAGGAGTGTACTTTGTCTCCCTTCAGAACGTCTCAAGGGGCTGTGGGCTTTGCAT 27960
|||||
```

```
Db 62800 GGGAGGAGTGTACTTTGTCTCCCTTCAGAACGTCTCAAGGGGCTGTGGGCTTTGCAT 62859
Oy 27961 CGACCGTTGAATCGTATTAATAATTAAAGGGGTACACGTTTATACGGGTAGGGCTCGT 28020
Db 62860 CGACCGTTGAATCGTATTAATAATTAAAGGGGTACACGTTTATACGGGTAGGGCTCGT 62919
Oy 28021 GTACGGTTTCCACCTCAGTGTATGACCTCAGAGAAAGATGCCCTCCGTGTGTGCAGG 28080
Db 62920 GTACGGTTTCCACCTCAGTGTATGACCTCAGAGAAAGATGCCCTCCGTGTGTGCAGG 62979
Oy 28081 ACTCTACGGTTTATCGGGTGTGAGAGATTAACCAACCAATGAGCCGAACCATGG 28140
Db 62980 ACTCTACGGTTTATCGGGTGTGAGAGATTAACCAACCAATGAGCCGAACCATGG 63039
Oy 28141 AGGACGGGAGCGTTTTCAGAGTGTGCTGTCGGGGGACTATGGGGTCACTCAAAATTAG 28200
Db 63040 AGGACGGGAGCGTTTTCAGAGTGTGCTGTCGGGGGACTATGGGGTCACTCAAAATTAG 63099
Oy 28201 CCATGACCATCGTAAAGGACACAGGGAATGCTGTGAGCGAGTATGCCGTATTTGGGT 28260
Db 63100 CCATGACCATCGTAAAGGACACAGGGAATGCTGTGAGCGAGTATGCCGTATTTGGGT 63159
Oy 28261 CCCACAGAAACGTCACAGACAGCCAGCTGATGTAGCATATCAATCAAGGGCTTTAACTCA 28320
Db 63160 CCCACAGAAACGTCACAGACAGCCAGCTGATGTAGCATATCAATCAAGGGCTTTAACTCA 63219
Oy 28321 ATTATTTGGTCAATGACAGCAACCCCTTAAAACTCTCCACAGAGAACAGTGTATACA 28380
Db 63220 ATTATTTGGTCAATGACAGCAACCCCTTAAAACTCTCCACAGAGAACAGTGTATACA 63279
Oy 28381 CCTCCGCCAAGCATATATGTCGGGCTTCACACCCCAACACACACCTCATCTACTAA 28440
Db 63280 CCTCCGCCAAGCATATATGTCGGGCTTCACACCCCAACACACACCTCATCTACTAA 63339
Oy 28441 TAAATAAAAAAGCAAAATGAAAAATGTGTTTATTCAGTCCAACACAGCGCACGG 28500
Db 63340 TAAATAAAAAAGCAAAATGAAAAATGTGTTTATTCAGTCCAACACAGCGCACGG 63399
Oy 28501 ATAGTTGTATTTCCACACACCGGGGGGTGCGCCGATAGTTTGAACGACCAAGAACGCC 28560
Db 63400 ATAGTTGTATTTCCACACACCGGGGGGTGCGCCGATAGTTTGAACGACCAAGAACGCC 63459
Oy 28561 CGGGCCCTGGGTTTGAAGTATGCCCCCGCCCGGTCGAGGTATACGTCCTCTAGG 28620
Db 63460 CGGGCCCTGGGTTTGAAGTATGCCCCCGCCCGGTCGAGGTATACGTCCTCTAGG 63519
Oy 28621 GCCCTGGTGTACCAACATTAATACGTCGATACACGTTGACAGTCCCTCGGTGACGC 28680
Db 63520 GCCCTGGTGTACCAACATTAATACGTCGATACACGTTGACAGTCCCTCGGTGACGC 63579
Oy 28681 GCGCCTCTTGCAGGGCGGACGAACACGCGCCTTGTACGATGATGCAATCGTCGCT 28740
Db 63580 GCGCCTCTTGCAGGGCGGACGAACACGCGCCTTGTACGATGATGCAATCGTCGCT 63639
Oy 28741 GTCTGAAGTGAACACAGTCAATCAATCAGTGGGCGCGGCTCTCATTCGGCGCTCA 28800
Db 63640 GTCTGAAGTGAACACAGTCAATCAATCAGTGGGCGCGGCTCTCATTCGGCGCTCA 63699
Oy 28801 TTGCTCCCATGTCTCAACAGAGCGCTGGTCTGCTCACTTGTGCTCATCTGAAATTAAT 28860
Db 63700 TTGCTCCCATGTCTCAACAGAGCGCTGGTCTGCTCACTTGTGCTCATCTGAAATTAAT 63759
Oy 28861 GGTCTCTTGTCTGCAAGTGTATCAGCAACACAGGTTCTTCTCATCGGAAGACCATCC 28920
Db 63760 GGTCTCTTGTCTGCAAGTGTATCAGCAACACAGGTTCTTCTCATCGGAAGACCATCC 63819
Oy 28921 GCCCTCTGCCGTGATCTAGATATATACCTGACACAGGGGCGAGGCCGTCGGCGAATA 28980
Db 63820 GCCCTCTGCCGTGATCTAGATATATACCTGACACAGGGGCGAGGCCGTCGGCGAATA 63879
Oy 28981 GCGCTGACGTTCTCCGCCACTTCAATCACTGTCTCTGATCATCTATAAAAAATCGTC 29040
Db 63880 GCGCTGACGTTCTCCGCCACTTCAATCACTGTCTCTGATCATCTATAAAAAATCGTC 63939
```

OY	29041	TTGCGTGTCTGATTACAGATGACTGTGGGTGCGCGTGTGGCCAGTAAACCGCAACGGG	29100
Dp	63940	TTGCGTGTCTGATTACAGATGACTGTGGGTGCGCGTGTGGCCAGTAAACCGCAACGGG	63999
OY	29101	CCGGGACCAACCAAGCGGTCAAGTGGCGGGCGGCGTCGGGGGTGGTGGGACACTGT	29160
Dp	64000	CCGGGACCAACCAAGCGGTCAAGTGGCGGGCGGCGTCGGGGGTGGTGGGACACTGT	64059
OY	29161	CGAAGTAAATACCGGTAGGTAGCCGGCGGCTGTGGTTAAAGAGATCCACGCTCCGGTGC	29220
Dp	64060	CGAAGTAAATACCGGTAGGTAGCCGGCGGCGGCTGTGGTTAAAGAGATCCACGCTCCGGTGC	64119
OY	29221	CGGATCTATTCTAGAGTGGGAGAGAACCGGCGGTCTGTCTTCTTCAATCCATCACTGTGA	29280
Dp	64120	CGGATCTATTCTAGAGTGGGAGAGAACCGGCGGTCTGTCTTCTTCAATCCATCACTGTGA	64179
OY	29281	GTCGCTGTCTCCGAATGAGATGAGTGGCTGTGGCGTTTGGAGTAAAGTGGAGGGGA	29340
Dp	64180	GTCGCTGTCTCCGAATGAGATGAGTGGCTGTGGCGTTTGGAGTAAAGTGGAGGGGA	64239
OY	29341	ATCTTGCTCAAAAAACATCTCCAGGTGCAGTCAATCAATCACTGGGGGACCTCCGTAACC	29400
Dp	64240	ATCTTGCTCAAAAAACATCTCCAGGTGCAGTCAATCAATCACTGGGGGACCTCCGTAACC	64259
OY	29401	GGCGCGTACCGGCAACCCCGTACGGGAGCCGCGGCAACAAAAAGTCTTGTCTCTTTT	29460
Dp	64300	GGCGCGTACCGGCAACCCCGTACGGGAGCCGCGGCAACAAAAAGTCTTGTCTCTTTT	64359
OY	29461	CCTTAGGTGCCCCGGGAAATCGGCAGCATCTGAGAGTGGCGGCGGGGTCTTGACGGGTG	29520
Dp	64360	CCTTAGGTGCCCCGGGAAATCGGCAGCATCTGAGAGTGGCGGCGGGGTCTTGACGGGTG	64419
OY	29521	GGATTAACAAATAGCCATGGGCCCAAAAGTTCACTGTGAAAAAGCACATGGCTATCCCGAT	29580
Dp	64420	GGATTAACAAATAGCCATGGGCCCAAAAGTTCACTGTGAAAAAGCACATGGCTATCCCGAT	64479
OY	29581	CAGTTAAATATTCAGTCAACGGGCAACCCCTCCATCTCGAATGATAGTCAATTCCGCAAGT	29640
Dp	64480	CAGTTAAATATTCAGTCAACGGGCAACCCCTCCATCTCGAATGATAGTCAATTCCGCAAGT	64539
OY	29641	TTTAAATGTTTGCAGCTTAAAACTGCGGCGAGGAGAACCGGTTGCGCGGTGGCGGTA	29700
Dp	64540	TTTAAATGTTTGCAGCTTAAAACTGCGGCGAGGAGAACCGGTTGCGCGGTGGCGGTA	64599
OY	29701	GCCAGGGGAACGAGATGGCGGCTTGAGAGACAGATGTCGTGCTGCTTTATCACGCTG	29760
Dp	64600	GCCAGGGGAACGAGATGGCGGCTTGAGAGACAGATGTCGTGCTGCTTTATCACGCTG	64659
OY	29761	GCCTTGTCTATAGCGCTTCTTCCCAACAGCATAAAAAGCAGCCTCGAAGCTTGGCAGAA	29820
Dp	64660	GCCTTGTCTATAGCGCTTCTTCCCAACAGCATAAAAAGCAGCCTCGAAGCTTGGCAGAA	64719
OY	29821	AGCAGACTTATATGTAAGCTGTGAACCAATCCAGCAAGTGGCGGTGTGACCCGCG	29880
Dp	64720	AGCAGACTTATATGTAAGCTGTGAACCAATCCAGCAAGTGGCGGTGTGTGACCCGCG	64779
OY	29881	TTCCCTCTTTCACCGGTCAAGTGGGTTTAAAAAGAGAACTCCGCTTTGGCCAAAG	29940
Dp	64780	TTCCCTCTTTCACCGGTCAAGTGGGTTTAAAAAGAGAACTCCGCTTTGGCCAAAG	64839
OY	29941	TCTTAAGCAACCGGTAGAAAGAGCGGTGAACCCAGGTACAGTATGGCTATCTCTTTAAAA	30000
Dp	64840	TCTTAAGCAACCGGTAGAAAGAGCGGTGAACCCAGGTACAGTATGGCTATCTCTTTAAAA	64899
OY	30001	ATATTTTGAAGCTTGGAGGTATACTGTAGTCCGAGCAACCGTTAAAGGCTATGTCGGTG	30060
Dp	64900	ATATTTTGAAGCTTGGAGGTATACTGTAGTCCGAGCAACCGTTAAAGGCTATGTCGGTG	64959
OY	30061	GCTTGACCGGAGTGAAGATCTCTGGCCAAAGATACAGACTTAAATATCTCCGGTTGG	30120
Dp	64960	GCTTGACCGGAGTGAAGATCTCTGGCCAAAGATACAGACTTAAATATCTCCGGTTGG	65019

QY	30121	CAACAATACGACCAACCAATTAATCTATCTATCGGGGAAATATCAGCTTACGTTGC	30108
Db	65020	CAACAATAAGCAACCAACCAATTAATCTATCTATCGGGGAAATATCAGCTTACGTTGC	65079
QY	30181	ATATCCATTAACGGCCTTCACACAGACGCCGACGCTTCGTTTAAATAATGAGAAAGATT	30240
Db	65080	ATATCCATTAACGGCCTTCACACAGACGCCGACGCTTCGTTTAAATAATGAGAAAGATT	65139
QY	30241	AAAAATTCAGGCCATGAGTGGCTAAGTAGACAGCTTGTGTGGAGGGTTCCTTAACACT	30300
Db	65140	AAAAATTCAGGCCATGAGTGGCTAAGTAGACAGCTTGTGTGGAGGGTTCCTTAACACT	65199
QY	30301	TCGTGGTACATTTTACTTCACAACTATTGTTTAAAGCCAAACCTTCCTTAATCCCGCGTC	30360
Db	65200	TCGTGGTACATTTTACTTCACAACTATTGTTTAAAGCCAAACCTTCCTTAATCCCGCGTC	65259
QY	30361	TGGTAATTTACTTTCACGTATACGTGAACCTTTTACTCTGTGTGAATAATCCAAACGAG	30420
Db	65260	TGGTAATTTACTTTCACGTATACGTGAACCTTTTACTCTGTGTGAATAATCCAAACGAG	65319
QY	30421	GTGGCCCGCGATAAGACAGTTCGCGTTTCACTACCGTTTATGTGAAGTCTTCAAACTCGG	30480
Db	65320	GTGGCCCGCGATAAGACAGTTCGCGTTTCACTACCGTTTATGTGAAGTCTTCAAACTCGG	65379
QY	30481	CTAAAAAATCTATCAAGCACTATTGGCATATATATTCACAACTTAAGACTCTTCTGTGGGA	30540
Db	65380	CTAAAAAATCTATCAAGCACTATTGGCATATATATTCACAACTTAAGACTCTTCTGTGGGA	65439
QY	30541	CACGTGAATTTAATCTGTACAAAATCGCTTAAAAAAAGCCGTAAGGTGAATCCATTTTA	30600
Db	65440	CACGTGAATTTAATCTGTGTACAAAATCGCTTAAAAAAAGCCGTAAGGTGAATCCATTTTA	65499
QY	30601	CACATATTTCTGTGGTGTAGACGATCAAGCTTATATGCAATGTTGCTGTACACAGCCCTG	30660
Db	65500	CACATATTTCTGTGGTGTAGACGATCAAGCTTATATGCAATGTTGCTGTACACAGCCCTG	65559
QY	30661	GACATTAAGCTAAATTTGTTAAATGAAGAAGCAATCTCAAAAGCCTCCGGAATATTA	30720
Db	65560	GACATTAAGCTAAATTTGTTAAATGAAGAAGCAATCTCAAAAGCCTCCGGAATATTA	65619
QY	30721	AGTCACATAGGGATTAATTTTCAACATAGGATTTCTACAAACCGCGGTACCAATGTAA	30780
Db	65620	AGTCACATAGGGATTAATTTTCAACATAGGATTTCTACAAACCGCGGTACCAATGTAA	65679
QY	30781	TTAAAAAAAATCCACATGTATAATTAATTAAGGTATATGCATCTTCTCATGTTTTTAA	30840
Db	65680	TTAAAAAAAATCCACATGTATAATTAATTAAGGTATATGCATCTTCTCATGTTTTTAA	65739
QY	30841	CATATATATGAACGCTAATGCTGTACTTATATTAATGTATAGAAATATGCCAATACAGTC	30900
Db	65740	CATATATATGAACGCTAATGCTGTACTTATATTAATGTATAGAAATATGCCAATACAGTC	65799
QY	30901	ATGTGAATGATTTTAAAGGCATTAATGCCAAACATCAATTAATTAACAAAAATGACCGC	30960
Db	65800	ATGTGAATGATTTTAAAGGCATTAATGCCAAACATCAATTAATTAACAAAAATGACCGC	65859
QY	30961	TTCCGGAATATCCGCCAGCTGTATTAACCCGAATAATACGAATGTACTACAAACACACCT	31020
Db	65860	TTCCGGAATATCCGCCAGCTGTATTAACCCGAATAATACGAATGTACTACAAACACACCT	65919
QY	31021	GAACCAATTTTATCTCAACATATGCAACAAATATTTCAAGGGTAACACCATGTTAATTA	31080
Db	65920	GAACCAATTTTATCTCAACATATGCAACAAATATTTCAAGGGTAACACCATGTTAATTA	65979
QY	31081	ATACGACGATGACATTTTATAGTAAAGTCTCTCAAGACAAATTTCTCTCAATTGATG	31140
Db	65980	ATACGACGATGACATTTTATAGTAAAGTCTCTCTCAAGACAAATTTCTCTCAATTGATG	66039
QY	31141	ACTCATCAACCTGGGTTCCGCTGTATATGTGCGAAATATATGTAGGTCCAGAGTACCCTCGT	31200
Db	66040	ACTCATCAACCTGGGTTCCGCTGTATATGTGCGAAATATATGTAGGTCCAGAGTACCCTCGT	66099
QY	31201	CATGCCACAAATTAATTTCCAGGGCTGTAAATATATCATCCAGTGAATCAGCTGCTAATG	31260

```
Db 66100 CATGCCCAAAATTAATTCAGGGCTGTAAATATCAATCCAGTAATACGTGCTAATG 66159
Qy 31261 TCAAGATGTTGTTCTAATTTTAAAGCCATCCAAATGGTGAAGTGGTACACTTTGGGAC 31320
Db 66160 TCAAGATGTTGTTCTAATTTTAAAGCCATCCAAATGGTGAAGTGGTGAACACTTTGGGAC 66219
Qy 31321 AAGACCCCGTAAATTTGGCAGCTCCACAAAGGAGATGATTTGATCGTTCAGCA 31380
Db 66220 AAGACCCCGTAAATTTGGCAGCTCCACAAAGGAGATGATTTGATCGTTCAGCA 66279
Qy 31381 GGGGAGCATTTTATTTTAAATACATGAGAACCGGACCGGTCAATGACGACATATG 31440
Db 66280 GGGGAGCATTTTATTTTAAATACATGAGAACCGGACCGGTCAATGACGACATATG 66339
Qy 31441 CCATTAGATTGAGTCTGTCGACTGTTGAATGACGTGAAAAAAATGATTTCTGT 31500
Db 66340 CCATTAGATTGAGTCTGTCGACTGTTGAATGACGTGAAAAAAATGATTTCTGT 66399
Qy 31501 CACATGCTACTATTTTAAACACAGAGGGCGGAATTAACGGTCCCGGCGTAA 31560
Db 66400 CACATGCTACTATTTTAAACACAGAGGGCGGAATTAACGGTCCCGGCGTAA 66459
Qy 31561 GGCGGTGATGGGACGAGCGCTCATTTGCCATTTCAGATTTGTTAAATCTGTGAA 31620
Db 66460 GGCGGTGATGGGACGAGCGCTCATTTGCCATTTCAGATTTGTTAAATCTGTGAA 66519
Qy 31621 CATACGAGTCTAAATCAAGTATAACACAGACAAAGTTCAAAACGAGGCAACGCGCTGG 31680
Db 66520 CATACGAGTCTAAATCAAGTATAACACAGACAAAGTTCAAAACGAGGCAACGCGCTGG 66579
Qy 31681 TTTCCACCCGAGCATCCCGCTCCACAAACCCGAACTCTCTAGGAACGACATCAAAAGGT 31740
Db 66580 TTTCCACCCGAGCATCCCGCTCCACAAACCCGAACTCTCTAGGAACGACATCAAAAGGT 66639
Qy 31741 TCAGACAAATTCGGAACCAAAACCCAGTCTTACAGCACCATCGTTAAATCTGTGAG 31800
Db 66640 TCAGACAAATTCGGAACCAAAACCCAGTCTTACAGCACCATCGTTAAATCTGTGAG 66699
Qy 31801 TTAAGAGCAGAGCGGCCACACACTGCTCTGTGAGATTCAGTTAGTGGCTGCAGG 31860
Db 66700 TTAAGAGCAGAGCGGCCACACACTGCTCTGTGAGATTCAGTTAGTGGCTGCAGG 66759
Qy 31861 CTTGCTGACAGCCGCTAGCTGCTGGGGGCTGCGCCGACCTTTGAACGCCGACGCCA 31920
Db 66760 CTTGCTGACAGCCGCTAGCTGCTGGGGGCTGCGCCGACCTTTGAACGCCGACGCCA 66819
Qy 31921 GTTCAGAGCAGAGCGAGAGGCTCTTGCAGTCGCGCCATATCTCGGCCATAGAGAT 31980
Db 66820 GTTCAGAGCAGAGCGAGAGGCTCTTGCAGTCGCGCCATATCTCGGCCATAGAGAT 66879
Qy 31981 CGCTGCGGTATCTTTTAGTGATATATCTGTTGGTAACAAACCTCACTCCCTGA 32040
Db 66880 CGCTGCGGTATCTTTTAGTGATATATCTGTTGGTAACAAACCTCACTCCCTGA 66939
Qy 32041 AAAAGGGAATAGGTCCTTTCTATCGTTTCTCGAATCTATATGTACATCTTAA 32100
Db 66940 AAAAGGGAATAGGTCCTTTCTATCGTTTCTCGAATCTATATGTACATCTTAA 66999
Qy 32101 GTATACCAAGAGCGCTAAACCAAGATGTGACACCTTTAAATAATGCAAAACCG 32160
Db 67000 GTATACCAAGAGCGCTAAACCAAGATGTGACACCTTTAAATAATGCAAAACCG 67059
Qy 32161 ACCGATGCTATATCCGCTTTCATGTCGTTCAAAAGTAGTCAGATGATCTCAGT 32220
Db 67060 ACCGATGCTATATCCGCTTTCATGTCGTTCAAAAGTAGTCAGATGATCTCAGT 67119
Qy 32221 TAGACTGCTCTCCCTGTTAAACCCCTTAATCTGAGATGAAACGCAATGACCGTGA 32280
Db 67120 TAGACTGCTCTCCCTGTTAAACCCCTTAATCTGAGATGAAACGCAATGACCGTGA 67179
Qy 32281 CTTCCTGATCTCTTAATACTTAACCCGGAACGAGTAAATCCATGATGCTGCACCC 32340
Db 67180 CTTCCTGATCTCTTAATACTTAACCCGGAACGAGTAAATCCATGATGCTGCACCC 67239
Qy 32341 CTACCCCAAGCAGCCGCCCTGACTATTAGACAGAGGTGAGTAACACGCTATCTTAA 32400
Db 67240 CTACCCCAAGCAGCCGCCCTGACTATTAGACAGAGGTGAGTAACACGCTATCTTAA 67299
Qy 32401 AAACCATACGTGGAGTTTGTAAAGTAAACAGCTGTGTATTTTCAACGCCCTGTCTA 32460
Db 67300 AAACCATACGTGGAGTTTGTAAAGTAAACAGCTGTGTATTTTCAACGCCCTGTCTA 67359
Qy 32461 AAATGATACGACACATCAATCAATTAACCTTTTATCAAGATTCAGAGGCGC 32520
Db 67360 AAATGATACGACACATCAATCAATTAACCTTTTATCAAGATTCAGAGGCGC 67419
Qy 32521 TGTTTACAGTGTGTAGTGGAGCATATCTGCCAATGGGAATGGCTGATGATCAACA 32580
Db 67420 TGTTTACAGTGTGTAGTGGAGCATATCTGCCAATGGGAATGGCTGATGATCAACA 67479
Qy 32581 CTTAGTGTGGATAGGTGCTCTGTGACTTTACTAGTGGCGATGAACCTAAATTTGGC 32640
Db 67480 CTTAGTGTGGATAGGTGCTCTGTGACTTTACTAGTGGCGATGAACCTAAATTTGGC 67539
Qy 32641 GTGTTAGTGTGTACCAACCAAAACCTGCGGCTGCGCTTTAGAAAGCTATGCA 32700
Db 67540 GTGTTAGTGTGTACCAACCAAAACCTGCGGCTGCGCTTTAGAAAGCTATGCA 67599
Qy 32701 GCTTTAATCTGTGTCATATGCTTCTTTAAATGCAATCTGTGATCTTTAAGCA 32760
Db 67600 GCTTTAATCTGTGTCATATGCTTCTTTAAATGCAATCTGTGATCTTTAAGCA 67659
Qy 32761 GTGGTCAAAAAAAGATTTAAACAGTTAAACAGTTAAACAGTTAAACAGTTAAAC 32820
Db 67660 GTGGTCAAAAAAAGATTTAAACAGTTAAACAGTTAAACAGTTAAACAGTTAAAC 67719
Qy 32821 TATATACCTCTCTCAACAAAGAAAAATTTTAAACCAACTGCGAGTACTGAACAT 32880
Db 67720 TATATACCTCTCTCAACAAAGAAAAATTTTAAACCAACTGCGAGTACTGAACAT 67779
Qy 32881 GGTACGACAGAGTCTGTAAGATGTCTATCATCTCTTCACTCCCTTTGAAGTTTG 32940
Db 67780 GGTACGACAGAGTCTGTAAGATGTCTATCATCTCTTCACTCCCTTTGAAGTTTG 67839
Qy 32941 GTTACAGCAGCATGTGATAGCAGCAGCAGCAGGAGGAGTGGATGAGAGGGGT 33000
Db 67840 GTTACAGCAGCATGTGATAGCAGCAGCAGCAGGAGGAGTGGATGAGAGGGGT 67889
Qy 33001 AAACATTCGTGGGCTGGGGGACTCCAGTTTAAAGATCTCCGAGGACGCTACGAGT 33060
Db 67900 AAACATTCGTGGGCTGGGGGACTCCAGTTTAAAGATCTCCGAGGACGCTACGAGT 67959
Qy 33061 TCTTCGTCAAATCTACGACGCGCATCCACACAGGGCAGTACTGATTAATAGTCC 33120
Db 67960 TCTTCGTCAAATCTACGACGCGCATCCACACAGGGCAGTACTGATTAATAGTCC 68019
Qy 33121 CGAATTCATGTCGTAAATTTTGGAGGCTCTTAAACAGTAACCATGTGCTCGCA 33180
Db 68020 CGAATTCATGTCGTAAATTTTGGAGGCTCTTAAACAGTAACCATGTGCTCGCA 68079
Qy 33181 CACTGCGGTACGATCAACCGCTCTCTGTCTGTGTTTCATAGAGCAGCTGAGTATCTTA 33240
Db 68080 CACTGCGGTACGATCAACCGCTCTCTGTCTGTGTTTCATAGAGCAGCTGAGTATCTTA 68139
Qy 33241 GACAGATTAAGGCGCGTTCACACTTAAGGTTGCCCTGTGTGAGAGCGATTCGGGCA 33300
Db 68140 GACAGATTAAGGCGCGTTCACACTTAAGGTTGCCCTGTGTGAGAGCGATTCGGGCA 68199
Qy 33301 TTGAGAGTCATGTGTATTTCAACCGCATATCATGCCGATGGCGGATATGGAATTTG 33360
Db 68200 TTGAGAGTCATGTGTATTTCAACCGCATATCATGCCGATGGCGGATATGGAATTTG 68259
Qy 33361 TACATATGATTTAAAGATGCTTCCCGTAATGAGCAGCATGATGCTGTTTAAAGT 33420
Db 68260 TACATATGATTTAAAGATGCTTCCCGTAATGAGCAGCATGATGCTGTTTAAAGT 68319
```

QY 33421 TCACAGGGGTGTTAAAAAACTCAGAGAGTCTGCTGGACAATTGCGGAGCTCCGAA 33480
 Db 68920 TCACAGGGGTGTTAAAAAACTCAGAGAGTCTGCTGGACAATTGCGGAGCTCCGAA 68979
 QY 33481 CCGCTCAGGGATTAAGCTGTACACAGCGGTGCTTTATTAACGAAGCATACGTCAAAAA 33540
 Db 68980 CCGCTCAGGGATTAAGCTGTACACAGCGGTGCTTTATTAACGAAGCATACGTCAAAAA 68939
 QY 33541 CATACCCACGCTGACCTAAATAAGCTCACAGAAAGCTGTGATGATGTAATGAA 33600
 Db 68440 CATACCCACGCTGACCTAAATAAGCTCACAGAAAGCTGTGATGATGTAATGAA 68499
 QY 33601 TGTGCTCCCTCGGGTCCCATCTCGGGCTCATCCGAGATGTAATCTTTAACTGTTTC 33660
 Db 68550 TGTGCTCCCTCGGGTCCCATCTCGGGCTCATCCGAGATGTAATCTTTAACTGTTTC 68559
 QY 33661 TGCCTACCGGGGTTCCTCCGGTTAAAAACCCGCGGGGCGCCACCTGTAACTGTCCTGC 33720
 Db 68560 TGCCTACCGGGGTTCCTCCGGTTAAAAACCCGCGGGGCGCCACCTGTAACTGTCCTGC 68619
 QY 33721 GCACAAATGCGCCGAGGCGATGTAATCTACCGAGAGGCGCTTTGTTGTAACGAA 33780
 Db 68620 GCACAAATGCGCCGAGGCGATGTAATCTACCGAGAGGCGCTTTGTTGTAACGAA 68679
 QY 33781 AAGATGTTCAATAGCTGCTGCTGAGCGGGGTGCTTATACCGCCCAAGTTGGCCAGAGTT 33840
 Db 68680 AAGATGTTCAATAGCTGCTGCTGAGCGGGGTGCTTATACCGCCCAAGTTGGCCAGAGTT 68739
 QY 33841 CTGCACGACGCTACGCGGAAATGAAGGCCAAGTGTGGGGCGTGGCGTCTCATTA 33900
 Db 68740 CTGCACGACGCTACGCGGAAATGAAGGCCAAGTGTGGGGCGTGGCGTCTCATTA 68799
 QY 33901 TGTGACGCGGGGCTATCATGGCTATGCGGAGCTGCGGCTGACCTAATAACCTG 33960
 Db 68800 TGTGACGCGGGGCTATCATGGCTATGCGGAGCTGCGGCTGACCTAATAACCTG 68859
 QY 33961 GATGCGGAGGGAATGGAATCTAGACTCAAGCACTGTGCAAACTGTTTTCACACC 34020
 Db 68860 GATGCGGAGGGAATGGAATCTAGACTCAAGCACTGTGCAAACTGTTTTCACACC 68919
 QY 34021 ATCTTTCTTCAAGAAATCTTAAGCCCTATGCACTACTGCGCAACGGGAGAGTGTCT 34080
 Db 68920 ATCTTTCTTCAAGAAATCTTAAGCCCTATGCACTACTGCGCAACGGGAGAGTGTCT 68979
 QY 34081 GACAAATTAATTTACATCACCGGTACGCGCGAGAAAGGCGCCGTGCTGACTGGAAGT 34140
 Db 68980 GACAAATTAATTTACATCACCGGTACGCGCGAGAAAGGCGCCGTGCTGACTGGAAGT 69039
 QY 34141 ACTAGCGGATGACGTGTCCGGGAAGCAGCCTGTGCCGATTCCTTAATCTGCAAGTA 34200
 Db 69040 ACTAGCGGATGACGTGTCCGGGAAGCAGCCTGTGCCGATTCCTTAATCTGCAAGTA 69099
 QY 34201 TGGCAACCGGGGCTTTCGCCGCAACCCCTGCTGACCTCAATGTTTGAAGAAATCCA 34260
 Db 69100 TGGCAACCGGGGCTTTCGCCGCAACCCCTGCTGACCTCAATGTTTGAAGAAATCCA 69159
 QY 34261 GAATATCATCTCAGCGCCGACCCCTGAGTCAATTTGTCACAAACACGACCCGAGT 34320
 Db 69160 GAATATCATCTCAGCGCCGACCCCTGAGTCAATTTGTCACAAACACGACCCGAGT 69219
 QY 34321 CTGCGCTAGTCAGTCAGATTAATTAAGCCCAACGAGGCGTGTCCCGGCAATGTTT 34380
 Db 69220 CTGCGCTAGTCAGTCAGATTAATTAAGCCCAACGAGGCGTGTCCCGGCAATGTTT 69279
 QY 34381 ATGACACAGTGAAGAGGGGTGTCAAGAGCATTCACACGACGACAGCCCTATTTTG 34440
 Db 69280 ATGACACAGTGAAGAGGGGTGTCAAGAGCATTCACACGACGACAGCCCTATTTTG 69339
 QY 34441 GCCGCGCACTAACCGGTTGACATCTGCGGCCCTGGCCGCAATATGCAATGTTCCCA 34500
 Db 69340 GCCGCGCACTAACCGGTTGACATCTGCGGCCCTGGCCGCAATATGCAATGTTCCCA 69399

QY 34501 GTTCCGCGCACGCTCCGAGAGTGGAAGGGTCCGCGGGCGTGCATTTGCGGGAACACAGA 34560
 Db 69400 GTTCCGCGCACGCTCCGAGAGTGGAAGGGTCCGCGGGCGTGCATTTGCGGGAACACAGA 69459
 QY 34561 TGCCTCCGACAGCCCGGTTAACCCCAATGTCCTCCGCAAGAGAGATGGAACGGTACA 34620
 Db 69460 TGCCTCCGACAGCCCGGTTAACCCCAATGTCCTCCGCAAGAGAGATGGAACGGTACA 69519
 QY 34621 CAGTTGGGAACGCTCCGTAATAAAGTCCACATTCGAGGCGCGGTATACGTCCTCATG 34680
 Db 69520 CAGTTGGGAACGCTCCGTAATAAAGTCCACATTCGAGGCGCGGTATACGTCCTCATG 69579
 QY 34681 GTTATATATACCAATTAATAGACTTAACGTCCTCCGTCAGGGTCCGCGCAAGATCCGCGCAT 34740
 Db 69580 GTTATATATACCAATTAATAGACTTAACGTCCTCCGTCAGGGTCCGCGCAAGATCCGCGCAT 69639
 QY 34741 ATGCGCAACACTCCAGAGTCCCGCATGGCGGGCGCTCTCCGCCCTTGCCGAAACGCC 34800
 Db 69640 ATGCGCAACACTCCAGAGTCCCGCATGGCGGGCGCTCTCCGCCCTTGCCGAAACGCC 69699
 QY 34801 GCACGGTCCCGCTAAGAGAAAGCAGCAGCGGAGGAGCGTGGCAACAAAGACTGAG 34860
 Db 69700 GCACGGTCCCGCTAAGAGAAAGCAGCAGCGGAGGAGCGTGGCAACAAAGACTGAG 69759
 QY 34861 GCGCAGCTTCGGGGCGCGCAACAGTAACCACTTTCGCGGAGCGTCCGCGATGCGC 34920
 Db 69760 GCGCAGCTTCGGGGCGCGCAACAGTAACCACTTTCGCGGAGCGTCCGCGATGCGC 69819
 QY 34921 GTTCCGACGACAGGGCTTAATGATTTAATGCAAGGCTCCACGATTAACCGCGAAGCA 34980
 Db 69820 GTTCCGACGACAGGGCTTAATGATTTAATGCAAGGCTCCACGATTAACCGCGAAGCA 69879
 QY 34981 TCTGACCCCAAAAGCAGCAGCATGCTAGCGGCTATCTACAGGACCTGTATGACTA 35040
 Db 69880 TCTGACCCCAAAAGCAGCAGCATGCTAGCGGCTATCTACAGGACCTGTATGACTA 69939
 QY 35041 CAGTCCCGCCCGGCATGATTCCTCCCTCCAGCAACTCGCAATGAGAGATATTTCCA 35100
 Db 69940 CAGTCCCGCCCGGCATGATTCCTCCCTCCAGCAACTCGCAATGAGAGATATTTCCA 69999
 QY 35101 G 35101
 Db 70000 G 70000

RESULT 3
 ID AAI64297 standard; DNA; 524 BP.
 AAI64297;
 22-APR-2002 (first entry)
 JMW Orf24 nucleotide sequence from cosmid 3 fragment 3 SP6.
 RRV; rhesus rhadinovirus; Japanese macaque virus; multiple sclerosis;
 JMW; cytostatic; antileukemic; antiallergic; dermatological;
 inflammatory; gene therapy; leucopenia; thrombocytopenia;
 inflammatory disease; asthma; allergy; dermatitis; ds.
 Japanese macaque herpesvirus.
 OS
 XX
 XX
 FH Key Location/Qualifiers
 FT CDS 3..524
 FT /tag= a
 FT /partial
 FT /note= "no start or stop codon present"
 PN MO200188203-A1.
 XX
 XX 22-NOV-2001.
 XX 17-MAY-2001; 2001WO-US16274.
 PP

```

XX 18-MAY-2000; 2000US-205652P.
PR (UYOR-) UNIV OREGON HEALTH SCI.
XX
XX Wong SW, Axthelm MK;
PI
XX MPI: 2002-075323/10.
DR P-PSDB: AAG78585.
XX
XX New Japanese macaque virus (JMHV) and nucleic acid sequences of open
PT reading frames in virus, useful for producing animal models for
PT assessing efficacy of drugs for treatment or prevention of multiple
PT sclerosis
XX
XX Claim 9; Page 68-69; 175pp; English.
XX
XX The invention relates to an isolated virus (Japanese macaque virus (JMHV)
CC as deposited with ATCC as deposit accession number PTA-1884. Non-human
CC primate models infected with the new virus are useful for testing the
CC efficacy of a drug for treating a condition associated with JMHV,
CC preferably a drug used to treat multiple sclerosis. This involves
CC administering the drug to a non-human primate infected with JMHV and
CC observing the non-human primate to determine if the drug prevents or
CC reduces the presentation of one or more symptoms associated with JMHV
CC infection. Methods of the invention are also useful for testing the
CC efficacy of candidate vaccine against JMHV infection, or conditions
CC associated with JMHV infection e.g., multiple sclerosis. Methods of the
CC invention are useful for diagnosing the presence of JMHV or a related
CC virus in a biological specimen. JMHV genome possesses an interleukin
CC (IL)-6 gene which encodes IL-6 proteins. The IL-6 proteins may be used
CC to induce stimulation of haematopoietic stem cells to enhance
CC proliferation, differentiation and terminal maturation of erythroid
CC cells from haematopoietic cells. Thus, JMHV IL-6 may be used in vivo or
CC ex vivo to treat diseases involving leukopenia or thrombocytopenia.
CC The JMHV IL-6 may also be used to stimulate growth of megakaryocytes
CC and platelets, and for the inhibition of tumour growth and for treating
CC leukemia. Additionally, JMHV IL-6 may be used for research, diagnostic
CC purposes, to produce antibodies for diagnostic purposes to diagnose
CC diseases characterized by increased or decreased production of IL-6,
CC and as a targeting molecule for identifying cells with receptors for
CC IL-6, etc. The JMHV macrophage inflammatory protein (MIP protein) is
CC useful for treating wounds and other inflammatory diseases including
CC asthma, allergies and dermatitis. They are also useful for producing
CC antibodies for diagnostic purposes, and as a targeting molecule for
CC identifying cells with receptors for MIP, etc. Nucleic acids encoding
CC the JMHV proteins are useful in gene therapy techniques for treating
CC the above mentioned conditions. The current sequence represents the
CC JMHV Orf21 nucleotide sequence from cosmid 3 fragment 3 SP6. The function
CC of Orf 24 is unknown.
XX
XX Sequence 524 BP; 157 A; 134 C; 104 G; 129 T; 0 other;
SQ
XX
XX Query Match 0.2%; Score 66; DB 24; Length 524;
XX Best Local Similarity 100.0%; Pred. No. 5,3e-17;
XX Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

XX Human glycerol-3-phosphate dehydrogenase cDNA SEQ ID NO:13.
DE
XX
XX Human: glycerol-3-phosphate dehydrogenase; enzyme;
KW tumour; lipid associated gene; lipid metabolism; lipid synthesis;
XX chromosome 2q24.1; gene; ss.
XX
XX Homo sapiens.
OS
XX
XX WO200227028-A1.
PN
XX
XX 04-APR-2002.
PD
XX
XX 27-SEP-2001; 2001WO-US30366.
PF
XX
XX 28-SEP-2000; 2000US-0676052.
PR
XX
XX (ATAI-) ATAIRGIN TECHNOLOGIES INC.
PA
XX Skinner MK, Patton JL, Chaudhary J;
PI
XX
XX MPI: 2002-402054/43.
DR
XX
XX Identifying tumor characteristics in a tissue sample taken from a
PT patient, involves determining the copy number or expression level of
PT genes associated with lipid metabolism, synthesis or action
XX
XX Example 1; Page 72; 113pp; English.
PS
XX
XX The present invention describes a method for identifying tumour
CC characteristics, comprising measuring a copy number or expression level
CC of at least two genes associated with lipid metabolism, synthesis, or
CC action in cells from a patient tissue sample, and comparing the results
CC with a copy number or expression level of the genes in a normal cell.
CC Also described is an array of nucleic acid polymers immobilised on a
CC solid support, comprising a solid support, at least two different nucleic
CC acid polymers which are each specific for a different gene associated
CC with lipid metabolism, synthesis or action, where each nucleic acid
CC polymer is located at a predetermined position on the solid support, and
CC the array comprises nucleic acid polymers which are specific for less
CC than 100 genes other than the selected genes. The method is useful for
CC determining tumour characteristics in a tissue sample taken from a
CC patient. The present sequence represents a human lipid-associated gene
CC related cDNA sequence, which is used in the exemplification of the
CC present invention.
XX
XX Sequence 1606 BP; 402 A; 372 C; 449 G; 383 T; 0 other;
SQ
XX
XX Query Match 0.1%; Score 24; DB 24; Length 1606;
XX Best Local Similarity 100.0%; Pred. No. 19;
XX Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

XX
XX 3118 GCACGTGATTTGATTATTAATACATATTTGTAAGAAACGAGATTTGAAGTTGTCG 3177
DB 203 GCACGTGATTTGATTTGATTAATACATATTTGTAAGAAACGAGATTTGAAGTTGTCG 144
OY 3178 TAAACT 3183
DB 143 TAAACT 138

```

```

XX
XX 8723 GCTGGGCTCGGGGACACCTGTCGTC 8746
DB 98 GCTGGGCTCGGGGACACCTGTCGTC 121
OY
DB
XX
XX AADA2098;
XX
XX 04-NOV-2002 (first entry)
DE
XX
XX Poly adenosine diphosphate-ribose glycohydrolase (PARG) gene.
XX
XX Poly adenosine diphosphate-ribose glycohydrolase; PARC; enzyme;
KW ADP-ribose; neoplastic disorder; genotoxic oxidative stress; neurotoxic;
KW cardiac disorder; neuronal disorder; reperfusion injury; neurotoxicity;
KW Alzheimer's disease; Huntington's disease; Parkinson's disease; cardiac;
KW cytostatic; vasotropic; neuroprotective; anticonvulsant; gene therapy;
KW antisense therapy; gene; ds.

```

OS	Caenorhabditis elegans.
XX	Location/Qualifiers
XH	Key
FH	CDS
FT	/tag- a
FT	3591..9540
FT	/product- "CEPARG"
FT	3591..3635
FT	/tag- b
FT	/number- 1
FT	3636..3680
FT	/tag- c
FT	3681..4121
FT	/tag- d
FT	/number- 2
FT	4122..5064
FT	/tag- e
FT	5065..5235
FT	/tag- f
FT	/number- 3
FT	5236..5929
FT	/tag- g
FT	5930..6152
FT	/tag- h
FT	/number- 4
FT	6153..6199
FT	/tag- i
FT	6200..6267
FT	/tag- j
FT	/number- 5
FT	6268..7245
FT	/tag- k
FT	7246..7338
FT	/tag- l
FT	/number- 6
FT	7339..7385
FT	/tag- m
FT	7386..7553
FT	/tag- n
FT	/number- 7
FT	7554..7737
FT	/tag- o
FT	7738..7853
FT	/tag- p
FT	/number- 8
FT	7854..8152
FT	/tag- q
FT	8153..8435
FT	/tag- r
FT	/number- 9
FT	8436..8486
FT	/tag- s
FT	8487..8610
FT	/tag- t
FT	/number- 10
FT	8611..8661
FT	/tag- u
FT	8662..8952
FT	/tag- v
FT	/number- 11
FT	8953..9382
FT	/tag- w
FT	9383..9540
FT	/tag- x
FT	/number- 12
XX	US6395543-B1.
XX	
XX	28-MAY-2002.
PD	
XX	23-FEB-2000; 200005-05113507.
EP	
XX	01-MAY-1998; 9805-083768P.

PR	30-APR-1999;	99U5-0302812.
XX	(KENT) UNIV KENTUCKY RES FOUND.	
PA	Jacobson MK, Jacobson EL, Ame J, Lin W;	
XX	WPI: 2002-535664/57.	
DR	P-PSDB: AAE25633.	
PT	New nucleic acid molecule encoding bovine poly adenosine	
PT	diphosphate-ribose glycohydrolase involved in cellular response to DNA	
PT	damage, inhibition of which is useful for treating neoplastic disorders	
XX	and neurodegenerative diseases	
PS	Example 14; Column 89-116; 77pp; English.	
XX	The invention relates to an isolated nucleic acid molecule which encodes	
CC	a bovine poly (adenosine diphosphate (ADP)-ribose) glycohydrolase (bPARG)	
CC	which catalyzes release of ADP-ribose from an ADP ribose polymer. The	
CC	invention is useful as probes and primer molecules that can used in	
CC	hybridisation assays and polymerase chain reaction (PCR) amplification.	
CC	The knowledge of the nucleotide sequence of the PARC gene permits the	
CC	preparation of antisense therapeutics containing sequences complementary	
CC	to the mRNA of PARC gene. The antisense therapeutic are useful to treat	
CC	neoplastic disorders and conditions caused by genotoxic oxidative stress	
CC	e.g., cardiac disorders, neuronal disorders, reperfusion injury,	
CC	neurotoxicity, Alzheimer's disease, Huntington's disease and Parkinson's	
CC	disease. The invention is useful in gene therapy and antisense therapy.	
XX	The present sequence is CePARC gene.	
SQ	Sequence 29793 BP; 9945 A; 4952 C; 5003 G; 9893 T; 0 other:	
Query Match	0.1%; Score 24; DB 24; Length 29793;	
Best Local Similarity	100.0%; Pred. No. 15;	
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
Oy	11807 AGTAAAAACCTAGTTGATTGTCTCA 11830 	
Db	21745 AGTAAAAAACCTAGTTGATTGTCTCA 21722	
<hr/>		
RESULT 6		
ID	ABK14930/C	
XX	ABK14930 standard; DNA; 29793 BP.	
AC		
XX	ABK14930;	
DT	08-MAY-2002 (first entry)	
XX		
DE	Worm poly(ADP-ribose) glycohydrolase (PARC) sequence from cosmid F20C5.	
XX		
KW	Worm; poly(ADP-ribose).glycohydrolase; PARC; PARC modulator;	
KW	ADP-ribose; adenosine diphosphate-ribose; DNA repair; apoptosis;	
KW	neoplasia; inherited genetic disease; myocardial infarction; cancer;	
KW	vascular stroke; aging; neurodegeneration; Huntington's disease;	
KW	Parkinson's disease; Alzheimer's disease; neurotoxicity; gene; ds.	
XX		
OS	Caenorhabditis elegans.	
XX		
FH	Key	Location/Qualifiers
FT	CDS	3591..9540
FT		/tag= a
FT		/product= "Worm poly(ADP-ribose) glycohydrolase (PARC)"
FT	exon	3591..3635
FT		/tag= b
FT		/number= 1
FT	Intron	3636..3680
FT		/tag= c
FT		/number= 1
FT	exon	3681..4121
FT		/tag= d
FT		/number= 2
FT	Intron	4122..5064

FT	/tag= h
FT	/number= 4
FT	6153..6199
FT	Intron
FT	/tag= i
FT	/number= 4
FT	6200..6267
FT	exon
FT	/tag= j
FT	/number= 5
FT	6268..7245
FT	Intron
FT	/tag= k
FT	/number= 5
FT	7246..7338
FT	exon
FT	/tag= l
FT	/number= 6
FT	7339..7385
FT	Intron
FT	/tag= m
FT	/number= 6
FT	7386..7553
FT	exon
FT	/tag= n
FT	/number= 7
FT	7554..7737
FT	Intron
FT	/tag= o
FT	/number= 7
FT	7738..7853
FT	exon
FT	/tag= p
FT	/number= 8
FT	7854..8152
FT	Intron
FT	/tag= q
FT	/number= 8
FT	8153..8435
FT	exon
FT	/tag= r
FT	/number= 9
FT	8436..8486
FT	Intron
FT	/tag= s
FT	/number= 9
FT	8487..8610
FT	exon
FT	/tag= t
FT	/number= 10
FT	8611..8661
FT	Intron
FT	/tag= u
FT	/number= 10
FT	8662..8952
FT	exon
FT	/tag= v
FT	/number= 11
FT	8953..9382
FT	Intron
FT	/tag= w
FT	/number= 11
FT	9383..9540
FT	exon
FT	/tag= x
FT	/number= 12
XX	
PN	US637202-B1.
XX	
PD	08-JAN-2002.
XX	
PE	23-FEB-2000; 2000US-0511477.
XX	
PR	01-MAY-1998; 98US-083768P.
PR	30-APR-1999; 99US-030281Z.
XX	
PA	(KENT) UNIV KENTUCKY RES FOUND.
XX	
PJ	Jacobson MK, Jacobson EL, Ame J, Lin W;
XX	
DR	WPI; 2002-163240/21.
XX	
PT	Novel isolated and purified poly(ADP-ribose) glycohydrolase protein
PT	which catalyses release of ADP-ribose from ADP-ribose polymer, useful
PT	for treating neoplastic and neurological disorders, heart attack and
XX	stroke -
PS	
XX	Example 14; Column 91-116; 81pp; English.

CC	The present invention relates to a new poly(ADP-ribose) glycohydrolase
CC	(PARG) protein which catalyses release of ADP-ribose from an ADP
CC	(adenosine diphosphate)-ribose polymer. The PARG molecule of the
CC	invention is useful for generating antibodies and can be inhibited or
CC	activated for diagnosing and treating neoplastic disorders such as
CC	adenocarcinoma, leukaemia, lymphoma, melanoma, myeloma, sarcoma,
CC	teratocarcinoma, hyperplasia and hypertrophy, reperfusion following
CC	ischaemia, heart attack, stroke, neurodegenerative diseases,
CC	neurological disorders including Alzheimer's, Huntington's and
CC	Parkinson's diseases, and related conditions. PARG levels may be
CC	enhanced to suppress DNA repair and increase the cell's susceptibility
CC	to chemotherapy drugs. Antagonists of PARC are administered to treat or
CC	prevent neoplastic disorders. The present nucleic acid sequence
CC	represents the worm PARC DNA sequence of the invention. This sequence
CC	was isolated from cosmid F20C5.
SQ	Sequence 29793 BP; 9945 A; 4952 C; 5003 G; 9893 T; 0 other;
Query Match	0.1%; Score 24; DB 24; Length 29793;
Best Local Similarity	100.0%; Pred. No. 15;
Matches 24; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
CY	11807 AGTAAAAAACGTAGTTGGATTCGA 11830
Db	21745 AGTAAAAAACGTAGTTGGATTCGA 21722
RESULT 8	
ABX14494/C	
ID	ABX14494 standard; DNA; 29793 BP.
XX	
AC	ABX14494;
XX	
DT	13-MAR-2003 (first entry)
XX	
DE	Cosmid F20C5 containing C. elegans PARC genomic DNA.
XX	
KM	Poly(ADP-ribose) glycohydrolase; PARC; PARC expression;
KW	cellular response; DNA damage; neoplastic disorder inducing agent;
KW	oxidative stress; neoplastic disorder; myocardial infarction;
KW	vascular stroke; neurodegenerative disorder; Alzheimer's disease;
KW	Parkinson's disease; Huntington's disease; Inborn genetic error;
KW	reperfusion; Ischaemia; aging; neurotoxicity; PARC activity;
KW	cytostatic; neuroprotective; nootropic; antiparkinsonian; cardiact;
KW	vasotropic; anticonvulsant; cerebroprotective; gene; cosmid F20C5; ds.
XX	
OS	Caenorhabditis elegans.
OS	Synthetic.
XX	
PN	US2002132328-A1.
XX	
PD	19-SEP-2002.
XX	
PF	09-OCT-2001; 2001US-0973451.
XX	
PR	01-MAY-1998; 98US-083768P.
XX	
PR	30-APR-1999; 99US-0302812.
XX	
PA	(JACO/) JACOBSON M K.
PA	(JACO/) JACOBSON E L.
PA	(AMEJ/) AME J.
PA	(LINW/) LIN W.
XX	
PI	Jacobson MK, Jacobson EL, Ame J, Lin W;
XX	
DR	WPI; 2003-155895/15.
PT	New nucleic acid molecule encoding a polypeptide with poly(ADP-ribose)
PT	glycohydrolase activity, for preventing, treating, or ameliorating a
PT	disease condition, e.g. neoplastic disorder, myocardial infarction or
PT	vascular stroke -
XX	
PS	Example 14; Page 49-62; 86pp; English.

XX The present invention relates to the isolation of poly(ADP-ribose) glycohydrolase (PARG) from several species, and the polynucleotide sequences encoding them. Methods for inhibiting PARG expression or overexpressing PARG are also disclosed. PARG is involved in the cellular response to DNA damage, and is associated with the body's response to neoplastic disorder inducing agents and oxidative stress. The polynucleotide sequences encoding PARG and PARG modulators are useful for preventing, treating, or ameliorating diseases such as neoplastic disorders, myocardial infarction, vascular stroke, neurodegenerative disorders (e.g. Alzheimer's disease, Parkinson's disease or Huntington's disease), inborn genetic errors, reperfusion following ischemia, aging, and neurotoxicity. The polynucleotide sequences are also useful in gene therapy. The methods are useful for identifying an agent that modulates PARG activity, identifying a mutant PARG allele in an individual, or screening candidate molecules for PARG modulating activity. The present DNA sequence represents cosmid F20C5 (Genbank Accession number 268161) which contains Caenorhabditis elegans PARG genomic DNA.

SQ Sequence 29793 BP; 9945 A; 4952 C; 5003 G; 9893 T; 0 other;

Query Match 0.1%; Score 24; DB 25; Length 29793;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11807 AGTAAACCTGATTGATTGCA 11830
|||||
DB 21745 AGTAAACCTGATTGATTGCA 21722

RESULT 9
AAT30688
ID AAT30688 standard; DNA; 918 BP.
XX
AC AAT30688;
XX
DT 11-SEP-1996 (first entry)
XX
DE Kaposi's sarcoma associated herpesvirus ORF26.
XX
KW Kaposi's sarcoma associated herpesvirus; KSHV; gamma-2 herpesvirus;
KM therapy; diagnosis; antisense; triplex; vaccine; AIDS; ss.
XX
OS Kaposi's sarcoma associated herpesvirus.
XX
PN WO9615779-A1.
XX
PD 30-MAY-1996.
XX
PE 21-NOV-1995; 95WO-US15138.
XX
PR 11-APR-1995; 95US-0420235.
PR 21-NOV-1994; 94US-0343101.
XX
PA (UYCO) UNIV COLUMBIA NEW YORK.
XX
PI Chang Y, Moore PS;
XX
DR WPI; 1996-268320/27.
DR P-PSDB; AAR97836.
XX
PT Herpes virus associated with Kaposi's sarcoma - also definitive DNA
PT sequences; useful for diagnosis of and to develop prods. for
PT treatment of Kaposi's sarcoma
XX
PS Claim 17; Page 213-215; 277pp; English.
XX
CC Lambda clone KS5 (AAT30681) has 17 protein-coding regions (AAT30682-98),
CC 15 of which are complete ORFs, including ORF26 (AAT30688) (nts 11913-
CC 12830), which codes for virion polypeptide VP23 (AAR97836). KS5 is a
CC fragment of a newly identified human gamma-2 herpesvirus associated
CC with Kaposi's sarcoma (KS). The ORFs were identified by sequence and

CC positional homology to known herpesvirus sequences. Probes that bind
CC specifically to the KS associated herpesvirus can be used for KS
CC diagnosis. Antisense or triplex oligonucleotides are useful for
CC prophylaxis or treatment of KS, and the protein products (see also
CC AAR97830-46) of the 17 open reading frames are useful as vaccines.
XX

SQ Sequence 918 BP; 204 A; 258 C; 229 G; 227 T; 0 other;

Query Match 0.1%; Score 23; DB 17; Length 918;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9414 AGTCACGTCATATTTATCT 9436
|||||
DB 823 AGTCACGTCATATTTATCT 845

RESULT 10
AAT16818
ID AAT16818 standard; DNA; 918 BP.
XX
AC AAT16818;
XX
DT 25-MAR-2003 (updated)
DT 13-AUG-1996 (first entry)
XX
DE Kaposi's sarcoma associated herpesvirus ORF26.
XX
KW Kaposi's sarcoma; KSHV; lymphoma; AIDS; vaccine; diagnosis; therapy;
KM virion polypeptide; ss.
XX
OS Kaposi's sarcoma associated herpesvirus.
XX
PN WO9606159-A1.
XX
PD 29-FEB-1996.
XX
PE 11-AUG-1995; 95WO-US10194.
XX
PR 18-AUG-1994; 94US-0292365.
PR 21-NOV-1994; 94US-0343101.
PR 11-APR-1995; 95US-0420235.
XX
PA (UYCO) UNIV COLUMBIA NEW YORK.
PA (GRANT) GRANT D E.
PA (VIELE) VIELE L.
XX
PI Chang Y, Moore PS, Grant DE, Vile L;
XX
DR WPI; 1996-151362/15.
DR P-PSDB; AAR93612.
XX
PT Herpesvirus DNA associated with Kaposi's sarcoma - also associated
PT vectors and proteins, used in detection and vaccination.
XX
PS Claim 17; Page 226-228; 305pp; English.
XX
CC Kaposi's sarcoma associated herpes virus (KHSV) clone KS5 (AAT16806),
CC obid. from a KS lesion genomic library, includes 15 complete ORFs and
CC 2 incomplete ORFs (AAT16807-23) named according to their herpesvirus
CC salmieri positional homologues. ORF26 (AAT16818) codes for the virion
CC polypeptide (AAR93612). KSHV DNA may be incorporated into a
CC vector and expressed in host cells to produce peptides useful in
CC vaccines or for raising antibodies. The DNA may itself be used to
CC immunise a subject, or used to design therapeutic antisense and
CC triplex molecules or diagnostic probes, or to raise transgenic
CC animals.
CC (Updated on 25-MAR-2003 to correct PR field.)
CC
SQ Sequence 918 BP; 204 A; 258 C; 229 G; 227 T; 0 other;
XX
Query Match 0.1%; Score 23; DB 17; Length 918;
Best Local Similarity 100.0%; Pred. No. 52;


```

XX 29-FEB-1996.
XX
XX 11-AUG-1995; 95MO-US10194.
XX
XX 18-AUG-1994; 94US-0292365.
XX
XX 21-NOV-1994; 94US-0343101.
XX
XX 11-APR-1995; 95US-0420235.
XX
XX (UYCO ) UNIV COLUMBIA NEW YORK.
XX
XX (GRAN/) GRANT D E.
XX
XX (VIE/) VIELE L.
XX
XX Chang Y, Moore PS, Grant DE, Viele L;
XX
XX WPI; 1996-151362/15.
XX
XX Herpesvirus DNA associated with Kaposi's sarcoma - also associated
XX
XX PT vectors and proteins, used in detection and vaccination.
XX
XX PS Claim 16; Page 177-188; 305pp; English.
XX
XX Representational difference analysis was used to identify unique
XX
XX CC DNA sequences in Kaposi's sarcoma (KS) tissue. An isolated sequence. A
XX
XX CC KS30Bam (AAT16824), was used to screen a KS lesion genomic library. A
XX
XX CC lambda phage, KS5, was identified and the sequence of its insert
XX
XX CC (AAT16808) was detd. This represents a novel infectious agent
XX
XX CC associated with AIDS-KS, Kaposi's sarcoma associated herpesvirus (KSHV).
XX
XX CC The KS5 fragment has 15 complete ORFs and 2 incomplete ORFs (see also
XX
XX CC AAT16807-23). Portions of the sequence may be incorporated into a
XX
XX CC vector and expressed in host cells to produce peptides (see also
XX
XX CC AAR91601-117) useful in vaccines or for raising antibodies. The DNA may
XX
XX CC itself be used to immunise a subject, or used to design therapeutic
XX
XX CC antisense and triplex molecules or diagnostic probes, or to raise
XX
XX CC transgenic animals.
XX
XX CC (Updated on 25-MAR-2003 to correct PR field.)
XX
XX
XX SO Sequence 20710 BP; 4628 A; 5526 C; 5666 G; 4890 T; 0 other;
XX
XX
XX Query Match 0.1%; Score 23; DB 17; Length 20710;
XX
XX Best Local Similarity 100.0%; Pred. No. 40;
XX
XX Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX
XX QY 9414 AGCTCAGTCTATTATTATCT 9436
XX
XX 12735 AGTCTCAGTCTATTATTATCT 12757
XX
XX
XX Db
XX
XX
XX RESULT 13
XX
XX AAV73803
XX
XX ID AAV73803 standard; DNA: 35100 BP.
XX
XX
XX AC AAV73803;
XX
XX
XX DT 25-FEB-1999 (first entry)
XX
XX
XX DE KSHV LUR DNA (nucleotides 35,101-70,200).
XX
XX
XX XX Kaposi's sarcoma; acquired immune deficiency syndrome; AIDS; DHFR; Bcl-2;
XX
XX KM dihydrofolate reductase; LUR; long unique region; vaccine; prophylaxis;
XX
XX KM diagnosis; treatment; HHV8; thymidine kinase; glycoprotein H;
XX
XX KM capsid protein; packaging protein; helicase primase; glycoprotein M;
XX
XX KM viral protein kinase; alkaline exonuclease; virion assembly protein;
XX
XX KM uracil DNA glycosylase; UDG; glycoprotein L; ds.
XX
XX
XX OS Kaposi's sarcoma-associated herpesvirus.
XX
XX
XX PN US5849564-A.
XX
XX
XX PD 15-DEC-1998.
XX
XX
XX PF 29-NOV-1996; 96US-0770379.
XX
XX

```

```

PR 29-NOV-1996; 96US-0770379.
XX
XX
XX PA (UYCO ) UNIV COLUMBIA NEW YORK.
XX
XX
XX PI Bohenzky RA, Chang Y, Edelman IS, Moore PS, Russo JI;
XX
XX DR WPI; 1999-069741/06.
XX
XX
XX PT Kaposi's sarcoma-associated herpes virus nucleic acid - encodes
XX
XX PT dihydrofolate reductase and is useful for treatment, prophylaxis
XX
XX PT or diagnosis of Kaposi's sarcoma
XX
XX
XX PS Disclosure; Column 97-126; 109pp; English.
XX
XX
XX CC This sequence is a fragment of the Kaposi's sarcoma-associated
XX
XX CC herpesvirus (KSHV) LUR (long unique region). This fragment contains
XX
XX CC coding regions for ORF20, ORF21 which encodes thymidine kinase, ORF22
XX
XX CC which encodes glycoprotein H, ORF23, ORF24, ORF25 which encodes the
XX
XX CC major capsid protein, ORF26 which encodes capsid protein II, ORF27,
XX
XX CC ORF28, ORF29b which encodes packaging protein II, ORF30, ORF31, ORF32,
XX
XX CC ORF33, ORF29a which encodes packaging protein I, ORF34, ORF35, ORF36
XX
XX CC which encodes viral protein kinase, ORF37 which encodes alkaline
XX
XX CC exonuclease, ORF38, ORF39 which encodes glycoprotein M, ORF40 which
XX
XX CC encodes helicase primase subunit I, ORF41 which encodes helicase primase
XX
XX CC subunit II, ORF42, ORF43 which encodes capsid protein III, ORF44 which
XX
XX CC encodes helicase primase subunit III, ORF45 which encodes the virion
XX
XX CC assembly protein, ORF46 which encodes uracil DNA glycosylase (UDG),
XX
XX CC ORF47 which encodes glycoprotein L. KSHV is a new human Herpesvirus
XX
XX CC (HHV8) believed to cause Kaposi's sarcoma (KS) which is the most common
XX
XX CC form of neoplasm occurring in persons with acquired immune deficiency
XX
XX CC syndrome (AIDS). The DHFR protein is useful for vaccination, prophylaxis,
XX
XX CC diagnosis and treatment of a subject with Kaposi's sarcoma and for
XX
XX CC detecting expression of a DNA virus associated with Kaposi's sarcoma in a
XX
XX CC cell.
XX
XX
XX SO Sequence 35100 BP; 8016 A; 9231 C; 9477 G; 8376 T; 0 other;
XX
XX
XX Query Match 0.1%; Score 23; DB 20; Length 35100;
XX
XX Best Local Similarity 100.0%; Pred. No. 38;
XX
XX Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX
XX QY 9414 AGCTCAGTCTATTATTATCT 9436
XX
XX 12655 AGTCTCAGTCTATTATTATCT 12677
XX
XX
XX Db
XX
XX
XX RESULT 14
XX
XX AAV19941
XX
XX ID AAV19941 standard; DNA: 137507 BP.
XX
XX
XX AC AAV19941;
XX
XX
XX DT 03-AUG-1998 (first entry)
XX
XX
XX DE KSHV long unique coding region and terminal repeat.
XX
XX
XX XX KSHV; HHV8; human herpes virus 8; macrophage inflammatory protein II;
XX
XX KM interleukin-6; IL-6; interferon regulatory factor; rheumatoid arthritis;
XX
XX KM complement-binding protein; glycoprotein; capsid protein IV; infection;
XX
XX KM immediate early protein; Kaposi's sarcoma; protective vaccine; lymphoma;
XX
XX KM lymphoproliferative disease; leukaemia; splenomegaly; mycosis fungoides;
XX
XX KM HIV immune status; anti-inflammatory agent; therapy; ds.
XX
XX
XX OS Kaposi's sarcoma-associated herpes virus.
XX
XX
XX FH Key Location/Qualifiers
XX
XX FT CDS 1142..2794
XX
XX FT /*tag= a
XX
XX FT /product= complement-binding protein
XX
XX FT 8699..11236
XX
XX FT /*tag= b
XX
XX FT /product= glycoprotein B
XX
XX FT complement (17261..17875)
XX
XX

```


CC proteins are useful for preventing, ameliorating or treating medical
 CC conditions, e.g. by protein or gene therapy. The genes are isolated
 CC from a range of human tissues disclosed in the specification. The
 CC nucleic acids, proteins, antibodies and (ant)agonists are useful in
 CC the diagnosis, treatment and prevention of: (a) cancer, e.g. breast
 CC and ovarian cancer, and other cancers of the adrenal gland, bone, bone
 CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
 CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune
 CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
 CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative
 CC colitis; (c) cardiovascular disorders such as myocardial ischaemia; (d)
 CC wound healing; (e) neurological diseases e.g. cerebral anoxia and
 CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
 CC and parasitic infections.

XX Sequence 1060 BP; 316 A; 212 C; 217 G; 311 T; 4 other;
 SQ

Query Match 0.1%; Score 22; DB 21; Length 1060;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02; Mismatches 0; Gaps 0;
 Matches 22; Conservative 0; Indels 0;

QY 21007 AAAATGTATACGTATACAAAC 21028
 |||||||||||||||||||
 Db 367 AAAATGTATACGTATACAAAC 346

RESULT 16
 ABR63559
 ID ABR63559 standard; cDNA; 1451 BP.
 XX
 AC ABR63559;
 XX
 DT 18-JUN-2002 (first entry)
 XX
 DE Rat sequence differentially expressed in response to a hepatotoxin #1466.
 XX
 KM Rat; ss: hepatotoxin; expressed sequence tag; EST; drug screening;
 XX differential expression; centrilobular necrosis; steatosis.
 OS Rattus norvegicus.
 XX
 PN M0200210453-A2.
 XX
 PD 07-FEB-2002.
 XX
 PF 30-JUL-2001; 2001WO-US23872.
 XX
 PR 31-JUL-2000; 2000US-222040P.
 PR 02-NOV-2000; 2000US-244880P.
 PR 11-MAY-2001; 2001US-280029P.
 PR 15-MAY-2001; 2001US-280645P.
 PR 22-MAY-2001; 2001US-292336P.
 PR 06-JUN-2001; 2001US-295798P.
 PR 13-JUN-2001; 2001US-297457P.
 PR 19-JUN-2001; 2001US-298884P.
 PR 09-JUL-2001; 2001US-303459P.
 XX
 PA (GENE-) GENE LOGIC INC.
 XX
 PI Mendrick D, Porter MW, Johnson KR, Castle AL, Elashoff MR;
 XX
 DR WPI; 2002-241625/29.
 XX
 PT Predicting toxic effects of compounds or the progression of these toxic
 PT effects by determining the changes in gene expression in tissues or
 PT cells exposed to the toxin and comparing these to gene expression in
 PT unexposed tissues or cells -
 XX
 XX Claim 1; Seq ID No 1466; 239pp; English.
 PS
 CC The invention relates to methods for predicting toxic effects of
 CC compounds or the progression of these toxic effects by determining the
 CC global changes in gene expression in tissues or cells exposed to the

CC toxin and comparing these to gene expression in unexposed tissues or
 CC cells. Also included are methods of predicting at least one toxic
 CC effect of a compound or progression of a toxic effect, preferably the
 CC hepatotoxicity of a compound, comprising detecting the level of
 CC expression in a tissue or cell sample exposed to the compound of two or
 CC more genes listed in the specification, where differential expression of
 CC the genes is indicative of at least one toxic effect or progression.
 CC The method can also be used to identify an agent which modulates the
 CC toxic response and predict cellular pathways that a compound modulates
 CC in a cell. The methods utilise a set of at least two probes (on a solid
 CC support in kit form), where each of the probes comprises a sequence that
 CC specifically hybridises to a gene listed in the specification, a computer
 CC system comprising a database containing information identifying the
 CC expression level in a tissue or cell sample exposed to a hepatotoxin of a
 CC set of genes comprising at least two genes listed in the specification,
 CC and a user interface to view the information used to present information
 CC identifying the expression level in a tissue or cell of at least one gene
 CC listed in the specification. The method is useful for elucidating global
 CC changes in gene expression and for identifying toxicity markers in
 CC tissues or cell exposed to a known toxin. The genes may be used as
 CC toxicity markers in drug screening and toxicity assays. The genes and
 CC gene expression information may be used as diagnostic markers for the
 CC prediction or identification of the physiological state of tissue or cell
 CC sample that has been exposed to a compound or agent. Hepatotoxicity
 CC is characterised by centrilobular necrosis and steatosis. The present
 CC sequence is an expressed sequence tag (EST) or cDNA derived from a gene
 CC which is differentially expressed in response to a hepatotoxic agent.

XX Sequence 1451 BP; 386 A; 374 C; 379 G; 312 T; 0 other;
 SQ

Query Match 0.1%; Score 22; DB 24; Length 1451;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02; Mismatches 0; Gaps 0;
 Matches 22; Conservative 0; Indels 0;

QY 25967 GAACAGCTGCTTCCAAAGATC 25988
 |||||||||||||||||||
 Db 1367 GAACAGCTGCTTCCAAAGATC 1388

RESULT 17
 ABA01689
 ID ABA01689 standard; mRNA; 2526 BP.
 XX
 AC ABA01689;
 XX
 DT 08-FEB-2002 (first entry)
 XX
 DE Mouse fibroblast growth factor receptor 1 mRNA SEQ ID NO:5.
 XX
 KM Fibroblast growth factor receptor 1; FGFR1; antisense oligonucleotide;
 XX phosphorothioate; diagnosis; ss.
 OS Mus sp.
 XX
 PN JP2001252085-A.
 XX
 PD 18-SEP-2001.
 XX
 PF 15-MAR-2000; 2000JP-0072741;
 XX
 PR 15-MAR-2000; 2000JP-0072741.
 XX
 PA (TOAG) TOA GOSSEI CHEM IND LTD.
 XX
 DR WPI; 2002-029661/04.
 XX
 PT An antisense nucleic acid compound used as a diagnostic and therapeutic
 PT agent -
 XX
 XX Example; Page 7-8; 10pp; Japanese.
 PS
 CC The present invention describes an antisense nucleic acid compound (I),
 CC used as a diagnostic and therapeutic agent. (I) comprises:

CC	(1) an antisense nucleic acid compound (II) having the base sequence
CC	TRGGTTT;
CC	(11) an antisense nucleic acid compound (III) having the above base
CC	sequence in which the base number is expressed by a base sequence
CC	between 10 and 60; and
CC	(111) an antisense nucleic acid molecule (IV) comprising one of the 3
CC	sequences given in ABA01686 to AAB01688, all comprising of 20 nucleic
CC	acids, and that inhibit the expression of fibroblast growth factor
CC	receptor 1 (FGFR1). (I) is useful as a treating agent, a diagnostic
CC	agent and a research reagent. The present sequence represents mouse
CC	FGFR1 mRNA, which is given in the exemplification of the present
CC	invention.
XX	
XX	
SO	Sequence 2526 BP; 576 A; 710 C; 712 G; 528 U; 0 other.
XX	
Query Match	0.18; Score 22; DB 24; Length 2526;
Best Local Similarity	77.38; Pred. No. 1.3e+02;
Matches 17; Conservative % 5; Mismatches 0; Indels 0; Gaps 0;	
OY	25967 GAAACAGCTGCTCTCCAAAGATC 25968
DB	1834 GAACAGCUGUCUCCAAAGATC 1855
XX	
RESULT 18	
AAV44041	
ID	AAV44041 standard; DNA; 3503 BP.
XX	
AC	AAV44041;
XX	
DT	25-MAR-2003 (updated)
DT	01-OCT-1998 (first entry)
XX	
DE	Mouse bFGF receptor DNA.
XX	
KW	Basic fibroblast growth factor receptor; bFGF; heparin binding; murine;
KW	antitumour agent; inhibitor; wound healing; ss.
XX	
OS	Mus sp.
XX	
FH	Key Location/Qualifiers
FT	CDS 282..2744
FT	/*tag= a
FT	/product= bFGF receptor
FT	/note= "basic fibroblast growth factor receptor"
XX	
PN	US5789182-A.
PD	
PD	04-AUG-1998.
XX	
PF	14-DEC-1993; 93US-0166717.
XX	
PR	20-DEC-1990; 90US-0631717.
PR	14-DEC-1993; 93US-0166717.
XX	
PA	(CHIL-) CHILDRENS MEDICAL CENT.
PA	(HARD) HARVARD COLLEGE.
PI	
PI	Flanagan JG, Klagsbrun M, Leder P, Ornitz DM, Yason A;
DR	WPI: 1998-446074/38.
DR	P-PSDB: AAM63844.
XX	
XX	
PT	Assays for high-affinity heparin-binding growth factor receptor
PT	ligands - using receptor-overexpressing cells or cell-free system
XX	
PS	Disclosure: Fig 9; 38pp; English.
XX	
CC	This sequence encodes a murine basic fibroblast growth factor (bFGF)
CC	which is a member of the heparin-binding growth factor receptor family.
CC	This protein is used in a method which assays the ability of a substance
CC	to bind to a high-affinity heparin-binding growth factor (HBGF) receptor.
CC	The assay screens for potential antitumour agents that inhibit binding of

CC	HBBE	to high-affinity receptors, or for potential wound healing agents
CC	that promote such binding.	
CC	(Updated on 25-MAR-2003 to correct PF field.)	
xx		
SQ	Sequence 3503 BP; 797 A; 995 C; 972 G; 730 T; 9 other:	
Query Match	0.1%; Score 22; DB 19; Length 3503;	
Best Local Similarity	100.0%; Pred. No. 1.2e+02;	
Matches 22:	Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
DQ	25967 GAACAGCTGTCGTCCAAAGATC 25988 	
Db	2052 GAACAGCTGTCGTCCAAAGATC 2073	
RESULT 19		
ID	ABL33920/C	
XX	ABL33920 standard; DNA; 12590 BP.	
AC		
XX	ABL33920;	
DT		
XX	26-MAR-2002 (first entry)	
DE		
XX	Human immune system associated gene SEQ ID NO: 1893.	
KW	Human; immune system disease; cytosine methylation; antisthmatic;	
KW	antiartherosclerotic; antihaemic; cyostatic; noctropic;	
KW	neuroprotective; anti-HIV; anticoagulant; ophthalmological;	
KW	antiinflammatory; antiarthritic; antidiabetic; antiporiatic;	
KW	antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;	
KW	acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;	
KW	neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;	
gene; ds.		
XX		
OS	Homo sapiens.	
XX		
PN	WO200200928-A2.	
PD		
XX	03-JAN-2002.	
PE		
XX	02-JUL-2001; 2001WO-EP07537.	
PR		
XX	30-JUN-2000; 2000DE-1032529.	
PR	01-SEP-2000; 2000DE-1043826.	
PA		
XX	(EPIC-) EPIGENOMICS AG.	
XX		
PI	Olek A, Piepenbrock C, Berlin K;	
DR		
XX	WPt: 2002-130909/17.	
Pt		
Pt	Nucleic acid comprising fragment of chemically modified gene, useful	
Pt	for diagnosis and treatment of diseases associated with abnormal	
Pt	cytosine methylation -	
PS		
XX	Claim 1: SEQ ID NO 1893; 32pp + Sequence Listing; German.	
XX		
CC	The present invention provides a number of human immune system associated	
CC	genes which are modified by the methylation of cytosines. The sequences	
CC	can be used in the diagnosis and treatment of immune system disorders,	
CC	including eye diseases such as retinopathy, neovascular glaucoma and	
CC	macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid	
CC	leukemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,	
CC	rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel	
CC	diseases. The present sequence is a gene of the invention.	
XX		
SQ	Sequence 12590 BP; 2516 A; 310 C; 3233 G; 6531 T; 0 other:	
Query Match	0.1%; Score 22; DB 24; Length 12590;	
Best Local Similarity	100.0%; Pred. No. 1.1e+02;	
Matches 22:	Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
yy	28429 TCATCTACTAATAATTAATAAAA 28450	


```

DB      5900 TCATCTACTAAATTAATTAATAA 5879
      |||||||||||||||||||
RESULT 20
AAH71549/c
ID      AAH71549 standard; cDNA; 752 BP.
XX
XX      AAH71549;
AC
XX      19-SEP-2001 (first entry)
DT
XX      Human cervical cancer marker nucleic acid 2823.
DE
XX      Cervical cancer; cytostatic; pre-malignant condition; gene therapy; ss.
XX      Homo sapiens.
OS
XX      WO200142467-A2.
PN
XX      14-JUN-2001.
PD
XX      08-DEC-2000; 2000WO-US33312.
PF
XX      08-DEC-1999; 99US-0169681.
PR      21-DEC-1999; 99US-0171350.
PR      14-MAR-2000; 2000US-0189315.
PR      12-MAY-2000; 2000US-0203791.
PR      09-JUN-2000; 2000US-0210600.
PR      21-JUL-2000; 2000US-0220114.
XX
XX      (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
PA
XX      Schlegel R, Deeds J, Berger A, Zhao X;
PI
XX      WPI: 2001-375006/39.
DR
XX      New isolated nucleic acid for diagnosing and treating cervical cancer
PT      and for assessing and detecting compounds for treating the cancer -
PI
XX      Claim 1; Page 579; 1051pp; English.
PS
XX      The invention relates to novel genes (AAH68727-AAH73383) associated with
CC      cervical cancer with cytostatic activity. The nucleic acids and encoded
CC      polypeptides are useful: to assess if a patient is afflicted with
CC      cervical cancer or has a pre-malignant condition; to monitor the
CC      progression of cervical cancer or a premalignant condition in a patient;
CC      and to select and/or assess the efficacy of a compound or therapy for
CC      inhibiting cervical cancer in a patient. The nucleic acids may also be
CC      useful for gene therapy.
CC
SQ      Sequence 752 BP; 219 A; 161 C; 189 G; 181 T; 2 other;
      Query Match          0.1%; Score 21; DB 22; Length 752;
      Best Local Similarity 100.0%; Pred. No. 3.7e+02;
      Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY      14343 AACCAAAAGATTGGCCCGT 14363
DB      483 AACCAAAAGATTGGCCCGT 463
      |||||||||||||||||||
RESULT 21
AAK04342/c
ID      AAK04342 standard; DNA; 1536 BP.
XX
XX      AAK04342;
AC
XX      13-APR-1999 (first entry)
DT
XX      Human secreted protein gene 32 clone HTLDQ11.
DE
XX      Human; secreted protein; fusion protein; gene therapy; protein therapy;
KM

```

```

KM      diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukemia;
KM      developmental abnormality; foetal deficiency; blood; allergy; renal; ds;
KM      immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
KM      inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
KM      cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
KM      osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
KM      endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
XX
XX      Homo sapiens.
OS
XX      WO9856804-A1.
PN
XX      17-DEC-1998.
PD
XX      11-JUN-1998; 98WO-US12125.
PF
XX      02-OCT-1997; 97US-0061060.
PR      13-JUN-1997; 97US-0049547.
PR      13-JUN-1997; 97US-0049548.
PR      13-JUN-1997; 97US-0049549.
PR      13-JUN-1997; 97US-0049550.
PR      13-JUN-1997; 97US-0049606.
PR      13-JUN-1997; 97US-0049607.
PR      13-JUN-1997; 97US-0049608.
PR      13-JUN-1997; 97US-0049609.
PR      13-JUN-1997; 97US-0049610.
PR      13-JUN-1997; 97US-0049611.
PR      13-JUN-1997; 97US-0050566.
PR      13-JUN-1997; 97US-0050901.
PR      08-JUL-1997; 97US-0052989.
PR      08-JUL-1997; 97US-0051919.
PR      18-AUG-1997; 97US-0055984.
PR      12-SEP-1997; 97US-0058665.
PR      12-SEP-1997; 97US-0058666.
PR      12-SEP-1997; 97US-0058669.
PR      12-SEP-1997; 97US-0058750.
PR      12-SEP-1997; 97US-0058971.
PR      12-SEP-1997; 97US-0058972.
PR      12-SEP-1997; 97US-0058973.
PR      02-OCT-1997; 97US-0060834.
PR      02-OCT-1997; 97US-0060841.
PR      02-OCT-1997; 97US-0060844.
PR      02-OCT-1997; 97US-0060865.
PR      02-OCT-1997; 97US-0061059.
XX
XX      (HUMA-) HUMAN GENOME SCI INC.
PA
XX      Brewer LA, Edner R, Ferris AM, Feng P, Greene JM, Lafleur DW;
PI
XX      Moore PA, Ni J, Olsen HS, Rosen CA, Ruben SM, Shi Y, Young P;
PI
XX      Xu GL;
PS
XX      WPI: 1999-080881/07.
DR
XX      P-PSDB; AAW78157.
DT
XX      New isolated human genes and the secreted polypeptides they encode -
PT
XX      useful for diagnosis and treatment of e.g. cancers, neurological
PT
XX      disorders, immune diseases, inflammation or blood disorders
XX
XX      Claim 1; Page 197-198; 380pp; English.
PS
XX      This sequence represents a nucleic acid molecule which encodes a
CC      secreted human protein. The gene number, and the clone it is derived
CC      from, are detailed in the descriptor line. The gene can be used to
CC      generate fusion proteins by linking to the gene to a human immunoglobulin
CC      Fc portion (e.g. AAK04302) for increasing the stability of the fused
CC      protein as compared to the human protein only.
CC      The invention relates to 86 novel genes and their fragments (nucleic
CC      acid sequences: AAK04311-X04410; amino acid sequences: AAW78126-W78225)
CC      which are useful for preventing, treating or ameliorating medical
CC      conditions e.g. by protein or gene therapy. Also, pathological
CC      conditions can be diagnosed by determining the amount of the new
CC      polypeptides in a sample or by determining the presence of mutations in
CC      the new polynucleotides. Specific uses are described for each of the 86

```

CC polynucleotides, based on which tissues they are most highly expressed in
 CC (see AAX04311 for described uses).

SO Sequence 1536 BP; 359 A; 382 C; 312 G; 469 T; 14 other;

Query Match 0.18; Score 21; DB 20; Length 1536;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10475 GGAATAATGCTGTAATACT 10495
 Db 649 GGAATAATGCTGTAATACT 629

RESULT 22
 ABA88869
 ID ABA88869 standard; DNA: 1557 BP.

AC ABA88869;

DT 11-FEB-2002 (first entry)

DE Escherichia coli polynucleotide SEQ ID NO 324.

KW Escherichia coli; B2/D+A-; antiinflammatory; antibacterial;
 KW immunosuppressive; extra-intestinal infection; phylogeny; meningitis;
 KW systemic infection; non-diarrhoeal infection; septicaemia;
 KW pyelonephritis; antibiotic resistance; ds.

OS Escherichia coli.

PN WO200166572-A2.

PD 13-SEP-2001.

PF 12-MAR-2001; 2001WO-EP03445.

PR 10-MAR-2001; 2000FR-0003145.

PR 02-FEB-2001; 2001FR-0001449.

PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.

PI Blingen E, Bonacorsi S, Clermont O, Nassif X, Tinsley C;

DR WPI; 2001-550253/61.

PT A library of DNA fragments of Escherichia coli strains for the
 PT phylogenic determination of a given strain comprises polynucleotides of
 PT nature B2/D+ A- -
 PS Example 6; Fig 6; 646pp; English.

CC The invention relates to a library of DNA fragments of Escherichia coli
 CC strains comprising polynucleotides (ABA88577-ABA88729 and ABA89533)
 CC and encoded proteins (ABBS2459-ABBS2919 and ABBS2954-ABBS3094) of nature
 CC B2/D+-. The polynucleotides have potential antiinflammatory,
 CC antibacterial and immunosuppressive activity as part of pharmaceutical
 CC compositions used to treat, palliate or prevent extra-intestinal E. coli
 CC infections. The polypeptides are useful for determining the phylogenic
 CC group of a given E. coli strain. These polypeptides can detect and treat
 CC an undesired development of E. coli, particularly an extra-intestinal
 CC infection that include systemic and non-diarrhoeal infections such as
 CC septicaemia, pyelonephritis and meningitis this is particularly
 CC advantageous as bacterial resistance is increasing with the more
 CC frequent use of broad spectrum antibiotics.

XX Sequence 1557 BP; 446 A; 337 C; 407 G; 367 T; 0 other;

Query Match 0.18; Score 21; DB 22; Length 1557;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 23363 CTGCTGCCACGCCGTGGTA 23383

Db 530 CTGCTGCCACGCCGTGGTA 550

RESULT 23
 ABZ09971/c
 ID ABZ09971 standard; DNA: 3628 BP.

AC ABZ09971;

DT 16-JAN-2003 (first entry)

DE Haematopoietic cell proliferation disorder related DNA sequence #111.

KW Human; haematopoietic cell proliferation disorder; cytostatic;
 KW gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia;
 KW cytosine methylation state; gene; ds.

OS Homo sapiens.

PN WO20027272-A2.

PD 03-OCT-2002.

PF 26-MAR-2002; 2002WO-EP03401.

PR 26-MAR-2001; 2001US-278333P.

PA (EPIC-) EPICENOMICS AG.

PI Berlin K, Braun A, Distler J, Guetig D, Howe A, Mueller J;
 PI Olek A, Piepenbrock C, Adorjan P, Grabs G, Lesche R, Leu E;
 PI Lewin A, Lipscher E, Maier S, Model F, Mueller V, Otto T;
 PI Pelet C, Schwöbe I, Ziebarth H;

DR WPI; 2003-018942/01.

PT Detecting and differentiating between hematopoietic cell proliferative
 PT disorders, comprises contacting a target nucleic acid with a reagent
 PT that distinguishes between methylated and non-methylated CpG
 PT dinucleotides -

PS Claim 28; SEQ ID 111; 117pp; English.

CC The present invention describes a method for detecting and
 CC differentiating between hematopoietic cell proliferative disorders
 CC associated with at least 1 gene and/or their regulatory regions in a
 CC subject. The method comprises contacting a target nucleic acid in a
 CC biological sample obtained from the subject with at least 1 reagent,
 CC which distinguishes between methylated and non-methylated CpG
 CC dinucleotides within the target nucleic acid. ABZ09861 to ABZ1118
 CC represent specifically claimed nucleotide sequences from the present
 CC invention. Oligonucleotides from the present invention can be used for
 CC differentiating between healthy haematopoietic cells and proliferative
 CC disorder haematopoietic cells; for differentiating between acute
 CC lymphocytic leukaemia and acute myelogenous leukaemia; as probes for
 CC determining the cytosine methylation state and/or single nucleotide
 CC polymorphisms (SNPs) of haematopoietic cell proliferation disorder
 CC related sequences and their complements; and as primers for the
 CC amplification of haematopoietic cell proliferation disorder related
 CC DNA sequences. The nucleotide sequences from the present invention can
 CC also be used for detecting a predisposition to, differentiation between
 CC subclasses, diagnosis, prognosis, treatment and/or monitoring of
 CC hematopoietic cell proliferative disorders. The present method enables
 CC a highly specific classification of haematopoietic cell proliferative
 CC disorders allowing for improved and informed treatment of patients.

XX Sequence 3628 BP; 734 A; 246 C; 1028 G; 1620 T; 0 other;

Query Match 0.18; Score 21; DB 25; Length 3628;
 Best Local Similarity 100.0%; Pred. No. 3.2e+02;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28433 CTACTAAATTAATAAACAA 28453
|||||
DB 1013 CTACTAAATTAATAAACAA 993

RESULT 24

AB210117/C
ID AB210117 standard; DNA; 3628 BP.

XX AB210117;

DT 16-JAN-2003 (first entry)

DE Haematopoietic cell proliferation disorder related DNA sequence #257.

XX Human; haematopoietic cell proliferation disorder; cytostatic;

KW gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia;

KW cytosine methylation state; gene; ds.

XX Homo sapiens.

XX WO20027272-A2.

PD 03-OCT-2002.

XX 26-MAR-2002; 2002MO-EP03401.

XX 26-MAR-2001; 2001US-278333P.

XX (EPIC-) EPIGENOMICS AG.

PI Berlin K, Braun A, Distler J, Guetig D, Howe A, Mueller J;

PI Olek A, Plepenbrock C, Adorjan P, Grabs G, Lesche R, Leu E;

PI Lewin A, Lipscher E, Maier S, Model F, Mueller V, Otto T;

PI Pelet C, Schwope I, Ziebarth H;

XX WPI; 2003-018942/01.

DR Detecting and differentiating between hematopoietic cell proliferative

PT disorders, comprises contacting a target nucleic acid with a reagent

PT that distinguishes between methylated and non-methylated CpG

PT dinucleotides -

XX Claim 28; SEQ ID 257; 117pp; English.

XX The present invention describes a method for detecting and

CC differentiating between haematopoietic cell proliferative disorders

CC associated with at least 1 gene and/or their regulatory regions in a

CC subject. The method comprises contacting a target nucleic acid in a

CC biological sample obtained from the subject with at least 1 reagent,

CC which distinguishes between methylated and non-methylated CpG

CC dinucleotides within the target nucleic acid. AB209861 to AB211118

CC represent specifically claimed nucleotide sequences from the present

CC invention. Oligonucleotides from the present invention can be used: for

CC differentiating between healthy haematopoietic cells and proliferative

CC disorder haematopoietic cells: for differentiating between acute

CC lymphocytic leukaemia and acute myelogenous leukaemia; as probes for

CC determining the cytosine methylation state and/or single nucleotide

CC polymorphisms (SNPs) of haematopoietic cell proliferation disorder

CC related sequences and their complements; and as primers for the

CC amplification of haematopoietic cell proliferation disorder related

CC DNA sequences. The nucleotide sequences from the present invention can

CC also be used for detecting a predisposition to, differentiation between

CC subclasses, diagnosis, prognosis, treatment and/or monitoring of

CC haematopoietic cell proliferative disorders. The present method enables

CC a highly specific classification of haematopoietic cell proliferative

CC disorders allowing for improved and informed treatment of patients.

XX Sequence 3628 BP; 734 A; 0 C; 1028 G; 1866 T; 0 other;

Query Match 0.1%; Score 21; DB 25; Length 3628;

Best Local Similarity 100.0%; Pred. No. 3.2e+02;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28433 CTACTAAATTAATAAACAA 28453
|||||
DB 1013 CTACTAAATTAATAAACAA 993

RESULT 25

ABL32593/C
ID ABL32593 standard; DNA; 6127 BP.

XX ABL32593;

DT 26-MAR-2002 (first entry)

DE Human immune system associated gene SEQ ID NO: 566.

XX Human; immune system disease; cytosine methylation; antiasthmatic;

KW antileukemic; anti-HIV; anticonvulsant; ophthalmological;

KW antineoplastic; antidiabetic; antidiabetic; antipsoriasis;

KW antineoplastic; cancer; eye disease; arteriosclerosis; anaemia;

KW acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;

KW neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;

XX gene; ds.

XX Homo sapiens.

XX WO200200928-A2.

PD 03-JAN-2002.

XX 02-JUL-2001; 2001MO-EP07537.

XX 30-JUN-2000; 2000DE-1032529.

XX 01-SEP-2000; 2000DE-1043826.

XX (EPIC-) EPIGENOMICS AG.

PI Berlin K;

PI Olek A, Plepenbrock C,

XX WPI; 2002-130909/17.

DR Nucleic acid comprising fragment of chemically modified gene, useful

PT for diagnosis and treatment of diseases associated with abnormal

PT cytosine methylation -

XX Claim 1; SEQ ID NO 566; 32pp + Sequence Listing; German.

XX The present invention provides a number of human immune system associated

CC genes which are modified by the methylation of cytosines. The sequences

CC can be used in the diagnosis and treatment of immune system disorders,

CC including eye diseases such as retinopathy, neovascular glaucoma and

CC macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid

CC leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,

CC rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel

CC diseases. The present sequence is a gene of the invention.

XX Sequence 6127 BP; 1578 A; 67 C; 1387 G; 3095 T; 0 other;

Query Match 0.1%; Score 21; DB 24; Length 6127;

Best Local Similarity 100.0%; Pred. No. 3.1e+02;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28433 CTACTAAATTAATAAACAA 28453
|||||
DB 2821 CTACTAAATTAATAAACAA 2801

RESULT 26

ABST9028

ID ABST9028 standard; DNA; 7636 BP.

XX ABST9028;

```

XX 17-DEC-2002 (first entry)
XX
XX E. coli CFT073 genomic sequence #195.
DE
XX Pathogenic; Escherichia coli CFT073 infection; livestock; pyelonephritis;
KW urinary tract infection; open reading frame; ORF; uropathogenic;
XX antibacterial; atrophic; nephrotropic; gene; ds.
XX
XX Escherichia coli.
XX
XX WO200259320-A2.
XX
XX 01-AUG-2002.
XX
XX 19-OCT-2001; 2001WO-US46833.
XX
XX 19-OCT-2000; 2000US-242412P.
XX
XX (WISC ) WISCONSIN ALUMNI RES FOUND.
XX
XX Blattner FR, Welch RA, Burland VD:
XX
XX WPI; 2002-691532/74.
XX
XX New DNA sequences of the pathogenic Escherichia coli CFT073 strain,
XX useful for preventing or treating E. coli CFT073 infection in humans or
XX livestock.
XX
XX Claim 1: Page 587-591; 765pp; English.
XX
XX The present invention relates to polynucleotide sequences from the
XX genome of the pathogenic Escherichia coli strain CFT073. Almost all
XX the sequences present in E. coli CFT073 are absent in the previously
XX sequenced laboratory strain K-12. The polynucleotide sequences of
XX the invention are useful for preventing, diagnosing or treating
XX E. coli CFT073 infection in humans or livestock. The polynucleotide
XX sequences are useful for preventing urinary tract infections and
XX pyelonephritis. Likewise, the polypeptides encoded by the different
XX open reading frames (ORF1-5) are useful for generating a vaccine
XX against uropathogenic E. coli strains. AB578834-AB579085 represent
XX genomic sequences from E. coli strain CFT073.
XX
XX Sequence 7636 BP; 2087 A; 1619 C; 1684 G; 2246 T; 0 other;
SQ
Query Match 0.1%; Score 21; DB 24; Length 7636;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 23363 CTGCTGCCACGCCGTGGGTA 23383
DB 6380 CTGCTGCCACGCCGTGGGTA 6400
RESULT 27
ABA88864
ID ABA88864 standard; DNA; 7646 BP.
XX
XX ABA88864.
XX
XX 11-FEB-2002 (first entry)
XX
XX Escherichia coli polynucleotide SEQ ID NO 315.
XX
XX Escherichia coli; B2/D+A-; antiinflammatory; antibacterial;
XX immunosuppressive; extra-intestinal infection; phylogeny; meningitis;
XX systemic infection; non-diarrhoeal infection; septicemia;
XX pyelonephritis; antibiotic resistance; ds.
XX
XX Escherichia coli.
XX
XX WO200166572-A2.
XX

```

```

PD 13-SEP-2001.
XX
XX 12-MAR-2001; 2001WO-EP03445.
XX
XX 10-MAR-2000; 2000FR-0003145.
XX
XX 02-FEB-2001; 2001FR-0001449.
XX
XX (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
XX
XX Bingen E, Bonacorsi S, Clermont O, Nassif X, Tinsley C;
XX
XX WPI; 2001-550253/61.
XX
XX A library of DNA fragments of Escherichia coli strains for the
XX phylogenetic determination of a given strain comprises polynucleotides of
XX nature B2/D+ A- -
XX
XX Example 6; Fig 6; 646pp; English.
XX
XX The invention relates to a library of DNA fragments of Escherichia coli
XX strains comprising polynucleotides (ABA88577-ABA88729 and ABA89533)
XX and encoded proteins (AB52459-AB52919 and AB52954-AB53094) of nature
XX B2/D+A-. The polynucleotides have potential antiinflammatory,
XX antibacterial and immunosuppressive activity as part of pharmaceutical
XX compositions used to treat, palliate or prevent extra-intestinal E. coli
XX infections. The polypeptides are useful for determining the phylogenic
XX group of a given E. coli strain. These polypeptides can detect and treat
XX an undesired development of E. coli, particularly an extra-intestinal
XX infection that include systemic and non-diarrhoeal infections such as
XX septicemia, pyelonephritis and meningitis this is particularly
XX advantageous as bacterial resistance is increasing with the more
XX frequent use of broad spectrum antibiotics.
XX
XX Sequence 7646 BP; 2089 A; 1619 C; 1686 G; 2252 T; 0 other;
SQ
Query Match 0.1%; Score 21; DB 22; Length 7646;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 23363 CTGCTGCCACGCCGTGGGTA 23383
DB 6381 CTGCTGCCACGCCGTGGGTA 6401
RESULT 28
AAQ90132/C
ID AAQ90132 standard; DNA; 8083 BP.
XX
XX AAQ90132;
XX
XX 25-MAR-2003 (updated)
XX
XX 11-NOV-1995 (first entry)
XX
XX Plasmid pBHVKex-3::p53.
XX
XX Plasmid pBHVKex-3::p53; vector; bovine viral diarrhoea virus 2724;
XX gp53 protein; major glycoprotein; cytomegalo virus promoter;
XX bovine somatotropin polyadenylation signal; attenuation;
XX recombinant vaccine; ds.
XX
XX Bovine viral diarrhoea virus (2724).
XX
XX WO9512682-A2.
XX
XX 11-MAY-1995.
XX
XX 31-OCT-1994; 94WO-0512198.
XX
XX 05-NOV-1993; 93US-0147810.
XX
XX (UPJO ) UPJOHN CO.
XX
XX Haanes EJ, Wardley RC;
XX

```

XX WPI: 1995-185781/24.
XX A replicating non-pathogenic virus containing a BVDV gene - for
PT vaccination against disease caused by bovine viral diarrhoea virus
XX
PS Claim 23; Page 22-25; 60pp; English.
XX
CC The sequence corresponds to plasmid PBHVKex-3::gIII/p53, which contains
CC a bovine viral diarrhoea virus (BVDV) major glycoprotein gp53 gene
CC inserted between a cytomegalovirus promoter and a bovine
CC somatotropin gene polyadenylation signal from plasmid
CC pHAS4-delta-Bxex-3, with no added signal peptide sequence. The
CC original gp53 gene has been inserted without site-directed
CC mutagenesis. The plasmid may be used to produce a replicating
CC non-pathogenic virus for use as a safe attenuated recombinant
CC vaccine against BVDV in animals.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 8083 BP; 1833 A; 2215 C; 2247 G; 1788 T; 0 other;

Query Match 0.1%; Score 21; DB 16; Length 8083;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7319 GTGACGCCCTGCGGCCAG 7339
DB 904 GTGACGCCCTGCGGCCAG 884
|||||

RESULT 29
AAO90134/C
ID AAO90134 standard; DNA; 8135 BP.
XX
AC AAO90134;
XX
DT 25-MAR-2003 (updated)
DT 11-NOV-1995 (first entry)
XX
DE Plasmid PBHVKex-1::gIII/p53.
XX
KM Plasmid PBHVKex-1::gIII/p53; vector; gp53 protein mutant;
KM bovine viral diarrhoea virus 2724; major glycoprotein;
KM pseudorabies virus gIII signal peptide; attenuation;
KM Plasmid pUC1564; Escherichia coli; recombinant vaccine; ds.
XX
OS Bovine viral diarrhoea virus (2724).
OS
PN WO9512682-A2.
PN
PD 11-MAY-1995.
PD
PF 31-OCT-1994; 94WO-US12198.
PF
PR 05-NOV-1993; 93US-0147810.
PR
XX (UPJO) UPJOHN CO.
PA
XX Haanes EJ, Wardley RC;
PI
XX WPI: 1995-185781/24.
DR
XX A replicating non-pathogenic virus containing a BVDV gene - for
PT vaccination against disease caused by bovine viral diarrhoea virus
XX
PS Claim 17; Page 30-34; 60pp; English.
XX
CC The sequence corresponds to plasmid PBHVKex-1::gIII/p53, which
CC contains a bovine viral diarrhoea virus (BVDV) major glycoprotein
CC gp53 mutant gene preceded by a pseudorabies virus gIII signal
CC peptide sequence in plasmid pHAS4-delta-Bxex-1. The plasmid
CC may be used to produce a replicating non-pathogenic virus, T11-3
CC (deposited as plasmid pUC1564 in Escherichia coli 15085, NRRL

CC B-21350), for use as a safe attenuated recombinant vaccine
CC against BVDV in animals.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 8135 BP; 1778 A; 2325 C; 2180 G; 1852 T; 0 other;

Query Match 0.1%; Score 21; DB 16; Length 8135;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7319 GTGACGCCCTGCGGCCAG 7339
DB 904 GTGACGCCCTGCGGCCAG 884
|||||

RESULT 30
AAO90136/C
ID AAO90136 standard; DNA; 8135 BP.
XX
AC AAO90136;
XX
DT 25-MAR-2003 (updated)
DT 11-NOV-1995 (first entry)
XX
DE Plasmid PBHVKex-3::gIII/p53.
XX
KM Plasmid PBHVKex-3::gIII/p53; vector; gp53 protein mutant;
KM bovine viral diarrhoea virus 2724; major glycoprotein;
KM pseudorabies virus gIII signal peptide; attenuation;
KM Plasmid pUC1565; Escherichia coli; recombinant vaccine; ds.
XX
OS Bovine viral diarrhoea virus (2724).
OS
PN WO9512682-A2.
PN
PD 11-MAY-1995.
PD
PF 31-OCT-1994; 94WO-US12198.
PF
PR 05-NOV-1993; 93US-0147810.
PR
XX (UPJO) UPJOHN CO.
PA
XX Haanes EJ, Wardley RC;
PI
XX WPI: 1995-185781/24.
DR
XX A replicating non-pathogenic virus containing a BVDV gene - for
PT vaccination against disease caused by bovine viral diarrhoea virus
XX
PS Claim 17; Page 39-43; 60pp; English.
XX
CC The sequence corresponds to plasmid PBHVKex-3::gIII/p53, which
CC contains a bovine viral diarrhoea virus (BVDV) major glycoprotein
CC gp53 mutant gene preceded by a pseudorabies virus gIII signal
CC peptide sequence in plasmid pHAS4-delta-Bxex-3. The plasmid
CC may be used to produce replicating non-pathogenic virus T11-8
CC (deposited as plasmid pUC1565 in Escherichia coli UC 15086, NRRL
CC B-21351), for use as a safe attenuated recombinant vaccine
CC against BVDV in animals.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 8135 BP; 1833 A; 2242 C; 2262 G; 1798 T; 0 other;

Query Match 0.1%; Score 21; DB 16; Length 8135;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7319 GTGACGCCCTGCGGCCAG 7339
DB 904 GTGACGCCCTGCGGCCAG 884
|||||

```
RESULT 31
AA090133/c
ID AA090133 standard; DNA: 8149 BP.
XX
XX
AC AA090133;
XX
XX
DT 25-MAR-2003 (updated)
DT 11-NOV-1995 (first entry)
XX
XX
DE Plasmid PBHVKex-1::gBGH/p53.
XX
XX
KW Plasmid PBHVKex-1::gBGH/p53; vector: gp53 protein mutant;
KW bovine viral diarrhoea virus 2724; major glycoprotein;
KW bovine somatotropin signal peptide; attenuation;
KW recombinant vaccine; ds.
XX
XX
OS Bovine viral diarrhoea virus (2724).
XX
XX
PN W09512682-A2.
XX
XX
PD 11-MAY-1995.
XX
XX
PF 31-OCT-1994; 94WO-US12198.
XX
XX
PR 05-NOV-1993; 93US-0147810.
XX
XX
PA (UPJO ) UPJOHN CO.
XX
XX
PI Haanes EJ, Wardley RC;
XX
XX
DR WPI: 1995-185781/24.
XX
XX
PT A replicating non-pathogenic virus containing a BVDV gene - for
PT vaccination against disease caused by bovine viral diarrhoea virus
XX
XX
XX
PS Claim 17; Page 26-30; 60pp; English.
XX
XX
XX
CC The sequence corresponds to plasmid PBHVKex-1::gBGH/p53, which
CC contains a bovine viral diarrhoea virus (BVDV) major glycoprotein
CC gp53 mutant gene preceded by a bovine somatotropin signal peptide
CC sequence in plasmid pHAS4-delta-BKex-1. The plasmid may be used
CC to produce a replicating non-pathogenic virus, T11-6 (deposited
CC as ATCC VR 2436) for use as a safe attenuated recombinant vaccine
CC against BVDV in animals.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
XX
SQ Sequence 8149 BP; 1784 A; 2324 C; 2185 G; 1856 T; 0 other;

Query Match 0.1%; Score 21; DB 16; Length 8149;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7319 GTGACGGCCCTGCGGCCAG 7339
DB 904 GTGACGGCCCTGCGGCCAG 884

RESULT 32
AA090135/c
ID AA090135 standard; DNA: 8149 BP.
XX
XX
AC AA090135;
XX
XX
DT 25-MAR-2003 (updated)
DT 11-NOV-1995 (first entry)
XX
XX
DE Plasmid PBHVKex-3::BGH/p53.
XX
XX
KW Plasmid PBHVKex-3::BGH/p53; vector: gp53 protein mutant;
KW bovine viral diarrhoea virus 2724; major glycoprotein;
KW bovine somatotropin signal peptide; attenuation;
KW recombinant vaccine; ds.
XX
XX
```

```
OS Bovine viral diarrhoea virus (2724).
XX
XX
PN W09512682-A2.
XX
XX
ED 11-MAY-1995.
XX
XX
PF 31-OCT-1994; 94WO-US12198.
XX
XX
PR 05-NOV-1993; 93US-0147810.
XX
XX
PA (UPJO ) UPJOHN CO.
XX
XX
PI Haanes EJ, Wardley RC;
XX
XX
DR WPI: 1995-185781/24.
XX
XX
PT A replicating non-pathogenic virus containing a BVDV gene - for
PT vaccination against disease caused by bovine viral diarrhoea virus
XX
XX
XX
PS Claim 17; Page 35-38; 60pp; English.
XX
XX
XX
CC The sequence corresponds to plasmid PBHVKex-3::BGH/p53, which
CC contains a bovine viral diarrhoea virus (BVDV) major glycoprotein
CC gp53 mutant gene preceded by a bovine somatotropin signal
CC peptide sequence in plasmid pHAS4-delta-BKex-3. The plasmid
CC may be used to produce a replicating non-pathogenic virus for use
CC as a safe attenuated recombinant vaccine against BVDV in animals.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
XX
SQ Sequence 8149 BP; 1836 A; 2246 C; 2263 G; 1804 T; 0 other;

Query Match 0.1%; Score 21; DB 16; Length 8149;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7319 GTGACGGCCCTGCGGCCAG 7339
DB 904 GTGACGGCCCTGCGGCCAG 884

RESULT 33
AAS45354
ID AAS45354 standard; DNA: 8513 BP.
XX
XX
AC AAS45354;
XX
XX
DT 18-DEC-2001 (first entry)
XX
XX
XX
CC Chemically pretreated genomic DNA associated with cell cycle #30.
XX
XX
DE Cell cycle: human; CPG dinucleotide; cytosine methylation; HIV; aging;
XX human immunodeficiency virus; neurodegenerative disorder; solid tumour;
XX graft-versus-host disease; glomerular disease; Lewy body disease; cancer;
XX arthritis; arteriosclerosis; anti-HIV; neuroprotective; antiarteriosclerotic;
XX immunosuppressive; antitumour; cytostatic; antiarteriosclerotic; ds;
XX PCR primer.
XX
XX
OS Homo sapiens.
XX
XX
PN W0200168911-A2.
XX
XX
PD 20-SEP-2001.
XX
XX
PE 15-MAR-2001; 2001WO-EP02945.
XX
XX
PF 15-MAR-2000; 2000DE-1013847.
XX
XX
PR 06-APR-2000; 2000DE-1019058.
XX
XX
PR 07-APR-2000; 2000DE-1019173.
XX
XX
PR 30-JUN-2000; 2000DE-1032529.
XX
XX
PR 01-SEP-2000; 2000DE-1043826.
XX
XX
PA (EPIG-) EPIGENOMICS AG.
XX
XX
```

PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-602751/68.
 XX
 PT Designing primers and probes for analysing diseases associated with
 PT cytosine methylation state e.g. arthritis, cancer, aging,
 PT arteriosclerosis comprising fragments of chemically modified genes
 PT associated with cell cycle -
 XX
 PS Claim 1; SEQ ID No 59; 28bp; English.
 XX
 CC Sequences AAS45296-AAS45520 represent chemically pretreated genomic DNA
 CC molecules associated with the cell cycle and specific PCR primers of the
 CC invention. The sequences are useful for detecting the methylation state
 CC of all CpG dinucleotides in a sequence and therefore for analysing
 CC associated diseases. By analysing cytosine methylations in the pretreated
 CC DNA, genetic and/or epigenetic parameters for the diagnosis and therapy
 CC of existing diseases or the predisposition to specific diseases can be
 CC ascertained. The parameters may be compared to another set of genetic
 CC and/or epigenetic parameters, the differences serving as basis for
 CC diagnosis and/or prognosis events which are disadvantageous to patients.
 CC The sequences of the invention are useful for the diagnosis and therapy
 CC of HIV infection, neurodegenerative disorders, graft-versus-host disease,
 CC aging, glomerular disease, Lewy body disease, arthritis,
 CC arteriosclerosis, solid tumours and cancers.
 CC
 SQ Sequence 8513 BP; 1821 A; 233 C; 2456 G; 4003 T; 0 other;
 Query Match 0.1%; Score 21; DB 22; Length 8513;
 Best Local Similarity 100.0%; Pred. No. 3e+02;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 16956 GAGTCGGGAGATTGTTT 16976
 DB 5725 GAGTCGGGAGATTGTTT 5745
 RESULT 34
 AAS46367
 ID AAS46367 standard; DNA; 8513 BP.
 XX
 AC AAS46367;
 XX
 DT 18-DEC-2001 (first entry)
 XX
 DE Tumour suppressor gene derived chemically modified sequence #89.
 XX
 KW Human; tumour suppressor gene; oncogene; antitumour; cytostatic;
 KW cancer; tumour; CpG dinucleotide; single-nucleotide polymorphism; SNP;
 KW cytosine methylation; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200168912-A2.
 XX
 PD 20-SEP-2001.
 XX
 PF 15-MAR-2001; 2001WO-EP02955.
 XX
 PR 15-MAR-2000; 2000DE-1013847.
 PR 06-APR-2000; 2000DE-1019058.
 PR 07-APR-2000; 2000DE-1019173.
 PR 30-JUN-2000; 2000DE-1032529.
 PR 01-SEP-2000; 2000DE-1043826.
 XX
 PA (EPIC-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-602752/68.
 XX
 PT Fragments of chemically modified genes associated with tumour suppressor
 PT genes and oncogenes, useful in designing primers and probes for

PT analysing diseases associated with cytosine methylation state e.g.
 PT cancer -
 XX
 PS Claim 1; SEQ ID No 89; 27bp; English.
 XX
 CC The invention relates to a nucleic acid comprising a sequence of 18
 CC bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with
 CC bisulphite, of genes associated with tumour suppression and
 CC oncogenes having a sequence taken from 536 (actually 533 since
 CC numbers 408; 458 and 500 are missing from the sequence listing) sequences
 CC (Ss) and sequences complementary to (Ss). The nucleic acid may be a
 CC peptide nucleic acid-oligonucleotide (PNA) of at least 9 nucleotides and may
 CC form part of a set of probes for detecting the cytosine methylation state
 CC and/or single nucleotide polymorphisms and also to be used in an
 CC array for analysing diseases associated with CpG dinucleotides e.g.
 CC cancers and tumours. The probes can also be used in a method for
 CC ascertaining genetic and/or epigenetic parameters for the diagnosis
 CC and/or therapy of existing diseases or the predisposition to specific
 CC diseases, by analysing cytosine methylations. The parameters may be
 CC compared to another set of genetic and/or epigenetic parameters, the
 CC differences serving as basis for diagnosis and/or prognosis events which
 CC are disadvantageous to patients. The present sequence is one of the
 CC 533 genomic sequences derived from tumour suppressor genes and
 CC oncogenes.
 CC Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic
 CC format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 CC
 SQ Sequence 8513 BP; 1821 A; 233 C; 2456 G; 4003 T; 0 other;
 Query Match 0.1%; Score 21; DB 22; Length 8513;
 Best Local Similarity 100.0%; Pred. No. 3e+02;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 16956 GAGTCGGGAGATTGTTT 16976
 DB 5725 GAGTCGGGAGATTGTTT 5745
 RESULT 35
 ABN80094
 ID ABN80094 standard; DNA; 8513 BP.
 XX
 AC ABN80094;
 XX
 DT 15-JUL-2002 (first entry)
 XX
 DE Human chemically modified disease associated gene SEQ ID NO 111.
 XX
 KW Human; development; homeobox gene; HOX; diabetes; cancer; apoptosis;
 KW heart disease; epilepsy; histone deacetylation; muscular dystrophy;
 KW dwarfism; single nucleotide polymorphism; SNP; cytosine methylation;
 KW antidiabetic; cytostatic; anticonvulsant; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200200927-A2.
 XX
 PD 03-JAN-2002.
 XX
 PF 02-JUL-2001; 2001WO-EP07536.
 XX
 PR 30-JUN-2000; 2000DE-1032529.
 PR 01-SEP-2000; 2000DE-1043826.
 XX
 PA (EPIC-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2002-130908/17.

PT Novel nucleic acid useful for diagnosis and therapy of diseases
PT associated with development genes such as diabetes, comprises a
PT sequence of a segment of chemically pretreated DNA of genes associated
PT with development
PS Claim 1; SEQ ID NO 111; 27pp; English.
XX
XX The invention relates to a nucleic acid (I) comprising a sequence at
CC least 18 bases in length of a segment of chemically pretreated DNA (II)
CC of genes associated with development selected from 87 genes listed in
CC the specification such as ACCPN, ADPN, or AFD and comprising one of 350
CC sequences (ABN79984-ABN80333) or their complements. The invention is
CC useful for the diagnosis or therapy of diseases associated with
CC development genes, in particular disease related to homeobox containing
CC genes (HOX), like diabetes, cancer, apoptosis related diseases, syndromes
CC associated with congenital heart disease, epilepsy, diseases related to
CC histone deacetylation, Currarino syndrome, diseases related with the
CC development of the brain and limb girdle muscular dystrophy and dwarfism.
CC Oligomers specific to each of the genes are useful for detecting the
CC methylation state of all CpG dinucleotides within the 350 sequences or
CC (II) and their complementary sequences, as primer oligonucleotides for
CC the amplification of the 350 sequences, (II) and/or their complements and
CC as oligomer probes for detecting the cytosine methylation state and/or
CC single nucleotide polymorphisms (SNPs).
CC Note: The sequence data for this patent did not form part of the printed
CC specification but is based on sequence information supplied to Derwent by
CC the European Patent Office.
XX
SQ Sequence 8513 BP; 1821 A; 233 C; 2456 G; 4003 T; 0 other;
Query Match 0.1%; Score 21; DB 24; Length 8513;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 16956 GAGTCGGGAGATTGTGTTT 16976
DB 5725 GAGTCGGGAGATTGTGTTT 5745
RESULT 36
ABK28187
ID ABK28187 standard; DNA: 8513 BP.
XX
AC ABK28187;
XX
DT 23-APR-2002 (first entry)
XX
DE DNA transcription associated genomic DNA #31.
XX
XX PNA transcription associated gene; peptide nucleic acid; PNA-oligomer;
KW PNA: cytosine methylation state; SNP; retroviral infection; gene; ds;
KW single nucleotide polymorphism; adenosine deaminase deficiency; cancer;
KW viral infection; Sezary syndrome; hematological disorder; tuberculosis;
KW immunological disorder; Werner syndrome; developmental disorder;
KW psoriasis; Rieger's syndrome; neurological disorder; erythropoiesis;
KW neurodegenerative disorder; Wardenburg syndrome; Niemann-Pick disease;
KW myelodysplastic syndrome; myocardial infarction; hypertension; arthritis;
KW angiodysplasia; congenital heart disease; HDR syndrome; gene therapy;
KW polyglutamine disorder; solid tumour.
OS Unidentified.
XX
XX WO200192565-A2.
XX
XX 06-DEC-2001.
XX
XX 06-APR-2001; 2001WO-EP03973.
XX
XX 06-APR-2000; 2000DE-1019058.
XX
XX 07-APR-2000; 2000DE-1019173.
XX
XX 30-JUN-2000; 2000DE-1032529.
XX
XX 01-SEP-2000; 2000DE-1043826.
XX

PA (EPIC-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI: 2002-090046/12.
XX
XX
XX New nucleic acids or oligomers, useful for diagnosing or treating
PT diseases associated with DNA transcription, e.g. immunological
PT disorders, Werner syndrome, psoriasis, myocardial infarction, solid
PT tumours or cancer
PS Claim 1; SEQ ID NO 61; 32pp; English.
XX
XX The invention relates to a nucleic acid, which comprises a segment of the
CC chemically pretreated DNA of genes associated with DNA transcription from
CC one of 346 sequences, and an oligomer, in particular an oligonucleotide
CC or peptide nucleic acid (PNA)-oligomer that hybridises to or is identical
CC to the chemically pretreated DNA of genes associated with DNA
CC transcription. The set of oligomer probes are useful for detecting the
CC cytosine methylation state and/or single nucleotide polymorphisms (SNPs)
CC in a chemically pretreated genomic DNA. The nucleic acids are useful for
CC diagnosing or treating diseases associated with DNA transcription
CC (particularly with the methylation status), e.g. adenosine deaminase
CC deficiency, viral infection, retroviral infection, Sezary syndrome,
CC haematological disorders, immunological disorders, Werner syndrome,
CC tuberculosis, developmental disorders, psoriasis, Rieger's syndrome,
CC neurological disorders, neurodegenerative disorders, Wardenburg
CC syndrome, Niemann-Pick disease, myelodysplastic syndrome, myocardial
CC infarction, hypertension, angiodysplasia, erythropoiesis, congenital heart
CC disease, HDR syndrome, arthritis, polyglutamine disorders, solid tumours
CC or cancer. Sequences ABK28127-ABK28472 represent DNA transcription
CC associated genomic DNA molecules of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification but was obtained in electronic format directly from the
CC European Patent Office.
XX
XX
SQ Sequence 8513 BP; 1821 A; 233 C; 2456 G; 4003 T; 0 other;
Query Match 0.1%; Score 21; DB 24; Length 8513;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 16956 GAGTCGGGAGATTGTGTTT 16976
DB 5725 GAGTCGGGAGATTGTGTTT 5745
RESULT 37
ABL05364/C
ID ABL05364 standard; cDNA: 36383 BP.
XX
XX ABL05364;
XX
XX 26-MAR-2002 (first entry)
XX
XX Drosophila melanogaster expressed polynucleotide SEQ ID NO 10574.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 10574.
XX
XX Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical; gene; ss.
XX
XX Drosophila melanogaster.
XX
XX WO200171042-A2.
XX
XX 27-SEP-2001.
XX
XX 23-MAR-2001; 2001WO-US09231.
XX
XX 23-MAR-2000; 2000US-191637P.
XX
XX 11-JUL-2000; 2000US-0614150.
XX
XX (PEKE) PE CORP NY.
XX

PI Venter JC, Adams M, Li PMD, Myers EW;
XX WPI: 2001-656860/75.
DR P-PSDB: ABB61261.
XX
XX
XX New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
XX
XX
XX Claim 1: SEQ ID NO 10574; 21bp + Sequence Listing; English.
XX
XX The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (AB16176-AB130511), expressed DNA
CC sequences (AB101840-AB16175) and the encoded proteins
CC (AB157737-AB172072).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 36383 BP; 10996 A; 6940 C; 6897 G; 11550 T; 0 other;
SQ
XX
XX Query Match 0.1%; Score 21; DB 23; Length 36383;
XX Best Local Similarity 100.0%; Pred. No. 2.6e+02;
XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 28437 TAAATAATAAATACACGCA 28457
DB 11364 TAAATAATAAATACACGCA 11344
AAH74201
ID AAH74201 standard; DNA; 124884 BP.
XX
XX AAH74201;
XX
XX 15-OCT-2001 (first entry)
XX
XX Nucleotide sequence of the Varicella virus Dumas strain.
XX
XX Dumas strain; pox vaccine; vaccine; poxvirus disease; chickenpox; ss.
XX
XX Varicella virus.
XX
XX WO200156600-A1.
XX
XX 09-AUG-2001.
XX
XX 31-JAN-2001; 2001WO-JP00678.
XX
XX 31-JAN-2000; 2000JP-0062734.
XX
XX (OSAU) UNITV OSAKA.
XX
XX Gomi Y, Sunamachi H, Takahashi M, Yamanishi K;
XX
XX WPI: 2001-488845/53.
XX
XX Method for checking absence of mutation at specific positions of
PT varicella virus genome for quality control of attenuated live varicella
PT vaccine -
XX
XX Claim 1: Page 61-105; 158pp; Japanese.
XX
XX The present sequence represents the nucleotide sequence of Varicella
CC virus, Dumas strain. The specification describes a method for the
CC quality control of an attenuated pox vaccine, characterised in that
CC the DNA sequence of specific parts of the viral genome in a sample is
CC determined and proved to be conserved rather than mutated in comparison

CC with the same parts of a reference viral genome. The method is useful
CC for quality control of vaccines for use in the prevention of poxvirus
CC diseases such as chickenpox.
XX
XX Sequence 124884 BP; 33789 A; 29295 C; 28177 G; 33623 T; 0 other;
SQ
XX
XX Query Match 0.1%; Score 21; DB 22; Length 124884;
XX Best Local Similarity 100.0%; Pred. No. 2.3e+02;
XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 26777 CATAGTATCGTCGTCGCC 26797
DB 96832 CATAGTATCGTCGTCGCC 96852
AAH74202
ID AAH74202 standard; DNA; 125157 BP.
XX
XX AAH74202;
XX
XX 15-OCT-2001 (first entry)
XX
XX Nucleotide sequence of the Varicella virus Oka strain.
XX
XX Oka strain; pox vaccine; vaccine; poxvirus disease; chickenpox; ss.
XX
XX Varicella virus.
XX
XX WO200156600-A1.
XX
XX 09-AUG-2001.
XX
XX 31-JAN-2001; 2001WO-JP00678.
XX
XX 31-JAN-2000; 2000JP-0062734.
XX
XX (OSAU) UNITV OSAKA.
XX
XX Gomi Y, Sunamachi H, Takahashi M, Yamanishi K;
XX
XX WPI: 2001-488845/53.
XX
XX Method for checking absence of mutation at specific positions of
PT varicella virus genome for quality control of attenuated live varicella
PT vaccine -
XX
XX Disclosure: Page 106-150; 158pp; Japanese.
XX
XX The present sequence represents the nucleotide sequence of Varicella
CC virus, Oka strain. The specification describes a method for the
CC quality control of an attenuated pox vaccine, characterised in that
CC the DNA sequence of specific parts of the viral genome in a sample is
CC determined and proved to be conserved rather than mutated in comparison
CC with the same parts of a reference viral genome. The method is useful
CC for quality control of vaccines for use in the prevention of poxvirus
CC diseases such as chickenpox.
XX
XX Sequence 125157 BP; 33776 A; 29439 C; 28285 G; 33624 T; 33 other;
SQ
XX
XX Query Match 0.1%; Score 21; DB 22; Length 125157;
XX Best Local Similarity 100.0%; Pred. No. 2.3e+02;
XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 26777 CATAGTATCGTCGTCGCC 26797
DB 96778 CATAGTATCGTCGTCGCC 96798
AAH74202
ID AAH74202 standard; DNA; 255 BP.
XX
XX RESULT 40
XX ABR80864/C
XX ABR80864 standard; DNA; 255 BP.

AC ABR80864;
XX 13-AUG-2002 (first entry)
XX
XX
DE Bacillus clausii genomic sequence tag (GST) #3707.
XX
XX Differential gene expression; genomic sequenced tag; GST;
KW altered culture condition; environmental stress;
KW physiological provocation; ds.
XX
OS Bacillus clausii.
XX
PN WO200229113-A2.
XX
PD 11-APR-2002.
XX
PE 05-OCT-2001; 2001WO-US31437.
XX
PR 06-OCT-2000; 2000US-0680598.
PR 27-MAR-2001; 2001US-279526P.
XX
XX (NOVO) NOVOZYMES BIOTECH INC.
PA (NOVO) NOVOZYMES AS.
XX
XX Berka R, Clausen IG;
PI
XX WPI; 2002-416684/44.
DR
XX
PT Monitoring differential expression of several genes in first Bacillus
PT cell relative to expression of same genes in one or more second
PT Bacillus cells, by using substrate containing Bacillus genomic
PT sequenced tag array
XX
XX
PS Claim 11; SEQ ID NO 8155; 200pp; English.
XX
XX The invention describes a method of monitoring differential expression of
CC genes in a first Bacillus cell relative to expression of the genes in
CC other Bacillus cells, comprising hybridising labeled nucleic acid probes
CC isolated from Bacillus cells to a substrate containing array of Bacillus
CC genomic sequenced tags (GST), examining the array, and determining
CC relative gene expression by an observed hybridisation reporter signal of
CC a spot in the array. The method is useful for measuring the expression of
CC genes in a first Bacillus cell relative to expression of the same genes
CC in one or more second Bacillus cells. The method is useful for monitoring
CC global expression of several genes from a Bacillus cell, discovering new
CC genes, identifying possible functions of unknown open reading frames and
CC monitoring gene copy number variation and stability. Monitoring changes
CC in expression of genes may be used to provide a representation of the way
CC in which Bacillus cells adapt to changes in culture conditions,
CC environmental stress or other physiological provocation. Extensive
CC follow-up characterisation is unnecessary, when one spot on an array
CC equals one gene or one open reading frame, since sequence information is
CC available. This sequence represents a genomic sequence tag (GST) used in
CC the method of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 255 BP; 71 A; 43 C; 68 G; 73 T; 0 other;
SQ
Query Match 0.1%; Score 20; DB 24; Length 255;
Best Local Similarity 100.0%; Pred. No. 1,1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 32834 CACACAGAAAAAATTTTGA 32853
DB 42 CACACAGAAAAAATTTTGA 23

RESULT 41
ABX74858/c
ID ABX74858 standard; cDNA: 282 BP.

XX
XX ABX74858;
AC
XX
XX 21-MAR-2003 (first entry)
DE Human cDNA sequence #109 up-regulated in CC-RCC patients.
XX
XX Human; microarray; solid surface; immobilised probe; CC-RCC;
KW differential expression profile; aggressive CC-RCC tumour type;
KW non-aggressive CC-RCC tumour type; clear cell renal carcinoma;
KW gene expression profiling; tumour tissue; gene; ss.
XX
XX Homo sapiens.
OS
PN WO200279411-A2.
XX
PD 10-OCT-2002.
XX
XX 29-MAR-2002; 2002WO-US09576.
PE
XX 29-MAR-2001; 2001US-279411P.
PR
XX (VAND-) VAN ANDEL INST.
PA
XX
XX Haab B, Rhodes D, Teh BT, Takashi M;
PI
XX WPI; 2003-040679/03.
DR
XX
PT New microarray, comprising a matrix of cDNA probe from a set of probes
PT immobilised to a solid surface in predetermined order, useful in the
PT prognosis of patients with clear cell renal carcinoma
XX
XX
PS Claim 35; SEQ ID NO 219; 179pp; English.
XX
XX The present invention relates to a microarray comprising a matrix of
CC at least one cDNA probe from a set of probes immobilised to a solid
CC surface in a predetermined order, where a row of pixels corresponds
CC to replicates of one distinct probe from the set. The probes are
CC complementary to nucleic acid sequences that are expressed
CC differentially in aggressive as compared to non-aggressive types of
CC clear cell renal carcinoma (CC-RCC) and that hybridise to the probes
CC under high stringency conditions. The microarray is useful for the
CC prognosis of patients with CC-RCC, wherein aggressive and
CC non-aggressive CC-RCC tumour types are characterised by differential
CC expression profiles of genes that hybridise with one or more probes
CC immobilised on the microarray. The arrays are useful for gene
CC expression profiling of tumour and normal tissues. The present
CC sequence represents a human cDNA sequence up-regulated in CC-RCC
CC patients.
XX
XX Sequence 282 BP; 109 A; 49 C; 39 G; 82 T; 3 other;
SQ
Query Match 0.1%; Score 20; DB 25; Length 282;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 3732 AAGTAACCCCAAAATGTTA 3751
DB 207 AAGTAACCCCAAAATGTTA 188

RESULT 42
ABV62066/c
ID ABV62066 standard; cDNA: 310 BP.
XX
XX ABV62066;
AC
XX
XX 13-SEP-2002 (first entry)
DE Human prostate expression marker cDNA 62057.
XX
XX Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW pharmacogenomic marker; gene; ss.

XX Homo sapiens.
 OS
 XX
 XX WO200160860-A2.
 PN
 XX
 PD 23-AUG-2001.
 XX
 PF 20-FEB-2001: 2001MO-US05171.
 XX
 XX 17-FEB-2000: 2000US-183319P.
 PR 16-MAR-2000: 2000US-189862P.
 PR 25-MAY-2000: 2000US-207454P.
 PR 09-JUN-2000: 2000US-211314P.
 PR 18-JUL-2000: 2000US-219007P.
 PR 13-DEC-2000: 2000US-255281P.
 XX
 XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 PA
 PI Schlegel R, Endege WO, Monahan JE;
 XX
 XX WPI: 2001-662795/76.
 DR
 XX Novel isolated nucleic acid molecule associated with cancerous state of
 PT prostate cells and correlating with presence of prostate cancer, useful
 PT for detecting presence of prostate cancer, stage of prostate cancer -
 XX
 PS Claim 1: Page 11728; 11750pp: English.
 XX
 XX The invention relates to an isolated nucleic acid molecule (1) comprising
 CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
 CC specification or its complement. (1) is useful for:
 CC (a) assessing whether a patient is afflicted with prostate cancer;
 CC (b) monitoring the progression of prostate cancer in a patient;
 CC (c) assessing the efficacy of a test compound to inhibit prostate
 CC cancer in a patient;
 CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
 CC in a patient;
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;
 CC (f) assessing the prostate cell carcinogenic potential of a compound;
 CC (g) determining whether prostate cancer has metastasized in a patient;
 CC (h) assessing the aggressiveness or indolence of prostate cancer in a
 CC patient;
 CC (1) is also useful as a pharmacodynamic or pharmacogenomic marker.
 CC
 SQ Sequence 310 BP; 94 A; 42 C; 59 G; 115 T; 0 other;
 Query Match 0.1%; Score 20; DB 23; Length 310;
 Best Local Similarity 100.0%; Pred. No. 1e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 30927 GCAACATCAATTAATATATA 30946
 Db 37 GCAACATCAATTAATATATA 18
 RESULT 43
 ABRK79195
 ID ABRK79195 standard; DNA; 356 BP.
 AC ABRK79195;
 XX
 DT 13-AUG-2002 (first entry)
 XX
 DE Bacillus clausii genomic sequence tag (GST) #2038.
 XX
 XX Differential gene expression; genomic sequenced tag; GST;
 KW altered culture condition; environmental stress;
 KW physiological provocation; ds.
 OS Bacillus clausii.
 XX
 XX WO200229113-A2.
 PN

PD 11-APR-2002.
 XX
 XX 05-OCT-2001: 2001MO-US31437.
 PE
 XX
 XX 06-OCT-2000: 2000US-0680598.
 PR 27-MAR-2001: 2001US-279526P.
 PR
 XX
 PA (NOVO) NOVOZYMES BIOTECH INC.
 PA (NOVO) NOVOZYMES AS.
 PI Berka R, Clausen IG;
 XX
 XX WPI: 2002-416684/44.
 DR
 XX
 XX Monitoring differential expression of several genes in first Bacillus
 PT cell relative to expression of same genes in one or more second
 PT Bacillus cells, by using substrate containing Bacillus genomic
 PT sequenced tag array -
 XX
 PS Claim 11: SEQ ID NO 6486; 200pp: English.
 XX
 XX The invention describes a method of monitoring differential expression of
 CC genes in a first Bacillus cell relative to expression of the genes in
 CC other Bacillus cells, comprising hybridising labelled nucleic acid probes
 CC isolated from Bacillus cells to a substrate containing array of Bacillus
 CC genomic sequenced tags (GST), examining the array, and determining
 CC relative gene expression by an observed hybridisation reporter signal of
 CC a spot in the array. The method is useful for measuring the expression of
 CC genes in a first Bacillus cell relative to expression of the same genes
 CC in one or more second Bacillus cells. The method is useful for monitoring
 CC global expression of several genes from a Bacillus cell, discovering new
 CC genes, identifying possible functions of unknown open reading frames and
 CC monitoring gene copy number variation and stability. Monitoring changes
 CC in expression of genes may be used to provide a representation of the way
 CC in which Bacillus cells adapt to changes in culture conditions,
 CC environmental stress or other physiological provocation. Extensive
 CC follow-up characterisation is unnecessary, when one spot on an array
 CC equals one gene or one open reading frame, since sequence information is
 CC available. This sequence represents a genomic sequence tag (GST) used in
 CC the method of the invention.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at
 CC ftp.wipo.int/pub/published_pct_sequences.
 CC
 SQ Sequence 356 BP; 107 A; 62 C; 89 G; 97 T; 1 other;
 Query Match 0.1%; Score 20; DB 24; Length 356;
 Best Local Similarity 100.0%; Pred. No. 1e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 26291 TGGTGTGGGAAAGTACCA 26310
 Db 68 TGGTGTGGGAAAGTACCA 87
 RESULT 44
 ABA14638/C
 ID ABA14638 standard; DNA; 456 BP.
 AC ABA14638;
 XX
 DT 23-JAN-2002 (first entry)
 XX
 DE Human nervous system related polynucleotide SEQ ID NO 6969.
 XX
 XX Human; nocitropic; neuroprotective; cyrostatic; dermatological; virocidic;
 KW immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnery;
 KW antiparkinsonian; antistoking; antianaemic; antiarthritic; cancer;
 KW antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;
 KW antiallergic; antidiabetic; anticonvulsant; antifungal;
 KW antiparasitic; cardiac; immune disorder; cardiovascular disorder;
 KW neurological disease; infection; nephrotropic; gene therapy; vaccine; ds.

XX Homo sapiens.
OS
XX
PN WO200159063-A2.
XX
PD 16-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01334.
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225215.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225477.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226868.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
XX

PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 20-OCT-2000; 2000US-0242221.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250391.
PR 01-DEC-2000; 2000US-0251160.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 06-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX

PA (HUMA-) HUMAN GENOME SCI INC.
 XX Rosen CA, Barash SC, Ruben SM;
 XX WPI; 2001-541565/60.
 DR Nucleic acids encoding 3224 human nervous system antigen polypeptides,
 XX useful for preventing, diagnosing and/or treating nervous system
 PT cancers and metastases -
 PS Disclosure; SEQ ID NO 6969; 1701pp + Sequence Listing; English.
 XX
 CC The invention relates to novel genes (ABAI1004-ABA2153) and proteins
 CC (ABAI4678-ABAI8001) useful for preventing, treating or ameliorating
 CC medical conditions e.g. by protein or gene therapy. The genes are
 CC isolated from a range of human tissues disclosed in the specification.
 CC The nucleic acids, proteins, antibodies and (ant)agonists are useful
 CC in the diagnosis, treatment and prevention of: (a) cancer e.g. breast
 CC and ovarian cancer and other cancers of the adrenal gland, bone, bone
 CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
 CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune
 CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
 CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative
 CC colitis; (c) cardiovascular disorders such as myocardial ischaemia;
 CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
 CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
 CC and parasitic infections.
 CC Note: The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 456 BP; 143 A; 63 C; 83 G; 167 T; 0 other;
 Query Match 0.1%; Score 20; DB 22; Length 456;
 Best Local Similarity 100.0%; Pred. No. 1e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 30927 GCAACATCAATTAATATA 30946
 DB 78 GCAACATCAATTAATATA 59
 RESULT 45
 ABN94325
 ID ABN94325 standard; DNA; 461 BP.
 XX
 AC ABN94325;
 XX
 DT 13-AUG-2002 (first entry)
 XX
 DE Gene #823 used to diagnose liver cancer.
 XX
 KW Gene; liver cancer; ds; hepatocellular carcinoma; hepatotropic;
 KW metastatic liver tumour; cytostatic; expression profile; disease state;
 KW disease progression; drug toxicity; drug efficacy; drug metabolism.
 XX
 OS Homo sapiens.
 XX
 PN WO200229103-A2.
 PD 11-APR-2002.
 XX
 PF 02-OCT-2001; 2001WO-US30589.
 XX
 PR 02-OCT-2000; 2000US-237054P.
 XX
 PA (GENE-) GENE LOGIC INC.
 XX
 PI Horne D, Alvares C, Peres-Da-Silva S, Vockley JG;
 DR WPI; 2002-426119/45.
 XX
 PT Diagnosing and detecting the progression of liver cancer,

PT hepatocellular carcinoma or metastatic liver tumor in a patient,
 PT involves detecting the level of expression of two or more genes in a
 PT liver tissue sample -
 XX
 PS Claim 1; SEQ ID NO 823; 298pp; English.
 XX
 CC The invention relates to a novel method for diagnosing and detecting the
 CC progression of liver cancer, hepatocellular carcinoma or metastatic liver
 CC tumour in a patient, and differentiating metastatic liver cancer from
 CC hepatocellular carcinoma in a patient, involving detecting the level of
 CC expression of two or more genes represented in ABN93503-ABN97455 in a
 CC tissue sample. The method of the invention has hepatotropic, and
 CC cytostatic activity. The method is useful for diagnosing and detecting
 CC the progression of liver cancer, hepatocellular carcinoma and metastatic
 CC liver carcinoma in a patient. The method is useful for identifying
 CC expression profiles which serve as useful diagnostic markers as well as
 CC markers that can be used to monitor disease states, disease progression,
 CC drug toxicity, drug efficacy and drug metabolism.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 461 BP; 162 A; 85 C; 62 G; 152 T; 0 other;
 Query Match 0.1%; Score 20; DB 24; Length 461;
 Best Local Similarity 100.0%; Pred. No. 1e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 30927 GCAACATCAATTAATATA 30946
 DB 360 GCAACATCAATTAATATA 379

Search completed: September 29, 2003; 20:40:34
 Job time : 28489 secs


```
FT /note="has similarity to KSHV ORF4"  
FT 6045..9443  
FT /tag= d  
FT /product= "ssDNA binding protein"  
FT /label= RV_ORF6  
FT /note="has similarity to KSHV ORF6"  
FT 9468..11528  
FT /tag= e  
FT /product= "transport protein"  
FT /label= RV_ORF7  
FT /note="has similarity to KSHV ORF7"  
FT 11515..14004  
FT /tag= f  
FT /product= "glycoprotein B"  
FT /label= RV_ORF8  
FT /note="has similarity to KSHV ORF8"  
FT 14122..17166  
FT /tag= g  
FT /product= "DNA polymerase protein"  
FT /label= RV_ORF9  
FT /note="has similarity to KSHV ORF9"  
FT 17261..18511  
FT /tag= h  
FT /label= RV_ORF10  
FT /note="has similarity to KSHV ORF10"  
FT 18520..19749  
FT /tag= i  
FT /label= RV_ORF11  
FT /note="has similarity to KSHV ORF11"  
FT complement (19921..20544)  
FT /tag= j  
FT /product= "RV R2"  
FT /label= RV_ORF  
FT /note="has similarity to KSHV interleukin (IL)-6 gene"  
FT complement (20777..21778)  
FT /tag= k  
FT /product= "thymidylate synthase"  
FT /label= RV_ORF70  
FT /note="has similarity to KSHV ORF70"  
FT complement (22245..22592)  
FT /tag= l  
FT /product= "RV R3"  
FT /note="has similarity to KSHV K4 viral MIP gene"  
FT 26846..27409  
FT /tag= m  
FT /product= "Bcl2-homologue"  
FT /label= RV_ORF16  
FT /note="has similarity to KSHV ORF16"  
FT complement (27515..29125)  
FT /tag= n  
FT /label= RV_ORF17  
FT /note="has similarity to KSHV ORF17"  
FT 28998..29897  
FT /tag= o  
FT /label= RV_ORF18  
FT /note="has similarity to KSHV ORF18"  
FT complement (29905..31548)  
FT /tag= p  
FT /product= "tegument protein"  
FT /label= RV_ORF19  
FT /note="has similarity to KSHV ORF19"  
FT complement (31043..32095)  
FT /tag= q  
FT /label= RV_ORF20  
FT /note="has similarity to KSHV ORF20"  
FT 32094..33767  
FT /tag= r  
FT /product= "thymidine kinase"  
FT /label= RV_ORF21  
FT /note="has similarity to KSHV ORF21"  
FT 33754..35868  
FT /tag= s  
FT /product= "glycoprotein H"  
FT  
  
FT /label= RV_ORF22  
FT /note="has similarity to KSHV ORF22"  
FT complement (35865..37073)  
FT /tag= t  
FT /label= RV_ORF23  
FT /note="has similarity to KSHV ORF23"  
FT complement (37123..39321)  
FT /tag= u  
FT /label= RV_ORF24  
FT /note="has similarity to KSHV ORF24"  
FT 39323..43459  
FT /tag= v  
FT /product= "major capsid protein"  
FT /label= RV_ORF25  
FT /note="has similarity to KSHV ORF25"  
FT 43491..44408  
FT /tag= w  
FT /product= "capsid protein"  
FT /label= RV_ORF26  
FT /note="has similarity to KSHV ORF26"  
FT 44433..45242  
FT /tag= x  
FT /label= RV_ORF27  
FT /note="has similarity to KSHV ORF27"  
FT 45408..45683  
FT /tag= y  
FT /label= RV_ORF28  
FT /note="has similarity to KSHV ORF28"  
FT complement (45733..46779)  
FT /tag= z  
FT /label= RV_ORF29b  
FT /note="has similarity to KSHV ORF29b"  
FT 46905..47135  
FT /tag= aa  
FT /label= RV_ORF30  
FT /note="has similarity to KSHV ORF30"  
FT 47093..47746  
FT /tag= ab  
FT /label= RV_ORF31  
FT /note="has similarity to KSHV ORF31"  
FT 47683..49077  
FT /tag= ac  
FT /label= RV_ORF32  
FT /note="has similarity to KSHV ORF32"  
FT 49049..50059  
FT /tag= ad  
FT /label= RV_ORF33  
FT /note="has similarity to KSHV ORF33"  
FT complement (49977..50960)  
FT /tag= ae  
FT /label= RV_ORF29a  
FT /note="has similarity to KSHV ORF29a"  
FT 50959..51942  
FT /tag= af  
FT /label= RV_ORF34  
FT /note="has similarity to KSHV ORF34"  
FT 51923..52372  
FT /tag= ag  
FT /label= RV_ORF35  
FT /note="has similarity to KSHV ORF35"  
FT 52278..53585  
FT /tag= ah  
FT /product= "kinase"  
FT /label= RV_ORF36  
FT /note="has similarity to KSHV ORF36"  
FT 53566..55008  
FT /tag= ai  
FT /product= "alkaline exonuclease"  
FT /label= RV_ORF37  
FT /note="has similarity to KSHV ORF37"  
FT 54963..55172  
FT /tag= aj  
FT /label= RV_ORF38
```

```
FT FT /note- "has similarity to KSHV ORF38"  
FT complement (55255..56391)  
FT /tag- ak  
FT /product- "glycoprotein M"  
FT /label- RVV_ORF39  
FT /note- "has similarity to KSHV ORF39"  
FT 56526..57932  
FT /tag- a1  
FT /product- "helicase/primase"  
FT /label- RVV_ORF40  
FT /note- "has similarity to KSHV ORF40"  
FT 57917..58528  
FT /tag- am  
FT /product- "helicase/primase"  
FT /label- RVV_ORF41  
FT /note- "has similarity to KSHV ORF41"  
FT complement (58525..59343)  
FT CDS  
FT /tag- an  
FT /label- RVV_ORF42  
FT /note- "has similarity to KSHV ORF42"  
FT complement (59297..61027)  
FT CDS  
FT /tag- ao  
FT /product- "capsid protein"  
FT /label- RVV_ORF43  
FT /note- "has similarity to KSHV ORF43"  
  
Query Match 100.0%; Score 35101; DB 24; Length 128139;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 35101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 CGACATGCTAGCGGCTATCTCTACAGACCTGTATGACTACAGTCCCGCGGCATCGA 60  
DB 64320 CGACATGCTAGCGGCTATCTCTACAGACCTGTATGACTACAGTCCCGCGGCATCGA 64379  
  
QY 61 TTCCCTCCAGACACTGAGACATGAGAGATATTTCCAGAGTTAGTCCGCATCTAG 120  
DB 64380 TTCCCTCCAGACACTGAGACATGAGAGATATTTCCAGAGTTAGTCCGCATCTAG 64439  
  
QY 121 CGGCGACGATCGGCTTGAAAGATGAGCCCAAGAGCAAGATCACACACCGAGACGTC 180  
DB 64440 CGGCGACGATCGGCTTGAAAGATGAGCCCAAGAGCAAGATCACACACCGAGACGTC 64499  
  
QY 181 CCACGCAACCCGGGCGATGCTTAACCGTAAAAATATGACCGGTTGAAAGTCCCTGGTG 240  
DB 64500 CCACGCAACCCGGGCGATGCTTAACCGTAAAAATATGACCGGTTGAAAGTCCCTGGTG 64559  
  
QY 241 CGACAAAAATGAGCTTAAACTTACCATTTTCTGTCTATTTGGGACACTAAAAATT 300  
DB 64560 CGACAAAAATGAGCTTAAACTTACCATTTTCTGTCTATTTGGGACACTAAAAATT 64619  
  
QY 301 GTGCGCAGTGGCGCAATTTTAAAGTCTGTAATGATGACCTTTTCAAGTTCTGTC 360  
DB 64620 GTGCGCAGTGGCGCAATTTTAAAGTCTGTAATGATGACCTTTTCAAGTTCTGTC 64679  
  
QY 361 CTAGAAATTTTCAATCCAGTTTCAATATATATAAGACACCTGTTTGTTCGTGAATC 420  
DB 64680 CTAGAAATTTTCAATCCAGTTTCAATATATATAAGACACCTGTTTGTTCGTGAATC 64739  
  
QY 421 TGGCGTGTATTTATCTTGAGAGCGCCCTTAAAAACATGCTCGTGTGAAACACACCCA 480  
DB 64740 TGGCGTGTATTTATCTTGAGAGCGCCCTTAAAAACATGCTCGTGTGAAACACACCCA 64799  
  
QY 481 AGAGACCCCAAGTCTGAATTTATGTCATATAGATCTCCACGAGGAAACACACGGGA 540  
DB 64800 AGAGACCCCAAGTCTGAATTTATGTCATATAGATCTCCACGAGGAAACACACGGGA 64859  
  
QY 541 TGGATTTCAAAACCTGTCTGTCAGCGCCAGATCTGCTCGGCTTATATCTATACG 600  
DB 64860 TGGATTTCAAAACCTGTCTGTCAGCGCCAGATCTGCTCGGCTTATATCTATACG 64919  
  
QY 601 AGAATAACGGCGCTTTTCCCAATAATGACAAATGACAGAGCAATACCGGACAGGTG 660  
DB 64920 AGAATAACGGCGCTTTTCCCAATAATGACAAATGACAGAGCAATACCGGACAGGTG 64979
```

```
QY 661 AAAGCTTCGAGAGCTAGCTGCGCGCACAGGTTTCTGCGGCTTCTGTCTACAGATGT 720  
DB 64980 AAAGCTTCGAGAGCTAGCTGCGCGCACAGGTTTCTGCGGCTTCTGTCTACAGATGT 65039  
  
QY 721 ATGGAACAAACACCGGAGAGGCGGTGTTCTAAAGACGTCGCGTCCGTAAAGCCT 780  
DB 65040 ATGGAACAAACACCGGAGAGGCGGTGTTCTAAAGACGTCGCGTCCGTAAAGCCT 65099  
  
QY 781 CGGCTGACATTAATTCAGCGGCGCTCCAGGCGTGTGCGCCAGCAAGGCACTTCACAG 840  
DB 65100 CGGCTGACATTAATTCAGCGGCGCTCCAGGCGTGTGCGCCAGCAAGGCACTTCACAG 65159  
  
QY 841 GGGCACATGCCGTATCTGACCGGATAGACAGACGAGTGGCGGTGACAAATAGACTACTCA 900  
DB 65160 GGGCACATGCCGTATCTGACCGGATAGACAGACGAGTGGCGGTGACAAATAGACTACTCA 65219  
  
QY 901 AGGTGAGTGGCGGCTGTGAGACAAACAAAGACCGCCCTTGCAGCCATCTTGTCTGC 960  
DB 65220 AGGTGAGTGGCGGCTGTGAGACAAACAAAGACCGCCCTTGCAGCCATCTTGTCTGC 65279  
  
QY 961 GTTCTATTTCTTTATGTTTAAACAGTAATGCTGTTTATTTAACTTGCATAGCCCG 1020  
DB 65280 GTTCTATTTCTTTATGTTTAAACAGTAATGCTGTTTATTTAACTTGCATAGCCCG 65339  
  
QY 1021 AACCGAACACTGTGCGATGCGATTATAAACGCAACCTGCGACACGTCAGATGAGACG 1080  
DB 65340 AACCGAACACTGTGCGATGCGATTATAAACGCAACCTGCGACACGTCAGATGAGACG 65399  
  
QY 1081 CAAACGCGCGCGGCGAGTGCAGACCTCAGGAAAAAATAAGCCCAACAGCTGCACAGG 1140  
DB 65400 CAAACGCGCGCGGCGAGTGCAGACCTCAGGAAAAAATAAGCCCAACAGCTGCACAGG 65459  
  
QY 1141 TACAAATTAAGCAAAATTTAGTATTTTAAAGTTTCCGAGGTTTCCCGTGGGCT 1200  
DB 65460 TACAAATTAAGCAAAATTTAGTATTTTAAAGTTTCCGAGGTTTCCCGTGGGCT 65519  
  
QY 1201 GCGGACACGCTGCGGCTTGTAGTGAATACCTCTCTAACAGACAGCTATTCACACAG 1260  
DB 65520 GCGGACACGCTGCGGCTTGTAGTGAATACCTCTCTAACAGACAGCTATTCACACAG 65579  
  
QY 1261 GAGCTGGAAGTAAACACGCAACTGACGCTCTCACCGCTCAACACAGAACCCCTTCAA 1320  
DB 65580 GAGCTGGAAGTAAACACGCAACTGACGCTCTCACCGCTCAACACAGAACCCCTTCAA 65639  
  
QY 1321 AAGCAGCATATTTTAAACAGATGATGATTTGATGTCGCAAAAACGGGACAGTAA 1380  
DB 65640 AAGCAGCATATTTTAAACAGATGATGATTTGATGTCGCAAAAACGGGACAGTAA 65699  
  
QY 1381 AAAAGCAGCATATTTTAAAGCAGCTGCGGTTACTGTTTAAACAGCTGAATGAT 1440  
DB 65700 AAAAGCAGCATATTTTAAAGCAGCTGCGGTTACTGTTTAAACAGCTGAATGAT 65759  
  
QY 1441 CTATTCACCCCTTCAATAAATAATTTTAAATAGCTTTCGCTGCTGCTCT 1500  
DB 65760 CTATTCACCCCTTCAATAAATAATTTTAAATAGCTTTCGCTGCTGCTCT 65819  
  
QY 1501 TAAACATTTTAAACATTTTATTTGGGAATTAAGGATTTATGGGATTAAGGATTTAATTT 1560  
DB 65820 TAAACATTTTAAACATTTTATTTGGGAATTAAGGATTTAAGGATTTAATTT 65879  
  
QY 1561 TTTGGATCATGGAATTTGGGAACATACGTCGGGATGGAAGTTATGCTTCATGGTGGG 1620  
DB 65880 TTTGGATCATGGAATTTGGGAACATACGTCGGGATGGAAGTTATGCTTCATGGTGGG 65939  
  
QY 1621 TGGCGTGAATTTGCAAGGAGAGGTCGGTGTGTCACCACTGCGACCTGCACAGATGGAAAT 1680  
DB 65940 TGGCGTGAATTTGCAAGGAGAGGTCGGTGTGTCACCACTGCGACCTGCACAGATGGAAAT 65999  
  
QY 1681 ACGAGGCGGTATACAGGCACTACTCGAAGAGTGCAGCAACATGAAAGCTTCGGGAGACC 1740  
DB 66000 ACGAGGCGGTATACAGGCACTACTCGAAGAGTGCAGCAACATGAAAGCTTCGGGAGACC 66059
```

OY	1741	TGAGCGGTTCGGGACACAAAGGGGCTGGAGCCAAAGACAAACACCGAAGCTAAATAT	1800
Dp	66060	TGGACGGTTCCGGGACAGCAAAAGGGGCTGGAGCCAAAGCAACACCGAAGCTAAATAT	66119
OY	1801	CGAATAACACCTTAACGTTGTGCATCAATCAAGGTCATAAATAAGAGCCGCTGGAGACAGCCGA	1860
Dp	66120	CGAATAACACCTTAAGGTTGTGCATCAATCAAGGTCATAAATAAGAGCCGCTGGAGACAGCCGA	66179
OY	1861	GGGCGGAATCATCATCACAGACCTGGCACAGCATCAAGAGGTTAAAGCTTCGATTAATCAA	1920
Dp	66180	GGGCGGAATCATCATCACAGACCTGGCACAGCATCAAGAGGTTAAAGCTTCGATTAATCAA	66239
OY	1921	CCCCGGAATTGGGCGCAACCACTCCCGGTAAATAATTCAGACTCCGGCGAGTCAAGTCAG	1980
Dp	66240	CCCCGGAATTGGGCGCAACCACTCCCGGTAAATAATTCAGACTCCGGCGAGTCAAGTCAG	66299
OY	1981	GTGGGACACCTCGGAACAGCGGCGCCACAGCGCTTCAATTAATGACACAAACGACATCTCA	2040
Dp	66300	GTGGGACACCTCGGAACAGCGGCGCCACAGCGCTTCAATTAATGACACAAACGACATCTCA	66359
OY	2041	ACCCATCTGGTCTGTGTTTTCAGAGCCATCCGTCGCGGCTCACAGCGATACCGAGC	2100
Dp	66360	ACCCATCTGGTCTGTGTTTTCAGAGCCATCCGTCGCGGCTCACAGCGATACCGAGC	66419
OY	2101	AGTCCGTTGGCGAATGCGGAACAGGTCACAGCAAGCATATGTAACCCCTGGCGCCCTTCCC	2160
Dp	66420	AGTCCGTTGGCGAATGCGGAACAGGTCACAGCAAGCATATGTAACCCCTGGCGCCCTTCCC	66479
OY	2161	TCTTTCAAGCGCAACACCTCGTCTCACAGGTCGCGGTACCCCTTGGCCCGCAACGATGG	2220
Dp	66480	TCTTTCAAGCGCAACACCTCGTCTCACAGGTCGCGGTACCCCTTGGCCCGCAACGATGG	66539
OY	2221	CAGAGATACGCCGAGGTGCGCAACATATGCGACCCAAATTTGACCGCAAGAATACACGCG	2280
Dp	66540	CAGAGATACGCCGAGGTGCGCAACATATGCGACCCAAATTTGACCGCAAGAATACACGCG	66599
OY	2281	GTCCGTTGAGAGAGTGGCCCGTATGAGACGCTGCACGGGACCTTCAAACGTCGCTGTAGAC	2340
Dp	66600	GTCCGTTGAGAGAGTGGCCCGTATGAGACGCTGCACGGGACCTTCAAACGTCGCTGTAGAC	66659
OY	2341	CAATTCCTCCCTTCGCGAGAGCCGCTGGGACCTGTTACACCCCTTGGGCTATGGCCGA	2400
Dp	66660	CAATTCCTCCCTTCGCGAGAGCCGCTGGGACCTGTTACACCCCTTGGGCTATGGCCGA	66719
OY	2401	ATATTTGGGCTCACAGATGCGCTTGTACACAGATATATCAAAATATATGACATAGAACTAC	2460
Dp	66720	ATATTTGGGCTCACAGATGCGCTTGTACACAGATATATCAAAATATATGACATAGAACTAC	66779
OY	2461	ACGACGCTTACAGGCGAATAAGGTTAATTTGACACACTAGTCCGCGCTTATATT	2520
Dp	66780	ACGACGCTTACAGGCGAATAAGGTTAATTTGACACACTAGTCCGCGCTTATATT	66839
OY	2521	CTGGTCTCTGAGACTGGGCGCCTCTCTCTGAGAGCCGCTCGCGCTGGCACGATTCG	2580
Dp	66840	CTGGTCTCTGAGACTGGGCGCCTCTCTCTGAGAGCCGCTCGCGCTGGCACGATTCG	66899
OY	2581	CCTCTGGTGTCTCTGTCATTAACAGCTCCACGCGGATACTAATTCGGCGAGGCGTCT	2640
Dp	66900	CCTCTGGTGTCTCTGTCATTAACAGCTCCACGCGGATACTAATTCGGCGAGGCGTCT	66959
OY	2641	TCCATCTGCCCCGGGCGTCAACAGGCTTGGCGCGTGGCCGCTCACTTAAGCTTCAATCTTA	2700
Dp	66960	TCCATCTGCCCCGGGCGTCAACAGGCTTGGCGCGTGGCCGCTCACTTAAGCTTCAATCTTA	67019
OY	2701	CGGGTTCCACGTTTACATAAAGCGCGAAAGGCGAGCTGGGATTTGGCCCTCTTCGGGG	2760
Dp	67020	CGGGTTCCACGTTTACATAAAGCGCGAAAGGCGAGCTGGGATTTGGCCCTCTTCGGGG	67079
OY	2761	TTAGAGATGACGGGAGTGGAGAGCCGAGCTGTGGATTCGCCAGAAATTTATCAGCTTTTGG	2820
Dp	67080	TTAGAGATGACGGGAGTGGAGAGCCGAGCTGTGGATTCGCCAGAAATTTATCAGCTTTTGG	67139
OY	2821	AGCTGCTTGTTTTCAACGGCAATTTTTCGACCTGAGCGGCTAATCTCTCATTTGTACG	2880

Dd	67140	AGCTGCTTGTTTTCAACGCAATTTTGGACCTGAGCGGCTAATCTCTCCATTGTGCAC	67199
Qy	2881	TCCTTTTGGGGGGCGCGCTTGGGACGCGTGGAAAGACATGGCAGCTACTACGATTAC	2940
Dd	67200	TCCTTTTGGGGGGCGCGCTTGGGACGCGTGGAAAGACATGGCAGCTACTACGATTAC	67259
Qy	2941	AGACTACAGCGGACGTTTAAATCTTACAGCGCGCCCTGAGGTACTCTGTCCGACG	3000
Dd	67260	AGACTACAGCGGACGTTTAAATCTTACAGCGCGCCCTGAGGTACTCTGTCCGACG	67319
Qy	3001	GTTTCACCAATTTAAAAAGCACATPATAGTTAGGTACAGAAATTTGCAACGGGACC	3060
Dd	67320	GTTTCACCAATTTAAAAAGCACATPATAGTTAGGTACAGAAATTTGCAACGGGACC	67379
Qy	3061	AGACACAGTTGATCATCCGCCCATATCTGAAAAAACCTAGACAGCACGGGCTGTACG	3120
Dd	67380	AGACACAGTTGATCATCCGCCCATATCTGAAAAAACCTAGACAGCACGGGCTGTACG	67439
Qy	3121	TCGCGCGAGCAATCATAGTCATPATAAAGAGGCGTTACGAGGAGACCGCGGAGGTTT	3180
Dd	67440	TCGCGCGAGCAATCATAGTCATPATAAAGAGGCGTTACGAGGAGACCGCGGAGGTTT	67499
Qy	3181	GTAATCACAGAGGCGCGCGCTTCCGTGATGTGAGAGAGTGGTGACGGTGGCGACACC	3240
Dd	67500	GTAATCACAGAGGCGCGCGCTTCCGTGATGTGAGAGAGTGGTGACGGTGGCGACACC	67559
Qy	3241	GGCAGACACAGATATTAAGACGCAACAGGCGTTACGCGACGACAAATTGACCTGTCA	3300
Dd	67560	GGCAGACACAGATATTAAGACGCAACAGGCGTTACGCGACGACAAATTGACCTGTCA	67619
Qy	3301	TTCAAGCGCGCGTTCGCGACGCAACCTCCACTTTGGCACGGCGCTCTCTTATATACT	3360
Dd	67620	TTCAAGCGCGCGTTCGCGACGCAACCTCCACTTTGGCACGGCGCTCTCTTATATACT	67679
Qy	3361	ACCGATTAAACATTTATGGCAGAGTGCAGCGCCCATAGCGTTCCGTACGCTTGACTCT	3420
Dd	67680	ACCGATTAAACATTTATGGCAGAGTGCAGCGCCCATAGCGTTCCGTACGCTTGACTCT	67739
Qy	3421	GTAAATTGAAATTAATACCAAAAAACAACTCATCTGTATAGCGTTACGCAAAATTTTC	3480
Dd	67740	GTAAATTGAAATTAATACCAAAAAACAACTCATCTGTATAGCGTTACGCAAAATTTTC	67799
Qy	3481	CCGTCGTGTCAACCGCGGAGAACCTCTAGTCTGTGCGCCCTGGGACTAAAAATTAACGCG	3540
Dd	67800	CCGTCGTGTCAACCGCGGAGAACCTCTAGTCTGTGCGCCCTGGGACTAAAAATTAACGCG	67859
Qy	3541	CGCCCGAGTGCAGATCTTCTAGGAGGAGCGCGACGATAGAGGTATPACACACGCG	3600
Dd	67860	CGCCCGAGTGCAGATCTTCTAGGAGGAGCGCGACGATAGAGGTATPACACACGCG	67919
Qy	3601	GACTTATAGATCAAGGGTATCTGTGAGAAATTAACATCATCGTTCCATAAAGACTAAAC	3660
Dd	67920	GACTTATAGATCAAGGGTATCTGTGAGAAATTAACATCATCGTTCCATAAAGACTAAAC	67979
Qy	3661	AGGTGCTACACTTTACCGGGGAGAAAGTCAAGCTCTCACTCATCGCTTTATGTACGCT	3720
Dd	67980	AGGTGCTACACTTTACCGGGGAGAAAGTCAAGCTCTCACTCATCGCTTTATGTACGCT	68039
Qy	3721	CGCCCGGGGCGCTAAAAATGCGGATPACTGAACCTTACCAATTAACCTGTGGAGGCTGAT	3780
Dd	68040	CGCCCGGGGCGCTAAAAATGCGGATPACTGAACCTTACCAATTAACCTGTGGAGGCTGAT	68099
Qy	3781	TTGATGTTTACGTCGCCCATATGATACCAATACCCCAACGACAGAAACCCCGTTTACGT	3840
Dd	68100	TTGATGTTTACGTCGCCCATATGATACCAATACCCCAACGACAGAAACCCCGTTTACGT	68159
Qy	3841	TGAGTTTGTATTATAGAGTCCACAGCTCAGCACCCCGCAGCTCCCAATATGTTGGGCG	3900
Dd	68160	TGAGTTTGTATTATAGAGTCCACAGCTCAGCACCCCGCAGCTCCCAATATGTTGGGCG	68219
Qy	3901	GCTCTGAGCTGGCGACAAAGGGGCTTACCGTGCAGCGGACCAATAGACCAAGTCTGTTGG	3960

Db 68220 GCTGTGAGTGGCGACAAAGGGGCTTACCGTCGACGGCACAATGAGACCACTGCTGG 68279
QY 3961 TACATCTGAGGTTTTTATACCTTACCAAAAGCCAAATAGATATACAGCAAAACGCCGA 4020
Db 68280 TACATCTGAGGTTTTTATACCTTACCAAAAGCCAAATAGATATACAGCAAAACGCCGA 68339
QY 4021 TATGTGAGTATGTTTTATCCAGAGAACACGTCACCAAGCGGGTGAACATTCCTTAGAT 4080
Db 68340 TATGTGAGTATGTTTTATCCAGAGAACACGTCACCAAGCGGGTGAACATTCCTTAGAT 68399
QY 4081 CCGGCGTACAACTCGGAGACACCTCCAGATATGTGTGGCCAAATAGGTTTACGACG 4140
Db 68400 CCGGCGTACAACTCGGAGAACCTCCAGATATGTGTGGCCAAATAGGTTTACGACG 68459
QY 4141 TGGCCAGCTGCCCAAAACCACCGCTCAACTCCGCACTCAAGCCAAACCGGAC 4200
Db 68460 TGGCCAGCTGCCCAAAACCACCGCTCAACTCCGCACTCAAGCCAAACCGGAC 68519
QY 4201 CGGAGACCGCCCGCGGCGCAAAAGGGGTGGGCTGTCAGGGTTATTAATTTTAAACATGG 4260
Db 68520 CGGAGACCGCCCGCGGCGCAAAAGGGGTGGGCTGTCAGGGTTATTAATTTTAAACATGG 68579
QY 4261 CATTAATTTTAAAGTGTGTTATTTTATTAATAAACAATCCAAATTAAGCTTAACCATGAGT 4320
Db 68580 CATTAATTTTAAAGTGTGTTATTTTATTAATAAACAATCCAAATTAAGCTTAACCATGAGT 68639
QY 4321 TGGCGATCTGTATTTATTTTGTCTGCGACGATATTTATCCGCAACCGCAACTGGGGCTC 4380
Db 68640 TGGCGATCTGTATTTATTTGTCTGCGACGATATTTATCCGCAACCGCAACTGGGGCTC 68699
QY 4381 GGTGTGCAATCAACCGGATGGAGGGGTGGAGACGCTTCGTCTTACCAACATTA 4440
Db 68700 GGTGTGCAATCAACCGGATGGAGGGGTGGAGACGCTTCGTCTTACCAACATTA 68759
QY 4441 TTATATTTCCGACGCCACGTCGACAGATCATCGAGCGATTCGTCGAGCAGTTTTC 4500
Db 68760 TTATATTTCCGACGCCACGTCGACAGATCATCGAGCGATTCGTCGAGCAGTTTTC 68819
QY 4501 ATTTCCAGAGTACACAGCTCTGTCGGCCGTTTATTAACAAGCGCGTCAAAAGCGCTC 4560
Db 68820 ATTTCCAGAGTACACAGCTCTGTCGGCCGTTTATTAACAAGCGCGTCAAAAGCGCTC 68879
QY 4561 TCGTCCACGTAATATATCCCTATAGCCAGGACAAACATGCGCTTCCAGATTAACGTTCTGT 4620
Db 68880 TCGTCCACGTAATATCCCTATAGCCAGGACAAACATGCGCTTCCAGATTAACGTTCTGT 68939
QY 4621 ATAGACTTATGCTTATGATATTTGAATCTTAACGTCCTCGGACCCCGGGGTAACTTA 4680
Db 68940 ATAGACTTATGCTTATGATATTTGAATCTTAACGTCCTCGGACCCCGGGGTAACTTA 68999
QY 4681 GCCGCGTCAAAAGCAGCAAGATATCTCGTTATTTTATTTGATTTGAAGGCCACAGATTA 4740
Db 69000 GCCGCGTCAAAAGCAGCAAGATATCTCGTTATTTTATTTGATTTGAAGGCCACAGATTA 69059
QY 4741 GTCTGCCGAAGGGGCGGCTGACATCTGTGCTGCTTACATCTCCCATATTCACGTC 4800
Db 69060 GTCTGCCGAAGGGGCGGCTGACATCTGTGCTGCTTACATCTCCCATATTCACGTC 69119
QY 4801 GGGGCGAGACCACTGCTATTTGCGTCCGCGAGTATAGGACACTGTTAAAGAGATCT 4860
Db 69120 GGGGCGAGACCACTGCTATTTGCGTCCGCGAGTATAGGACACTGTTAAAGAGATCT 69179
QY 4861 GGGAGGGAGATATTTGACATCTCCAGCGTCAAAAGGAGTAAACCCGCAACAGCTCA 4920
Db 69180 GGGAGGGAGATATTTGACATCTCCAGCGTCAAAAGGAGTAAACCCGCAACAGCTCA 69239
QY 4921 AAGCAACAGCGCGGCGCATTTGCCAAACAAATGATGATGAATTTAGGGCAATTTTCTC 4980
Db 69240 AAGCAACAGCGCGGCGCATTTGCCAAACAAATGATGATGAATTTAGGGCAATTTTCTC 69299
QY 4981 TACTAGTGAATATGCGCGAAGTATTTACGATATCTGACTGAAACGCAAGCAAGCGG 5040
Db 69300 TACTAGTGAATATGCGCGAAGTATTTACGATATCTGACTGAAACGCAAGCAAGCGG 69359

QY 5041 GTCCCTCTTGCGTGTCTCCAGCATCGGGGCGACGCGCTATATAATCTCCACATGCGCT 5100
Db 69360 GTCCCTCTTGCGTGTCTCCAGCATCGGGGCGACGCGCTATATAATCTCCACATGCGCT 69419
QY 5101 AATTAACCTGCTGCGCGGCAAGCGCCAGCGCGGGCGCAAGGTTTACCGTTGAT 5160
Db 69420 AATTAACCTGCTGCGCGGCAAGCGCCAGCGCGGGCGCAAGGTTTACCGTTGAT 69479
QY 5161 GGTGCTAACCTTACCGCGGTGGCGAGTTTATCTATTCCTTAACAGGTACGACCATGAG 5220
Db 69480 GGTGCTAACCTTACCGCGGTGGCGAGTTTATCTATTCCTTAACAGGTACGACCATGAG 69539
QY 5221 CTCGGATTAACATTAAGACCGCATTTGACTGCTCAACAGGAGAAATATCTGAACCAT 5280
Db 69540 CTCGGATTAACATTAAGACCGCATTTGACTGCTCAACAGGAGAAATATCTGAACCAT 69599
QY 5281 ATTAAGGTAATGAGTCAAAAGCGTCCGCGACAGACCAAAACATGACTGTTTAAATC 5340
Db 69600 ATTAAGGTAATGAGTCAAAAGCGTCCGCGACAGACCAAAACATGACTGTTTAAATC 69659
QY 5341 TAAGTGCGCGTGTCAAGGCAAGTTGCTGTGGCCCTAAGAAAGGTACAAATGAG 5400
Db 69660 TAAGTGCGCGTGTCAAGGCAAGTTGCTGTGGCCCTAAGAAAGGTACAAATGAG 69719
QY 5401 CCCATCCCGCTATTTGATGATTAACGCTGTGGGCTGCTGTGAGGCATCGTTTGTACTGGC 5460
Db 69720 CCCATCCCGCTATTTGATGATTAACGCTGTGGGCTGCTGTGAGGCATCGTTTGTACTGGC 69779
QY 5461 CGGCACTTTTATTTTCCAGTCTCATATATGACGCGGAGACGCTGCTGATCTTAAC 5520
Db 69780 CGGCACTTTTATTTTCCAGTCTCATATATGACGCGGAGACGCTGCTGATCTTAAC 69839
QY 5521 GAGGTTATTCAGTCCAGTCAAGGCGACAGCTTGTACCGTAAACCTTATGAGCAAT 5580
Db 69840 GAGGTTATTCAGTCCAGTCAAGGCGACAGCTTGTACCGTAAACCTTATGAGCAAT 69899
QY 5581 AGGGCGGCTATTCGGGGGCTCAGATTTCTTTGGAATTTGCCAATTTTGGGCGTATCT 5640
Db 69900 AGGGCGGCTATTCGGGGGCTCAGATTTCTTTGGAATTTGCCAATTTTGGGCGTATCT 69959
QY 5641 AAAATACAAATGCAACAGACGACGCTGAGTCCAGGCGCATGATCAAAACATCACTC 5700
Db 69960 AAAATACAAATGCAACAGACGACGCTGAGTCCAGGCGCATGATCAAAACATCACTC 70019
QY 5701 CATACGTGGGGGCTTGAATGCTGACCTCAAGGACCTGTACCTTCACTTCACTGTCAT 5760
Db 70020 CATACGTGGGGGCTTGAATGCTGACCTCAAGGACCTGTACCTTCACTTCACTGTCAT 70079
QY 5761 TTACGAGTGCATGACGACGACGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5820
Db 70080 TTACGAGTGCATGACGACGACGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 70139
QY 5821 GACCCCGCAACGGTTAAACCTCCGCACTGTGTGCGCGCTTAAAGAGATTTTAAAGA 5880
Db 70140 GACCCCGCAACGGTTAAACCTCCGCACTGTGTGCGCGCTTAAAGAGATTTTAAAGA 70199
QY 5881 GCACGTATGGAATTAACAATAAGCAAGCTACCTGAGTACTTACATTAACATTTTAAC 5940
Db 70200 GCACGTATGGAATTAACAATAAGCAAGCTACCTGAGTACTTACATTAACATTTTAAC 70259
QY 5941 CGTACCGCTCTCTCTCCGAGGAGTACGAATTTTCAGAGATAGCATGCAATGCTG 6000
Db 70260 CGTACCGCTCTCTCTCCGAGGAGTACGAATTTTCAGAGATAGCATGCAATGCTG 70319
QY 6001 GTGTGACATTCGAGAGACGTTGGGGGAAATATCATATGATTAATATGACGATTCACA 6060
Db 70320 GTGTGACATTCGAGAGACGTTGGGGGAAATATCATATGATTAATATGACGATTCACA 70379
QY 6061 GCTGAATCTTAACAAAGATTTATCCGCTCTGCTGACTGACGCGCCTAGATCTGATTC 6120
Db 70380 GCTGAATCTTAACAAAGATTTATCCGCTCTGCTGACTGACGCGCCTAGATCTGATTC 70439

QY 6121 CGAGGCCCCAAGAAACCTTTTACGGTGGCTTCAGAAATTCACATACAGTGGCA 6180
| | | | |
Db 70440 CGAGGCCCCAAGAAACCTTTTACGGTGGCTTCAGAAATTCACATACAGTGGCA 70499
QY 6181 GTTTTGAATTAACATATTTTGTCTAATGCAGCAGACTGATAGACGGCTAGAA 6240
| | | | |
Db 70500 GTTTTGAATTAACATATTTTGTCTAATGCAGCAGACTGATAGACGGCTAGAA 70559
QY 6241 ACAAAACATTTATCGTCCCGAAGACGCCAATTGCAAGGCTGCAGGATCAAGATCTCAC 6300
| | | | |
Db 70560 ACAAAACATTTATCGTCCCGAAGACGCCAATTGCAAGGCTGCAGGATCAAGATCTCAC 70619
QY 6301 CTCACGATATTTTACTGGACCTCGGCTATCTCAGCTACATTTAAACAACAAATTCCT 6360
| | | | |
Db 70620 CTCACGATATTTTACTGGACCTCGGCTATCTCAGCTACATTTAAACAACAAATTCCT 70679
QY 6361 AGTTTCACGCCAGATATTTTCAACCCAGACACTCCAGTTTATAGATGGGTGTGATTT 6420
| | | | |
Db 70680 AGTTTCACGCCAGATATTTTCAACCCAGACACTCCAGTTTATAGATGGGTGTGATTT 70739
QY 6421 TGAATCTAAAGGTAAACGGAAGGTAGACGACTCTAAACGATATCTACACATATGCGTAA 6480
| | | | |
Db 70740 TGAATCTAAAGGTAAACGGAAGGTAGACGACTCTAAACGATATCTACACATATGCGTAA 70799
QY 6481 GCTGGCGCAGTTCATTTAGAAACGTTGCAAGTTAATAGTCCACTTAAACCCAGACACC 6540
| | | | |
Db 70800 GCTGGCGCAGTTCATTTAGAAACGTTGCAAGTTAATAGTCCACTTAAACCCAGACACC 70859
QY 6541 CGTGTATTTTAAAGTCGGCTGTTCACGCCCTTAACCTGGCGGATATCTCAGACAC 6600
| | | | |
Db 70860 CGTGTATTTTAAAGTCGGCTGTTCACGCCCTTAACCTGGCGGATATCTCAGACAC 70919
QY 6601 CGCGTCTGTCTACTGTGACGCAAAAATAGAGATGAGAAATGTAAACCCGTTTCCAGCCG 6660
| | | | |
Db 70920 CGCGTCTGTCTACTGTGACGCAAAAATAGAGATGAGAAATGTAAACCCGTTTCCAGCCG 70979
QY 6661 ATACTGTTTGGGGGGTCCGCTCCACTCGTGTCCCGACGACATTTTAAACCGCGTGT 6720
| | | | |
Db 70980 ATACTGTTTGGGGGGTCCGCTCCACTCGTGTCCCGACGACATTTTAAACCGCGTGT 71039
QY 6721 TAAATCTGACACGCGGCTAGCCTCAGAGATATCTGAGATCTTAAAGATTAAGACATTT 6780
| | | | |
Db 71040 TAAATCTGACACGCGGCTAGCCTCAGAGATATCTGAGATCTTAAAGATTAAGACATTT 71099
QY 6781 TGAATCTGACATTTTACGCCAAGGGGAGATGCTGGCGCTACTGCTATTAAGTGTG 6840
| | | | |
Db 71100 TGAATCTGACATTTTACGCCAAGGGGAGATGCTGGCGCTACTGCTATTAAGTGTG 71159
QY 6841 CCCGGGGGGGAGAGCTGTCACGGCTCCTTAAATTTATCTGTCACCCCGGAAGAGTCAGA 6900
| | | | |
Db 71160 CCCGGGGGGGAGAGCTGTCACGGCTCCTTAAATTTATCTGTCACCCCGGAAGAGTCAGA 71219
QY 6901 TAAATCTGCGGCTATTTGAAAAACGCGTTTAAAGTTTCTAATCTGCTACATCACGCCCTG 6960
| | | | |
Db 71220 TAAATCTGCGGCTATTTGAAAAACGCGTTTAAAGTTTCTAATCTGCTACATCACGCCCTG 71279
QY 6961 AAATCTGTCTACCAAAAAGGCGCACCCTGTGACGGATCACTGACGAAAAAGAGGGCTT 7020
| | | | |
Db 71280 AAATCTGTCTACCAAAAAGGCGCACCCTGTGACGGATCACTGACGAAAAAGAGGGCTT 71339
QY 7021 TCTAGAAAAGCAAAACCAAGATTAATCTCCCAAAAACATCAGGACCTGGCGAAAAAAT 7080
| | | | |
Db 71340 TCTAGAAAAGCAAAACCAAGATTAATCTCCCAAAAACATCAGGACCTGGCGAAAAAAT 71399
QY 7081 TGAGGGAACACAGAAAAACCACTAATTGATTTGGGACAGGACCGAGTGTGGCCAAAAT 7140
| | | | |
Db 71400 TGAGGGAACACAGAAAAACCACTAATTGATTTGGGACAGGACCGAGTGTGGCCAAAAT 71459
QY 7141 ACAGATTAACATACAGCGTTTCTTCCGAGATGACCGCATGGCCAAATTTGATCTGTGAG 7200
| | | | |
Db 71460 ACAGATTAACATACAGCGTTTCTTCCGAGATGACCGCATGGCCAAATTTGATCTGTGAG 72519
QY 7201 CTTCATGCACTCCGAGACACATTTATACAATTTAAACCACAAAAAGGAAACACTTTT 7260

Db 71520 CTTCATGCACTCCGAGACACATTTATACAAGTTTAAACCAAAAAGGAAACACTTTT 71579
QY 7261 CTGTATTAATCAATTAAGCACCAGAAACCACTAGACAGTCCGTTATTTTAAACCTTACA 7320
| | | | |
Db 71580 CTGTATTAATCAATTAAGCACCAGAAACCACTAGACAGTCCGTTATTTTAAACCTTACA 71639
QY 7321 TTCCACAAAAGAAAGGAGGCTCAGCGTCACTTTATAGATCAGTGTCTTGTGCAAAATG 7380
| | | | |
Db 71640 TTCCACAAAAGAAAGGAGGCTCAGCGTCACTTTATAGATCAGTGTCTTGTGCAAAATG 71699
QY 7381 TTAATCAATTAAGCCCACTGACATTTTCAATTTATGTAACCATTAACGGGACGTAAGA 7440
| | | | |
Db 71700 TTAATCAATTAAGCCCACTGACATTTTCAATTTATGTAACCATTAACGGGACGTAAGA 71759
QY 7441 GACACGAATTAATCAATTCGTTGATGGGCCAGCTCTCCGCTACTTTTATTTTAAAC 7500
| | | | |
Db 71760 GACACGAATTAATCAATTCGTTGATGGGCCAGCTCTCCGCTACTTTTATTTTAAAC 71819
QY 7501 CGGTAACCCCAAAAACAAATCTGAGCAGATTTTGTTCGCAACGCTGAACATGGCAGAG 7560
| | | | |
Db 71820 CGGTAACCCCAAAAACAAATCTGAGCAGATTTTGTTCGCAACGCTGAACATGGCAGAG 71879
QY 7561 GCAATGCTGAGCTGGAATTAACATGAAGATATTTTGAAGGTAAGAAGACCCCTGTGGC 7620
| | | | |
Db 71880 GCAATGCTGAGCTGGAATTAACATGAAGATATTTTGAAGGTAAGAAGACCCCTGTGGC 71939
QY 7621 TCTTACGACTCCATTTTAAACCCGCAACTTATCAAAAGGCTCTTTTATACGATTTTACAT 7680
| | | | |
Db 71940 TCTTACGACTCCATTTTAAACCCGCAACTTATCAAAAGGCTCTTTTATACGATTTTACAT 71999
QY 7681 GCGGTATGTGTTCACGCACTAATTTTATAGGGGCAATATCATGCTGCACTTCA 7740
| | | | |
Db 72000 GCGGTATGTGTTCACGCACTAATTTTATAGGGGCAATATCATGCTGCACTTCA 72059
QY 7741 CGACTGCTCCTGGAGCAATGAGACGACCTGTCCCAAGCCGGAGCCGAACCCGTCAC 7800
| | | | |
Db 72060 CGACTGCTCCTGGAGCAATGAGACGACCTGTCCCAAGCCGGAGCCGAACCCGTCAC 72119
QY 7801 AACGCCGAACAGCTTCCGGAAGGGGCCAAATCACAAGTGTGGGTTTACTTAAATCCG 7860
| | | | |
Db 72120 AACGCCGAACAGCTTCCGGAAGGGGCCAAATCACAAGTGTGGGTTTACTTAAATCCG 72179
QY 7861 TAAAGATTCGATCTGAGAACCGCGGTAAATTTAGACCAATATCTCCACTTAACCGCTC 7920
| | | | |
Db 72180 TAAAGATTCGATCTGAGAACCGCGGTAAATTTAGACCAATATCTCCACTTAACCGCTC 72239
QY 7921 GCGATCTGATCCAGAACCGGTCGGGGTCCGCTCAACGATCAACCACTCAGGAGATA 7980
| | | | |
Db 72240 GCGATCTGATCCAGAACCGGTCGGGGTCCGCTCAACGATCAACCACTCAGGAGATA 72299
QY 7981 CGTCAAGAGATTCAAACCAACGTTGATGACCCGCTCATGAGAAACCGTGGCAGAGGG 8040
| | | | |
Db 72300 CGTCAAGAGATTCAAACCAACGTTGATGACCCGCTCATGAGAAACCGTGGCAGAGGG 72359
QY 8041 CGGTAAAGGAAAGGCCCGCTTATCCGCAAGAACCAATAGCTGCGCGGCTGACAGCAC 8100
| | | | |
Db 72360 CGGTAAAGGAAAGGCCCGCTTATCCGCAAGAACCAATAGCTGCGCGGCTGACAGCAC 72419
QY 8101 ATAGGCGCACGACTATCGGGGAAAGCCGCTTAAACGGGAGCATTTAAAGAGTCTATTAA 8160
| | | | |
Db 72420 ATAGGCGCACGACTATCGGGGAAAGCCGCTTAAACGGGAGCATTTAAAGAGTCTATTAA 72479
QY 8161 AAAGATGACCTTCATCCATCCACATGCTCTCTGCGGACAGATTAAGAAAGTATTCGAGGG 8220
| | | | |
Db 72480 AAAGATGACCTTCATCCATCCACATGCTCTCTGCGGACAGATTAAGAAAGTATTCGAGGG 72539
QY 8221 ACTGTTGCCAGCAGACCTGAGCAGTGTCTTATAGGTGTGCTGCGCGGCGCCACCGCT 8280
| | | | |
Db 72540 ACTGTTGCCAGCAGACCTGAGCAGTGTCTTATAGGTGTGCTGCGCGGCGCCACCGCT 72599
QY 8281 GCAACCCGAGGTTTCAAGGATCGACAGGTTTACCGCTTATGCAAGTCTGGGCGCGAG 8340
| | | | |

Dd 72600 GCAACCCGAGGTTGTCACGGATGACAGCTTACCGCTATAGTCAGTCTGGCGGCGCAG 72659
Qy 8341 AGAGCGCCTGCTGGCCAAAAAGTTAGCTGGCTAACTAACAGCCTATACAAACCCCT 8400
Dd 72660 AGAGCGCCTGCTGGCCAAAAAGTTAGCTGGCTAACTAACAGCCTATACAAACCCCT 72719
Qy 8401 GCTCAGCTTTGTGACGGGGGAAAAACAACAGGCCCACTGGTTGGCGACGGCCAAAAACAC 8460
Dd 72720 GCTCAGCTTTGTGACGGGGGAAAAACAACAGGCCCACTGGTTGGCGACGGCCAAAAACAC 72779
Qy 8461 GCTAGCCTCTGGGGGACCTCCAGGCTCTCGGGGCTTTATAGAGAAAGTCTGGGCTGGGC 8520
Dd 72780 GCTAGCCTCTGGGGGACCTCCAGGCTCTCGGGGCTTTATAGAGAAAGTCTGGGCTGGGC 72839
Qy 8521 CCAGCTGGCTGATCTCAAAAAGATGCTGAACGACAGCAACCTAGATATCATCTAGAG 8580
Dd 72840 CCAGCTGGCTGATCTCAAAAAGATGCTGAACGACAGCAACCTAGATATCATCTAGAG 72899
Qy 8581 CAGTAGTCAGAGCCTGTGACACCTGGTTCATCTCCAAAATCAGGCAATTTGCACATACAGTG 8640
Dd 72900 CAGTAGTCAGAGCCTGTGACACCTGGTTCATCTCCAAAATCAGGCAATTTGCACATACAGTG 72959
Qy 8641 CTTCCTGGAGATAGGGGTGAGGTTAGCTGGTGAACAGCTACTACTACCTGCTGCTAT 8700
Dd 72960 CTTCCTGGAGATAGGGGTGAGGTTAGCTGGTGAACAGCTACTACTACCTGCTGCTAT 73019
Qy 8701 AAATTAACCCGCTGGCGGAGCGCGCAACTGGCGGAGAGGTGAACCTGAATTTTAACT 8760
Dd 73020 AAATTAACCCGCTGGCGGAGCGCGCAACTGGCGGAGAGGTGAACCTGAATTTTAACT 73079
Qy 8761 CGGAATGCTGATGGGTTGCGCCCTAACCTTGGCGGCGCTCCTTGCAGAGCTAAAGTTGTC 8820
Dd 73080 CGGAATGCTGATGGGTTGCGCCCTAACCTTGGCGGCGCTCCTTGCAGAGCTAAAGTTGTC 73139
Qy 8821 TGGGGAAGGCTGACCTGTTAGTCTCTTCCCTGAGAAAATATAGACCGGGAAGTGTAT 8880
Dd 73140 TGGGGAAGGCTGACCTGTTAGTCTCTTCCCTGAGAAAATATAGACCGGGAAGTGTAT 73199
Qy 8881 GGGAGCTTTAAATCAATAGTGTGAGAGCACTACACCAAAATGTGTAGCGGAGTGTGT 8940
Dd 73200 GGGAGCTTTAAATCAATAGTGTGAGAGCACTACACCAAAATGTGTAGCGGAGTGTGT 73259
Qy 8941 CATTTACAACCCAGCCCATGTAGATCTGGGAAAACAACAGGAGCTTTTTTCTTTCC 9000
Dd 73260 CATTTACAACCCAGCCCATGTAGATCTGGGAAAACAACAGGAGCTTTTTTCTTTCC 73319
Qy 9001 AGGTATATATATTAACCATGATGTAGTAACTAGTTACGGTATTTATTCACGGGCGCTTAAA 9060
Dd 73320 AGGTATATATATTAACCATGATGTAGTAACTAGTTACGGTATTTATTCACGGGCGCTTAAA 73379
Qy 9061 TGCATAAACCACATAACAAAAATGTGTAAAAACAACAGCGCTCAAGCTTTTTC 9120
Dd 73380 TGCATAAACCACATAACAAAAATGTGTAAAAACAACAGCGGTCAAGCTTTTTC 73439
Qy 9121 TGCAGGCTCTGTGCTCGGAACAATAAGCAGATTCGCCACTAGCGGCACTTCTCT 9180
Dd 73440 TGCAGGCTCTGTGCTCGGAACAATAAGCAGATTCGCCACTAGCGGCACTTCTCT 73499
Qy 9181 ATAGCCCTGGTATACAGCGAGTGTATTTTACGGAAGGCCACATGAAGACGCTGGCGGGGT 9240
Dd 73500 ATAGCCCTGGTATACAGCGAGTGTATTTTACGGAAGGCCACATGAAGACGCTGGCGGGGT 73559
Qy 9241 GCGTAACAGTAACCCGGGTCCAATCGCGAGTTTACACAACATATAAAATAGGAGACCGT 9300
Dd 73560 GCGTAACAGTAACCCGGGTCCAATCGCGAGTTTACACAACATATAAAATAGGAGACCGT 73619
Qy 9301 TTATAGCGTTTATTTGACATACACACATTTTCAGGAGTTTCGCTTTTATATAAAT 9360
Dd 73620 TTATAGCGTTTATTTGACATACACACATTTTCAGGAGTTTCGCTTTTATATAAAT 73679
Qy 9361 CTTCATTCATTCAAAGTCCGATATTTTACGCTGTGTGGACACATATACATATACGCGC 9420
Dd 73680 CTTCATTCATTCAAAGTCCGATATTTTTCACGCTGTGTGGACACATATACATATACGCGC 73739

Qy 9421 CTGTGATTTGATTCCTCTCTCTCTGTATAGGAGACAGGACAGACCCAAATCTGTGCAAAACG 9480
Dd 73740 CTGTGATTTGATTCCTCTCTCTCTGTATAGGAGACAGGACAGACCCAAATCTGTGCAAAACG 73799
Qy 9481 ATCGGGTGGCCCGGAGTACAGAGGTCTGTGTGACTGGGCTTAATCTTAATCATGTATTCATC 9540
Dd 73800 ATCGGGTGGCCCGGAGTACAGAGGTCTGTGTGACTGGGCTTAATCTTAATCATGTATTCATC 73859
Qy 9541 GGTATCAAAAACGGGATGCTCCACAGATGGGACCGTCTGGTTGACAGGTTTGA 9600
Dd 73860 GGTATCAAAAACGGGATGCTCCACAGATGGGACCGTCTGGTTGACAGGTTTGA 73919
Qy 9601 GGTATTCGACGGAACCATTAATTAAGAAATCCATAGCATTCATTAATCCCATACTG 9660
Dd 73920 GGTATTCGACGGAACCATTAATTAAGAAATCCATAGCATTCATTAATCCCATACTG 73979
Qy 9661 ACAACTGCACAAAACAATGCCGCTCTCCAGGGCGGTGAACGCTTCACAACTGTCTCA 9720
Dd 73980 ACAACTGCACAAAACAATGCCGCTCTCCAGGGCGGTGAACGCTTCACAACTGTCTCA 74039
Qy 9721 CATATAATCGTCATTCATATTAAGGCGCGGGGGACACACAACTGAAGCGGCCGGGAGC 9780
Dd 74040 CATATAATCGTCATTCATATTAAGGCGCGGGGGACACACAACTGAAGCGGCCGGGAGC 74099
Qy 9781 CATGCAGACGTGTGTTCATTTTATCCGTTTGTCTGTGATTAACGAAACGCCCATCC 9840
Dd 74100 CATGCAGACGTGTGTTCATTTTATCCGTTTGTCTGTGATTAACGAAACGCCCATCC 74159
Qy 9841 AGAATGGGTAAAGTCTGTGCTTAAGAGACCCCATTAATTAACCTGAATATGCAATTA 9900
Dd 74160 AGAATGGGTAAAGTCTGTGCTTAAGAGACCCCATTAATTAACCTGAATATGCAATTA 74219
Qy 9901 TCCCCACGGGTCGTCACAGATGGCGCCCAACACAGCAAGACCGCTGATGTCAGATAG 9960
Dd 74220 TCCCCACGGGTCGTCACAGATGGCGCCCAACACAGCAAGACCGCTGATGTCAGATAG 74279
Qy 9961 CGGAGAGGCGTGTTCCTCCCGGGAACGCAACCGCGCCCTTGAATTTGCTGCTGCTAAC 10020
Dd 74280 CGGAGAGGCGTGTTCCTCCCGGGAACGCAACCGCGCCCTTGAATTTGCTGCTGCTAAC 74339
Qy 10021 GTCTTTCACCGGAGCGGTGTGGGTTCAGAGCGCTCGGTGGCGGGGGGCGTCAATGTGAA 10080
Dd 74340 GTCTTTCACCGGAGCGGTGTGGGTTCAGAGCGCTCGGTGGCGGGGGGCGTCAATGTGAA 74399
Qy 10081 GGTACCGGCGGAGCGGTGACGAATAGCCGAGCAGCTTAACTCCGTTATTCAGATAC 10140
Dd 74400 GGTACCGGCGGAGCGGTGACGAATAGCCGAGCAGCTTAACTCCGTTATTCAGATAC 74459
Qy 10141 CTTGCCGCGCTGTCGGCGCCCTTGGCGTTAAACATCCGAACCTCAAGCCCGCAGTTTC 10200
Dd 74460 CTTGCCGCGCTGTCGGCGCCCTTGGCGTTAAACATCCGAACCTCAAGCCCGCAGTTTC 74519
Qy 10201 TGGCGCTTACCCCAAGGCGCCGAGGCGACACCTGCTATACATCTTCATATGAGGCGAA 10260
Dd 74520 TGGCGCTTACCCCAAGGCGCCGAGGCGACACCTGCTATACATCTTCATATGAGGCGAA 74579
Qy 10261 CCTGAAGACACGTTTTCGAATGAATAAATCCGCTCAAAACGTCCTTTCTTCATGAA 10320
Dd 74580 CCTGAAGACACGTTTTCGAATGAATAAATCCGCTCAAAACGTCCTTTCTTCATGAA 74639
Qy 10321 ATAGGCACTTTTCTTATTCGACCACTATAGGCGGCGCTTGGCGTGGCCCACTAGACT 10380
Dd 74640 ATAGGCACTTTTCTTATTCGACCACTATAGGCGGCGCTTGGCGTGGCCCACTAGACT 74699
Qy 10381 CCGGAGCGGAAGGGGAGTGTTCCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 10440
Dd 74700 CCGGAGCGGAAGGGGAGTGTTCCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 74759
Qy 10441 AAGGTATCAAAATCCACAGACGACGGGCTGTAGTGGCGGACGACACCTGCTTTTTC 10500
Dd 74760 AAGGTATCAAAATCCACAGACGACGGGCTGTAGTGGCGGACGACACCTGCTTTTTC 74819

QY	10501	GTGCTGTGCCAAMAAACAGTCCGAAATACGTTTGGCAAAATTTGGCTGAGTACATCCATTC	10560
Db	74820	GTCTCTGTCCCAAAACAGTCCGAAATACGTTTGGCAAAATTTGGCTGAGTACATCCATTC	74879
QY	10561	TCGAAGTCCCATGGCGGAGGACACCGCTCTAGGTGGGCGCGACGTAGCCATGGCTGT	10620
Db	74880	TCGAAGTCCCATGGCGGAGGACACCGCTCTAGGTGGGCGCGACGTAGCCATGGCTGT	74939
QY	10621	ATATGCCAGGTTGATCTACACCGCTTTCAGTTTGTTTAAATTAACCAACATCCGCCAT	10680
Db	74940	ATATGCCAGGTTGATCTACACCGCTTTCAGTTTGTTTAAATTAACCAACATCCGCCAT	74999
QY	10681	CGCGCTACCGCCGTGGCGCGAGATGTGTGCAGCCGTGCACAAAAAAGATCCCACTCGGCA	10740
Db	75000	CGCGCTACCGCCGTGGCGCGAGATGTGTGCAGCCGTGCACAAAAAAGATCCCACTCGGCA	75059
QY	10741	ACTAATTCCTCCAGCGCGCGAGTGGGTACCGGTTCACTTCACTCACTCAGACAGCCCA	10800
Db	75060	ACTAATTCCTCCAGCGCGCGAGTGGGTACCGGTTCACTTCACTCACTCAGACAGCCCA	75119
QY	10801	CCCCATCATCTTCACCGCTGTTTCCCGCGTCCGAGTGTGCATTTGAATTTGGTCCGAGT	10860
Db	75120	CCCCATCATCTTCACCGCTGTTTCCCGCGTCCGAGTGTGCATTTGAATTTGGTCCGAGT	75179
QY	10861	CGCCCACTTACTGCTGGGTGATCGAGATTTGGCTGCTCCCTCTCTGGATCTTCATCT	10920
Db	75180	CGCCCACTTACTGCTGGGTGATCGAGATTTGGCTGCTCCCTCTCTGGATCTTCATCT	75239
QY	10921	GGAATGAACAGTGGGTGCGACCCCTCGATGATTACGTGCTCCGGGGGTAAACAACCT	10980
Db	75240	GGAATGAACAGTGGGTGCGACCCCTCGATGATTACGTGCTCCGGGGGTAAACAACCT	75299
QY	10981	CTGTACCGCATACAGAGAGAGTTTTCACACAGTAAACGAGTGCATGTGCGAGTGGCGAT	11040
Db	75300	CTGTACCGCATACAGAGAGAGTTTTCACACAGTAAACGAGTGCATGTGCGAGTGGCGAT	75359
QY	11041	CGACGGATTTCCGCGACGTGACCGACAGACACACAGGGCATTTGTGCATATTTCTAGTG	11100
Db	75360	CGACGGATTTCCGCGACGTGACCGACAGACACACAGGGCATTTGTGCATATTTCTAGTG	75419
QY	11101	GTTCGTCTCCAGGGTTCCGGGACCTTTCGAAGCTCTAGATATATCCATATCAAAA	11160
Db	75420	GTTCGTCTCCAGGGTTCCGGGACCTTTCGAAGCTCTAGATATATCCATATCAAAA	75479
QY	11161	CTGTAAACGGGTTGCTGTGATGCGAGGTCTTATCTCTCCATTTGTTAGTAAACACT	11220
Db	75480	CTGTAAACGGGTTGCTGTGATGCGAGGTCTTATCTCTCCATTTGTTAGTAAACACT	75539
QY	11221	TCATTTTCCCGGTTCTCAGGTTTCTTACGCCAAATGCGACATTCCTGAAGGTAATCAACA	11280
Db	75540	TCATTTTCCCGGTTCTCAGGTTTCTTACGCCAAATGCGACATTCCTGAAGGTAATCAACA	75599
QY	11281	CACCCCTTGTGACATTTTGTGATTAACCTTATAGATCTTCTGTGGAAACATGACGTCAA	11340
Db	75600	CACCCCTTGTGACATTTTGTGATTAACCTTATAGATCTTCTGTGGAAACATGACGTCAA	75659
QY	11341	CGAACCCCGGTGACGGTAAAAAACAAAGTCTCTCATCTTGGAAACAGACGGTGGCCAG	11400
Db	75660	CGAACCCCGGTGACGGTAAAAAACAAAGTCTCTCTCATCTTGGAAACAGACGGTGGCCAG	75719
QY	11401	CGAGGAGCGGACATGTGTCAGCTGACAGACCCGATTTCCAGACATGAACACGTTGAGGCCAA	11460
Db	75720	CGAGGAGCGGACATGTGTCAGCTGACAGACCCGATTTCCAGACATGAACACGTTGAGGCCAA	75779
QY	11461	CGGCTCTCCAAAATATAGAAAGTTAATTTGATGGCCCTCTGGACCGAGTCTGCGCA	11520
Db	75780	CGGCTCTCCAAAATATAGAAAGTTAATTTGATGGCCCTCTGGACCGAGTCTGCGCA	75839
QY	11521	CACGCTGTATTGTGCATTCGCACTCGAGCCAAATACGTTGCGGTAAAAAACCGCTTTC	11580
Db	75840	CACGCTGTATTGTGCATTCGCACTCGAGCCAAATACGTTTCCGGTAAAAAACCGCTTTC	75899
QY	11581	TTTTACGTTCCAGACCCACCCCTGTGCTGATTGGAACTCACTGATTAAACCAAGCACT	11640

Db	75900	TTTTACGCTCCAGACCCACC	CCCCCTGGTGCATTGGAACTC	ACATGATTTAAACCAAGGCAC	TT	75959
QY	11641	GAGTTTCGGTGGAGACAT	GAGATTATACATTTGCACAACT	TACACCGGTTCGGCAACA	TT	11700
Db	75960	GAGTTTGGGTGGAGACAT	GATATACACTTGCACAACTT	ACACCGGTTCGGCAACA	TT	76019
QY	11701	GGCGAAACAGTCTATAT	CGAGCACCCGGTGC	CCCATAGGCTTATTAATTAATTAAGCT	TT	11760
Db	76020	GGCGAAACAGTCTATAT	CGAGCACCCGGTGC	CCCATAGGCTTATTAATTAATTAAGCT	TT	76079
QY	11761	CTCGTATACCTTTTGT	GTGTCTCATGTGCTAC	AAGATCTCATTTTCCGAATCTG	CCAT	11820
Db	76080	CTCGTATACCTTTTGT	GTGTCTCATGTGCTAC	AAGATCTCATTTTCCGAATCTG	CCAT	76139
QY	11821	AGTGGAGCGGTTTTTGC	CCCGGACATATGCTCGCAT	GTGTTGGCATGTGCATCAAAAAACT	TT	11880
Db	76140	AGTGGAGCGGTTTTTGC	CCCGGACATATGCTCGCAT	GTGTTGGCATGTGCATCAAAAAACT	TT	76199
QY	11881	TCTCGCATATTCATAC	GGAGCCGATCTG	CATTTGTTTCACGGGACCCGGACACGG	TT	11940
Db	76200	TCTCGCATATTCATAC	GGAGCCGATCTG	CATTTGTTTCACGGGACCCGGACACGG	TT	76259
QY	11941	TCTTGTCCCTATCTT	CCCAACCAATCCGGGTACT	CGCCGATTCGACCCGGGCACGA	TT	12000
Db	76260	TCTTGTCCCTATCTT	CCCAACCAATCCGGGTACT	CGCCGATTCGACCCGGGCACGA	TT	76319
QY	12001	GCCAGGCCCTGATAT	GACATCTCACGGGCCGC	CAATTCGGGTATTTGGAGACTTGACGGATTC	TT	12060
Db	76320	GCCAGGCCCTGATAT	GACATCTCACGGGCCGC	CAATTCGGGTATTTGGAGACTTGACGGATTC	TT	76379
QY	12061	AGCTCTCAAGACAAAT	GAACCCCTTGCTCACGGGAC	CGCATTTCAATTAATGTATCTAAAT	TT	12120
Db	76380	AGCTCTCAAGACAAAT	GAACCCCTTGCTCACGGGAC	CGCATTTCAATTAATGTATCTAAAT	TT	76439
QY	12121	GACGGATGCTATGT	GCCCTTAACATATGTGCTA	AGACTACTCAAACTGTGTTAGGGGAAGA	TT	12180
Db	76440	GACGGATGCTATGT	GCCCTTAACATATGTGCTA	AGACTACTCAAACTGTGTTAGGGGAAGA	TT	76499
QY	12181	GTGCAAAACACCTGG	CACTCAATAAAATTTTG	AGTGGGCAATTCACCCGTCTCTCCG	TT	12240
Db	76500	GTGCAAAACACCTGG	CACTCAATAAAATTTTG	AGTGGGCAATTCACCCGTCTCTCCG	TT	76559
QY	12241	TGCTTATTAATTAAC	CCCCCATGCGCACCATAT	TCAAGGACAAAAACATCCAGATACAAAC	TT	12300
Db	76560	TGCTTATTAATTAAC	CCCCCATGCGCACCATAT	TCAAGGACAAAAACATCCAGATACAAAC	TT	76619
QY	12301	ACTTTATTAAGAT	TAGAAGCGCTCACCGGCT	CACAAAAACGGTTCGGCGGCACAGGTAA	TT	12360
Db	76620	ACTTTATTAAGAT	TAGAAGCGCTCACCGGCT	CACAAAAACGGTTCGGCGGCACAGGTAA	TT	76679
QY	12361	CATTAAACATTAG	GGGGGGGACACACGGCC	GCACAGACACTCGGGCACAGCTGATTAATTT	TT	12420
Db	76680	CATTAAACATTAG	GGGGGGGACACACGGCC	GCACAGACACTCGGGCACAGCTGATTAATTT	TT	76739
QY	12421	AGCGGTACAGT	GTGCTTCGATCCGCTCG	GGGTGTAGGTACGCCCCCAAAATATAGTTAA	TT	12480
Db	76740	AGCGGTACAGT	GTGCTTCGATCCGCTCG	GGGTGTAGGTACGCCCCCAAAATATAGTTAA	TT	76799
QY	12481	ACACACGCTTGT	GGAAGCGCGCTCCG	TCCGGAGATGTTCTGCGCATGGCTGTCAATATAG	TT	12540
Db	76800	ACACACGCTTGT	GGAAGCGCGCTCCG	TCCGGAGATGTTCTGCGCATGGCTGTCAATATAG	TT	76859
QY	12541	TCAACCAAGTTAA	TATGACGACACGSGT	TGGGGCACGACAGGACGCAACCGCCCCGGTTA	TT	12600
Db	76860	TCAACCAAGTTAA	TATGACGACACGSGT	TGGGGCACGACAGGACGCAACCGCCCCGGTTA	TT	76919
QY	12601	GATTTCGACGTTT	CCCTTGAACGAACGGC	CACAGGAATGCCCAACCATTAATGTAAATGGCG	TT	12660
Db	76920	GATTTCGACGTTT	CCCTTGAACGAACGGC	CACAGGAATGCCCAACCATTAATGTAAATGGCG	TT	76979
QY	12661	GAGGGTCTGGCCCC	CAAAACGCCAACC	CGGCAAAAGATCTTTATTCAGAGGAACGCAACGCC	TT	12720

Dd 76980 GAGGGTCGCGCCAAACGCCAACCCGGCAAAAGATCTTATCCAGGAAGCGCAACGCC 77039
Oy 12721 TCGGCTGAAACTGTGTAAGTGGCTGGAAATCTCCGACACAGTCCCTGCTGGCGATC 12780
Dd 77040 TCGGCTGAAACTGTGTAAGTGGCTGGAAATCTCCGACACAGTCCCTGCTGGCGATC 77099
Oy 12781 GGTGCGGGCGAATGTGCGCTTGAAGGGCGACGTTTCGACAAATGGGAGACACAGATGCGG 12840
Dd 77100 GGTGCGGGCGAATGTGCGCTTGAAGGGCGACGTTTCGACAAATGGGAGACACAGATGCGG 77159
Oy 12841 TTGGACGATTCAGTCACACACTTCACCAACTCTGTCCCATTAATAGTAAACATTTAGT 12900
Dd 77160 TTGGACGATTCAGTCACACACTTCACCAACTCTGTCCCATTAATAGTAAACATTTAGT 77219
Oy 12901 AGCATTCMAACTGTTCACCCCGGCTCCACCGGACAGTGTACCGAACCAGCGCGCA 12960
Dd 77220 AGCATTCMAACTGTTCACCCCGGCTCCACCGGACAGTGTACCGAACCAGCGCGCA 77279
Oy 12961 ACCGGACCAAACTTATTCACGGGCTCTCTCGCGCAACCCCGTAACATAGCAGTAGTGGCG 13020
Dd 77280 ACCGGACCAAACTTATTCACGGGCTCTCTCGCGCAACCCCGTAACATAGCAGTAGTGGCG 77339
Oy 13021 GAGGCTGTATGCGCAACGACACAGCACTCAAGTAAATGGTAAAGGCGAATGTGGG 13080
Dd 77340 GAGGCTGTATGCGCAACGACACAGCACTCAAGTAAATGGTAAAGGCGAATGTGGG 77399
Oy 13081 CATCTGTCCGATATGAGTGTGAAAGGTTGTCTTATGTGACAGCTCCGACAGGTTTGA 13140
Dd 77400 CATCTGTCCGATATGAGTGTGAAAGGTTGTCTTATGTGACAGCTCCGACAGGTTTGA 77459
Oy 13141 CTATGCGGTATGGGCGTGGATAGCCAGTTTGTGCAATTCCTTACGCGTTAATTCCTGCGCA 13200
Dd 77460 CTATGCGGTATGGGCGTGGATAGCCAGTTTGTGCAATTCCTTACGCGTTAATTCCTGCGCA 77519
Oy 13201 GCCCGGTGCAAGATGCCCCCTGGATGACAGTAAATGATTAATTTTTCGCCCTCC 13260
Dd 77520 GCCCGGTGCAAGATGCCCCCTGGATGACAGTAAATGATTAATTTTTCGCCCTCC 77579
Oy 13261 TCGACTCTGTGCTCCCTCTGTCTGCGATTCACAGGTATGCGAATTAAGTCTTTCCTGCG 13320
Dd 77580 TCGACTCTGTGCTCCCTCTGTCTGCGATTCACAGGTATGCGAATTAAGTCTTTCCTGCG 77639
Oy 13321 TCMAACCAACGATTCGCGGATGACAGCTGTCTGCGACATTCACACAGCCATCTCGA 13380
Dd 77640 TCMAACCAACGATTCGCGGATGACAGCTGTCTGCGACATTCACACAGCCATCTCGA 77699
Oy 13381 AGGCTGATGTTGGTGTGCTACACGACGCGCGCTCCATATCTCCGCGCGTGCAGAGGCA 13440
Dd 77700 AGGCTGATGTTGGTGTGCTACACGACGCGCGCTCCATATCTCCGCGCGTGCAGAGGCA 77759
Oy 13441 TGCMAACCTTGTCCAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 13500
Dd 77760 TGCMAACCTTGTCCAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 77819
Oy 13501 TGCMAACGGAATTTGTGCTCTAGTCTGCTGCGACAGTACCTTAAGCTTATTTTATCT 13560
Dd 77820 TGCMAACGGAATTTGTGCTCTAGTCTGCTGCGACAGTACCTTAAGCTTATTTTATCT 77879
Oy 13561 GTCGTGCACTCTGCGGCGGGAAGTTTGTGTTTATGACACACACCGGGAAGATTCATGT 13620
Dd 77880 GTCGTGCACTCTGCGGCGGGAAGTTTGTGTTTATGACACACACCGGGAAGATTCATGT 77939
Oy 13621 GTCCCTGCAACGCTGCTCTGACAGACACACAGAAATAGGAATCTGTGGGCTCTCTT 13680
Dd 77940 GTCCCTGCAACGCTGCTCTGACAGACACACAGAAATAGGAATCTGTGGGCTCTCTT 77999
Oy 13681 GGGCAACAGGCTGTGTGAGAGATCAGTGTGCGCGCTGCGACGCGCATGCGCTCTG 13740
Dd 78000 GGGCAACAGGCTGTGTGAGAGATCAGTGTGCGCGCTGCGACGCGCATGCGCTCTG 78059
Oy 13741 GTCCGGAAGAGGCGGAAGCTTCTCATGAAACCATGAAGTTAAATTTCTGTAG 13800
Dd 78060 GTCCGGAAGAGGCGGAAGCTTCTCATGAAACCATGAAGTTAAATTTCTGTAG 78119

Oy 13801 AGAGAACATGACCTCTGTTGATATATACCAATTAAGTCTTACCCGCGGTACA 13860
Dd 78120 AGAGAACATGACCTCTGTTGATATATACCAATTAAGTCTTACCCGCGGTACA 78179
Oy 13861 GCGTTTCCCTGCTTATTAATGACGTAACCTCGGTTTCTGTCGCTGATGATG 13920
Dd 78180 GCGTTTCCCTGCTTATTAATGACGTAACCTCGGTTTCTGTCGCTGATGATG 78239
Oy 13921 CCTGTTATGCGGACGACGATCGTTTATTTGGCTTATCTGTCGCGGCAATTTT 13980
Dd 78240 CCTGTTATGCGGACGACGATCGTTTATTTGGCTTATCTGTCGCGGCAATTTT 78299
Oy 13981 CACGATCTGAGATGGAACACAGACAGTGAACCCGGTCCATAGAAACAGATGACCGG 14040
Dd 78300 CACGATCTGAGATGGAACACAGACAGTGAACCCGGTCCATAGAAACAGATGACCGG 78359
Oy 14041 GATGGGAACCGGCGCGGATGCAACAGACACTCTCCGATCTTGGACGTGTATCA 14100
Dd 78360 GATGGGAACCGGCGCGGATGCAACAGACACTCTCCGATCTTGGGACGTGTATCA 78419
Oy 14101 GTCCGGAAGCGCAAAATTAACACCTGAAATTCACCGGCAAAAGGCAATTTGAT 14160
Dd 78420 GTCCGGAAGCGCAAAATTAACACCTGAAATTCACCGGCAAAAGGCAATTTGAT 78479
Oy 14161 GAGGACGCGGCTTCTGGACCCCGACAGATGTGCTCGGGCGTACGCTGATCTGTCG 14220
Dd 78480 GAGGACGCGGCTTCTGGACCCCGACAGATGTGCTCGGGCGTACGCTGATCTGTCG 78539
Oy 14221 GAGGACCAACGTGGGCAAGGGGCGGCGGCGGCAATTCGCCGCTTAACCCGATGCCAC 14280
Dd 78540 GAGGACCAACGTGGGCAAGGGGCGGCGGCGGCAATTCGCCGCTTAACCCGATGCCAC 78599
Oy 14281 ACACCTGCTCAAAATTAATTAATTCCTGACATTCATCAAGATATACGATAGC 14340
Dd 78600 ACACCTGCTCAAAATTAATTAATTCCTGACATTCATCAAGATATACGATAGC 78659
Oy 14341 ATCCGAATTCATCAAAAGTTTATACCGGAAGGCGGTCCAGCGCGCTGTCGCGCA 14400
Dd 78660 ATCCGAATTCATCAAAAGTTTATACCGGAAGGCGGTCCAGCGCGCTGTCGCGCA 78719
Oy 14401 CGACCCCATGCTCCACTTCTGGAATTCAGACATTCCTCCCTCAAAACCCCTCAAAATTCGTC 14460
Dd 78720 CGACCCCATGCTCCACTTCTGGAATTCAGACATTCCTCCCTCAAAACCCCTCAAAATTCGTC 78779
Oy 14461 TCTTACACTTACGAGGTTTCCATCTAGCCCAACCTGACAGCTCTCTCCACGCAGTAG 14520
Dd 78780 TCTTACACTTACGAGGTTTCCATCTAGCCCAACCTGACAGCTCTCTCCACGCAGTAG 78839
Oy 14521 CGACAACGCGTGGATTCAGCTGCGCCCTCTTCCAAAGACAGCTTAAAGCTTTTTCCTCC 14580
Dd 78840 CGACAACGCGTGGATTCAGCTGCGCCCTCTTCCAAAGACAGCTTAAAGCTTTTTCCTCC 78899
Oy 14581 CTCATGCAACCAAGTTAGGCTGTAATAGGTTTCTGCTTGAATGTAAGGCTCACCA 14640
Dd 78900 CTCATGCAACCAAGTTAGGCTGTAATAGGTTTCTGCTTGAATGTAAGGCTCACCA 78959
Oy 14641 TCTGATGAGGCTGTTAGTAATCTGCAAGTCCGCAAGGTAACCTATACAAATAG 14700
Dd 78960 TCTGATGAGGCTGTTAGTAATCTGCAAGTCCGCAAGGTAACCTATACAAATAG 79019
Oy 14701 GCGCATATGAGTGTACTTTTCCCTGATATTTGCAAGGCTCTATCTCCCAAAAG 14760
Dd 79020 GCGCATATGAGTGTACTTTTCCCTGATATTTGCAAGGCTCTATCTCCCAAAAG 79079
Oy 14761 TGCACCTGCGCTAAGCAACGCTCTAATTTCTGCACTTCCTCATTTATTAACCAATATG 14820
Dd 79080 TGCACCTGCGCTAAGCAACGCTCTAATTTCTGCACTTCCTCATTTATTAACCAATATG 79139
Oy 14821 TTTCTGCTCAGGTTTGGACGCTCAGCTGCAAGACAGCGGATAGATCCGCAATTCG 14880
Dd 79140 TTTCTGCTCAGGTTTGGACGCTCAGCTGCAAGACAGCGGATAGATCCGCAATTCG 79199

```
QY 14881 CTCTCCAGTGCCTTGACAAACACTGGCCAGATTAAAAAGTAGCAAAAGGCATTAGC 14940
D 14882 |
D 79200 CTCTCCAGTGCCTTGACAAACACTGGCCAGATTAAAAAGTAGCAAAAGGCATTAGC 79259
QY 14941 TTTTCGATTTAGTACCGGAGTAGTAGTGACATTAGAAAGTGTGTGGCCACACATT 15000
D 14942 |
D 79260 TTTTCGATTTAGTACCGGAGTAGTAGTGACATTAGAAAGTGTGTGGCCACACATT 79319
QY 15001 CAGGTGTGACACTCAAGCCCGACCAATATGGCAGCTGACCATTCCTCATCAACACTAG 15060
D 15002 |
D 79320 CAGGTGTGACACTCAAGCCCGACCAATATGGCAGCTGACCATTCCTCATCAACACTAG 79379
QY 15061 TACGAAAAAAGCAAAACACACGCGAGGTGACATTTTCCAGTTAGGAATTTATTAAG 15120
D 15062 |
D 79380 TACGAAAAAAGCAAAACACACGCGAGGTGACATTTTCCAGTTAGGAATTTATTAAG 79439
QY 15121 CCGGCGAATCATCTAACAACAAGCAAAATGTTTATTCAAAGTCCCTATAGATTCTGTT 15180
D 15122 |
D 79440 CCGGCGAATCATCTAACAACAAGCAAAATGTTTATTCAAAGTCCCTATAGATTCTGTT 79499
QY 15181 TGAATTAACATATATAGTATAGTAGAGCCCTGGAAGAGTTTGCTCTCGCCAGGGAACA 15240
D 15182 |
D 79500 TGAATTAACATATATAGTATAGTAGAGCCCTGGAAGAGTTTGCTCTCGCCAGGGAACA 79559
QY 15241 CCCGAAAAACCGAGTTTAAACAAGGCGCGGGGAGCCGCTGTGCGCGGGGAGGGGAGC 15300
D 15242 |
D 79560 CCCGAAAAACCGAGTTTAAACAAGGCGCGGGGAGCCGCTGTGCGCGGGGAGGGGAGC 79619
QY 15301 CTGGCCATATCAAGCAAAATATACATCATAGTCAAAATGCCACACAGCTCATCCGGTATG 15360
D 15302 |
D 79620 CTGGCCATATCAAGCAAAATATACATCATAGTCAAAATGCCACACAGCTCATCCGGTATG 79679
QY 15361 GCACGATGTGGCAAACTGTACGGGTCCAGGTTATTTCCGAAACCCACAGCTTAGAGCCC 15420
D 15362 |
D 79680 GCACGATGTGGCAAACTGTACGGGTCCAGGTTATTTCCGAAACCCACAGCTTAGAGCCC 79739
QY 15421 CCGGTAAATCTGAAACAATTAATTTCCCTGCTGCTGCTGAGAAATTTATTCATCCAGAGC 15480
D 15422 |
D 79740 CCGGTAAATCTGAAACAATTAATTTCCCTGCTGCTGAGAAATTTATTCATCCAGAGC 79799
QY 15481 CATTTCAAAAGCGTCTCGAGTCTCTGACACACAGACAGCTCATGCTGTGTGTATCGGA 15540
D 15482 |
D 79800 CATTTCAAAAGCGTCTCGAGTCTCTGACACACAGACAGCTCATGCTGTGTGTATCGGA 79859
QY 15541 GGAACACAGCGCTGGAAGGGGTCCATGCAAAACACACAGCTGTGCTCCGCTATTTGTT 15600
D 15542 |
D 79860 GGAACACAGCGCTGGAAGGGGTCCATGCAAAACACACAGCTGTGCTCCGCTATTTGTT 79919
QY 15601 GGTTTTGAAGATAGCTGATTTCCCTGCGGGTGGCTGTCAACAGCTCAGCTCAATTCG 15660
D 15602 |
D 79920 GGTTTTGAAGATAGCTGATTTCCCTGCGGGTGGCTGTCAACAGCTCAGCTCAATTCG 79979
QY 15661 CCATATATTAATCTTTTATATGATGACACCCCATGATGCCGGCAGATGGCGACGA 15720
D 15662 |
D 79980 CCATATATTAATCTTTTATATGATGACACCCCATGATGCCGGCAGATGGCGACGA 80039
QY 15721 CACGCCATAGTCTGGCGGCGAGAAAGCCGGAAGATAGCGTGCATGCTGCTCCGCG 15780
D 15722 |
D 80040 CACGCCATAGTCTGGCGGCGAGAAAGCCGGAAGATAGCGTGCATGCTGCTCCGCG 80099
QY 15781 TCGTGTCAATCTTGATGACCTTCCGATACCCGATCCGCTCTGTGATCACTTACGAGCGTCC 15840
D 15782 |
D 80100 TCGTGTCAATCTTGATGACCTTCCGATACCCGATCCGCTCTGTGATCACTTACGAGCGTCC 80159
QY 15841 GAAAGGCGGTGAAGCATTCGCGGCCGAGCATGGCAACCGCATTTATGGCAACCTCAAG 15900
D 15842 |
D 80160 GAAAGGCGGTGAAGCATTCGCGGCCGAGCATGGCAACCGCATTTATGGCAACCTCAAG 80219
QY 15901 CGGAGCGGCACACGCGGCGGAACACCGGACAAAGATCTTTCCGATAGACGAACCTTA 15960
D 15902 |
D 80220 CGGAGCGGCACACGCGGCGGAACACCGGACAAAGATCTTTCCGATAGACGAACCTTA 80279
QY 15961 AAGACCAGCGCGTGAAGGAAATGTAGTGGGAATTCCTTATCTTCCTCAAGATGAC 16020
D 15962 |
D 80280 AAGACCAGCGCGTGAAGGAAATGTAGTGGGAATTCCTTATCTTCCTCAAGATGAC 80339
QY 16021 TTTGCTTTTCTTACGGCTCCAGCAGCGCGCCCTGTGCTTGACACAGCTGTCTTCCA 16080
D 16022 |
D 80340 TTTGCTTTTCTTACGGCTCCAGCAGCGCGCCCTGTGCTTGACACAGCTGTCTTCCA 80399
QY 16081 GACGGCAGTGGAGTGTCTTTAACTACAGTAGGACATCATATGTGTGACCGTGGCTTGA 16140
D 16082 |
D 80400 GACGGCAGTGGAGTGTCTTTAACTACAGTAGGACATCATATGTGTGACCGTGGCTTGA 80459
QY 16141 TAATCATATTTGGAAACGAGCGGTGTAGCTGCCAACAACCGCTGTCTTGTGCTG 16200
D 16142 |
D 80460 TAATCATATTTGGAAACGAGCGGTGTAGCTGCCAACAACCGCTGTCTTGTGCTG 80519
QY 16201 TCTGCCAAAAACAGGCGCGGGGTACAGACACTATCGGCTTTGAAAGCTCACCACTTCCTTG 16260
D 16202 |
D 80520 TCTGCCAAAAACAGGCGCGGGGTACAGACACTATCGGCTTTGAAAGCTCACCACTTCCTTG 80579
QY 16261 AGGGCCATGCCATTAACAGATGGGCCCTTCTCGATATCCCGAGCGCCATGATTCAGTGC 16320
D 16262 |
D 80580 AGGGCCATGCCATTAACAGATGGGCCCTTCTCGATATCCCGAGCGCCATGATTCAGTGC 80639
QY 16321 GCAACGTTTAAACCCCATGTAAAGTTTCAGTTCAATTTAAATGACACAACTCGGCCAT 16380
D 16322 |
D 80640 GCAACGTTTAAACCCCATGTAAAGTTTCAGTTCAATTTAAATGACACAACTCGGCCAT 80699
QY 16381 GCTGTGCAAAACATTAAGAAAGTGGCACACGCTGCGCTTTGGCCGCTGTGATGAA 16440
D 16382 |
D 80700 GCTGTGCAAAACATTAAGAAAGTGGCACACGCTGCGCTTTGGCCGCTGTGATGAA 80759
QY 16441 CCGCGCGGTAACTACTTCTCCATACGCTGCGGAGGGTGTAGTACATATGCTTCC 16500
D 16442 |
D 80760 CCGCGCGGTAACTACTTCTCCATACGCTGCGGAGGGTGTAGTACATATGCTTCC 80819
QY 16501 CGTTGTTCGCGAAGACCGGACACCGGCTCCAGAGGTCCTCCCTGCTCATCTCC 16560
D 16502 |
D 80820 CGTTGTTCGCGAAGACCGGACACCGGCTCCAGAGGTCCTCCCTGCTCATCTCC 80879
QY 16561 CCGGGCACGCTTCTGACATCATCTGACACATCATATTCACACAGTACGGAAGTTTCAG 16620
D 16562 |
D 80880 CCGGGCACGCTTCTGACATCATCTGACACATCATATTCACACAGTACGGAAGTTTCAG 80939
QY 16621 GGCATATGGGAGCATCCCATGATTTTTCGAGTGTAGTACGCGGCACATGAAATTCACGC 16680
D 16622 |
D 80940 GGCATATGGGAGCATCCCATGATTTTTCGAGTGTAGTACGCGGCACATGAAATTCACGC 80999
QY 16681 ACATGACGCGGCGGAGACATCTCTGAGTGTGGCATCTCGCAGCTCCCTCAATATATG 16740
D 16682 |
D 81000 ACATGACGCGGCGGAGACATCTCTGAGTGTGGCATCTCGCAGCTCCCTCAATATATG 81059
QY 16741 CAAGAGATGACGCTTGGAGCGGCTGCGAAGGCCGACGCTCATATTAATTTCAAGATA 16800
D 16742 |
D 81060 CAAGAGATGACGCTTGGAGCGGCTGCGAAGGCCGACGCTCATATTAATTTCAAGATA 81119
QY 16801 GTTGTGCAATGCCGTATGTGTGCTTCCAGGTTTTCACACACATTCAGACATCCGT 16860
D 16802 |
D 81120 GTTGTGCAATGCCGTATGTGTGCTTCCAGGTTTTCACACACATTCAGACATCCGT 81179
QY 16861 CATTAACAGATCAAACTCTCTCGCATTTTCTGACAGGCTTCGAAATCTGCTCGG 16920
D 16862 |
D 81180 CATTAACAGATCAAACTCTCTCGCATTTTCTGACAGGCTTCGAAATCTGCTCGG 81239
QY 16921 AAACCTGCAAGGAATCACTGGGACGAGGCAAGAAACAGTCATGATTTATCGGCACA 16980
D 16922 |
D 81240 AAACCTGCAAGGAATCACTGGGACGAGGCAAGAAACAGTCATGATTTATCGGCACA 81299
QY 16981 ACACAGGTGCTCGGGACGTTTGGGATCAGAAAGGCGACATATATGACACCCGAGCGGC 17040
D 16982 |
D 81300 ACACAGGTGCTCGGGACGTTTGGGATCAGAAAGGCGACATATATGACACCCGAGCGGC 81359
QY 17041 TCGCAAAATTTGAACTCGAGCTGTCTCCAAAGTAAAGAAAGATACCTCAAGCGCCC 17100
D 17042 |
```

Db 81360 TCGCAAAATTTGAACTCCGAGCTTCTCTCAAAAGTAAAAAGATACCTCAACGCCCC 81419
Qy 17101 TAGCAGAGTTGGCAGAGAAGTCTCGTAGTCTTGATTTCCCTTTATAAAGGAGAC 17160
Db 81420 TAGCAGAGTTGGCAGAGAAGTCTCGTAGTCTTGATTTCCCTTTATAAAGGAGAC 81479
Qy 17161 TCTCAGTGGCCCTTAGCCCTCGGCCGCCGTGTCTCTCGAAACATCCTCTCGAAGCA 17220
Db 81480 TCTCAGTGGCCCTTAGCCCTCGGCCGCCGTGTCTCTCGAAACATCCTCTCGAAGCA 81539
Qy 17221 ACTGCCCATGGAAACGCTATGCAACGATGTGTGCGCATGAGGTACACAGATCGCAGCC 17280
Db 81540 ACTGCCCATGGAAACGCTATGCAACGATGTGTGCGCATGAGGTACACAGATCGCAGCC 81599
Qy 17281 CACCGTAACCTCAGAGAACATTTGAAAGAGTCTGATCTTCCCGAGAGAGCCGCCGCC 17340
Db 81600 CACCGTAACCTCAGAGAACATTTGAAAGAGTCTGATCTTCCCGAGAGAGCCGCCGCC 81659
Qy 17341 CTTCGTCGCGGTGTGACGCTCCCTCAAAATACCTGTGAGATCTCACTGATATACATCT 17400
Db 81660 CTTCGTCGCGGTGTGACGCTCCCTCAAAATACCTGTGAGATCTCACTGATATACATCT 81719
Qy 17401 AATTTCTTAAATTTCTGGGCACTGTGAACCGGTTTGACACACGCCAGCGCTGACAA 17460
Db 81720 AATTTCTTAAATTTCTGGGCACTGTGAACCGGTTTGACACACGCCAGCGCTGACAA 81779
Qy 17461 ATCGCAATATCTGTTATATCTCATCGACGCGAGCTGTGGGTGACCGGTTGACAG 17520
Db 81780 ATCGCAATATCTGTTATATCTCATCGACGCGAGCTGTGGGTGACCGGTTGACAG 81839
Qy 17521 GACAGGTAAATGTCTTGTCTGTCTCATCCCATTCACATCCGCGGTTATCGTTAGACT 17580
Db 81840 GACAGGTAAATGTCTTGTCTGTCTCATCCCATTCACATCCGCGGTTATCGTTAGACT 81899
Qy 17581 CAGGCGCTCGATGAACCAAGCTTTAAATCCATATCGGGTTCGCCCATCTGCCGATTC 17640
Db 81900 CAGGCGCTCGATGAACCAAGCTTTAAATCCATATCGGGTTCGCCCATCTGCCGATTC 81959
Qy 17641 ATACCTGTACCGAGCGGCTCAGTTAAATACCGAGCCCGAGAACCCAGGCTCCGTA 17700
Db 81960 ATACCTGTACCGAGCGGCTCAGTTAAATACCGAGCCCGAGAACCCAGGCTCCGTA 82019
Qy 17701 ACAAAGGATCTAGATCTGAAGAAGCTTAATATATACGCCACCGGAAAACTCTGTA 17760
Db 82020 ACAAAGGATCTAGATCTGAAGAAGCTTAATATATACGCCACCGGAAAACTCTGTA 82079
Qy 17761 ACAAAGGATCTAGATCTGAAGAAGCTTAATATATACGCCACCGGAAAACTCTGTA 17820
Db 82080 ACAAAGGATCTAGATCTGAAGAAGCTTAATATATACGCCACCGGAAAACTCTGTA 82139
Qy 17821 TCAACCAAGGATCTAGATCTGAAGAAGCTTAATATATACGCCACCGGAAAACTCTGTA 17880
Db 82140 TCAACCAAGGATCTAGATCTGAAGAAGCTTAATATATACGCCACCGGAAAACTCTGTA 82199
Qy 17881 GTTCTCATATGCGGTGAGCAAAAGCTTACATATATTAAGACAGTGTGAGAGA 17940
Db 82200 GTTCTCATATGCGGTGAGCAAAAGCTTACATATATTAAGACAGTGTGAGAGA 82259
Qy 17941 AAACCTTATGAGGAGGAGGCAAAAGCAAGCTGTGACGCTATACAGATGTGACACTG 18000
Db 82260 AAACCTTATGAGGAGGAGGCAAAAGCAAGCTGTGACGCTATACAGATGTGACACTG 82319
Qy 18001 GGGCGCATCCCGCAGCGCCGCAACAGACACTCTGCAAAATTTGAATGAGAGGAGAT 18060
Db 82320 GGGCGCATCCCGCAGCGCCGCAACAGACACTCTGCAAAATTTGAATGAGAGGAGAT 82379
Qy 18061 TGTGGGACAGGCTGCGCTTCCGAGTGGGAAAGCGCTCTTAGTGAAGAGAGCATAGGC 18120
Db 82380 TGTGGGACAGGCTGCGCTTCCGAGTGGGAAAGCGCTCTTAGTGAAGAGAGCATAGGC 82439
Qy 18121 GGGCTGAATGCGGCTTCCGAGTGGGAGGAGGCTGACACCGACATCATATTTGGCCAG 18180
Db 82440 GGGCTGAATGCGGCTTCCGAGTGGGAGGAGGCTGACACCGACATCATATTTGGCCAG 82499

Qy 18181 GCAAAACACGCGCAGAACTCGCGCTTGTATATATATCAACCGGCTCCAGCAACTCC 18240
Db 82500 GCAAAACACGCGCAGAACTCGCGCTTGTATATATATCAACCGGCTCCAGCAACTCC 82559
Qy 18241 GTTACCCAGAGGAAGGCTGGAAGCTGACCCATATACGAAATGTAATCCAGACCCGTC 18300
Db 82560 GTTACCCAGAGGAAGGCTGGAAGCTGACCCATATACGAAATGTAATCCAGACCCGTC 82619
Qy 18301 TGGCAATATCAACCCCGCTATATCTCTTCCCGACCCCTTTAGCATCTCTGTCTG 18360
Db 82620 TGGCAATATCAACCCCGCTATATCTCTTCCCGACCCCTTTAGCATCTCTGTCTG 82679
Qy 18361 GTGAGAAACATATCTGTGGGCTATGCGGCAACAGGCGCTTTCGCGCAATCCGCG 18420
Db 82680 GTGAGAAACATATCTGTGGGCTATGCGGCAACAGGCGCTTTCGCGCAATCCGCG 82739
Qy 18421 ACAACGTCCTTCAAGTGTGCTTGGCGCGGCAACAGCGAACGCCGTTGGCGCA 18480
Db 82740 ACAACGTCCTTCAAGTGTGCTTGGCGCGGCAACAGCGAACGCCGTTGGCGCA 82799
Qy 18481 CCGGACCTCATGTTCCCAACCAAGCCCATATGTAATTAACCAAGCCGTAAGCATCA 18540
Db 82800 CCGGACCTCATGTTCCCAACCAAGCCCATATGTAATTAACCAAGCCGTAAGCATCA 82859
Qy 18541 ACACGTCTCCCGCTGCGCTCCCAAGGCGCTTCTGATCTCATCCGCGGCAAGATACCG 18600
Db 82860 ACACGTCTCCCGCTGCGCTCCCAAGGCGCTTCTGATCTCATCCGCGGCAAGATACCG 82919
Qy 18601 GAATCTGGCGGTTACCTCGTTGCGTACGTGCAAGAGATGCGCGGTTGCGCTTCG 18660
Db 82920 GAATCTGGCGGTTACCTCGTTGCGTACGTGCAAGAGATGCGCGGTTGCGCTTCG 82979
Qy 18661 GTTACAGAGGCGGCAAGATCGTAACAAGATGCGCAACAGCGCAATACGCGGCTGTT 18720
Db 82980 GTTACAGAGGCGGCAAGATCGTAACAAGATGCGCAACAGCGCAATACGCGGCTGTT 83039
Qy 18721 AGGCGCGGCGCGCAGAGGTTCTCTAGTGAATACATCTTGTGAGCGTGTGAGCGG 18780
Db 83040 AGGCGCGGCGCGCAGAGGTTCTCTAGTGAATACATCTTGTGAGCGTGTGAGCGG 83099
Qy 18781 TATACGCTGGCCAAACAGTTTTCATCTTCCGACGCTCAATCTGTCTGACGCTG 18840
Db 83100 TATACGCTGGCCAAACAGTTTTCATCTTCCGACGCTCAATCTGTCTGACGCTG 83159
Qy 18841 CCGTATGCTTAAATGCAATATGCAATATGCAATATGCAATATGCAATATGCAATAT 18900
Db 83160 CCGTATGCTTAAATGCAATATGCAATATGCAATATGCAATATGCAATATGCAATAT 83219
Qy 18901 ACCCGCGGCTTAAATGATTCGAAGGTAAACGAACAGAGTCTTTCCTCATCCAGCCA 18960
Db 83220 ACCCGCGGCTTAAATGATTCGAAGGTAAACGAACAGAGTCTTTCCTCATCCAGCCA 83279
Qy 18961 ATGCAATTCAGAGTCTTATCATTTATCGCAACATCGAGCAACATGCTTCCAGGCG 19020
Db 83280 ATGCAATTCAGAGTCTTATCATTTATCGCAACATCGAGCAACATGCTTCCAGGCG 83339
Qy 19021 CCGCGGTTTACGCGGATGAGCCGCTGCTTCCGCAATCTCGAGGAGGCGCGTCCG 19080
Db 83340 CCGCGGTTTACGCGGATGAGCCGCTGCTTCCGCAATCTCGAGGAGGCGCGTCCG 83399
Qy 19081 ATAACTGGCTTAAATATCTATCCCGCCCGGTGACACTGTACTTTACAGTCAACCTTC 19140
Db 83400 ATAACTGGCTTAAATATCTATCCCGCCCGGTGACACTGTACTTTACAGTCAACCTTC 83459
Qy 19141 GGCACAGCGCGTAGGCGTGGGAGGAGGCAACCGACAGCACTATTTTTCATCTTACGCG 19200
Db 83460 GGCACAGCGCGTAGGCGTGGGAGGAGGCAACCGACAGCACTATTTTTCATCTTACGCG 83519
Qy 19201 CCTACTAGGGAATCTGGGCTGTAACAAATCCACGAGCGCGGCAATGTACCATGAG 19260
Db 83520 CCTACTAGGGAATCTGGGCTGTAACAAATCCACGAGCGCGCGCAATGTACCATGAG 83579

OY	19261	TCATTCATCTCTGACACATCACCAAAGTGACAGGACCTGCGGCTCTTTTACTGAGCCAG	19320
Db	83580	TCATTCATCTCTGACACATCACCAAAGTGACAGGACCTGCGGCTCTTTTACTGAGCCAG	83639
OY	19321	GGCAGCCCCCAAGGTAAAGAGTGACCTGCTTGGGAAACAGTGTCGGCGGGAACGGGAG	19380
Db	83640	GGCAGCCCCCAAGGTAAAGAGTGACCTGCTTGGGAAACAGTGTCGGCGGGAACGGGAG	83699
OY	19381	ACCGGGGAGTCTGCGCAGTAGACCCATTAACATAGAAGATTTGATTTTGACAGAGATC	19440
Db	83700	ACCGGGGAGTCTGCGCAGTAGACCCATTAACATAGAAGATTTGATTTTGACAGAGATC	83759
OY	19441	GCACAGCCGTTGTGCGTGCTCCCTCTGCGTGCTTCCCTGCGACGCAACCTGTGCGC	19500
Db	83760	GCACAGCCGTTGTGCGTGCTCCCTCTGCGTGCTTCCCTGCGACGCAACCTGTGCGC	83819
OY	19501	TGCTTCGTATTCCACATACATCCCAAGTCATTTGGCATAGCAAAAAGAGCCCTCTCAC	19560
Db	83820	TGCTTCGTATTCCACATACATCCCAAGTCATTTGGCATAGCAAAAAGAGCCCTCTCAC	83879
OY	19561	ACCGTTTATATATCTACACAGGTTTCTCTGCTCCGCGCTTACGCGCCCATCCAACT	19620
Db	83880	ACCGTTTATATATCTACACAGGTTTCTCTGCTCCGCGCTTACGCGCCCATCCAACT	83939
OY	19621	GAGGTTTTGGAAGCCACATCTTATAGCTGTCCCATAGAAACACTGTCGACCCGGTTTGG	19680
Db	83940	GAGGTTTTGGAAGCCACATCTTATAGCTGTCCCATAGAAACACTGTCGACCCGGTTTGG	83999
OY	19681	GGTCTTGGCGTTATGCAATCGATACCCCTGACGGTCGTGGGACGTGTCCGCTACCA	19740
Db	84000	GGTCTTGGCGTTATGCAATCGATACCCCTGACGGTCGTGGGACGTGTCCGCTACCA	84059
OY	19741	GCGACCCCAATAAAAATCTGATACGTATAGCCGCCCAAAATGAGATCTGTGTCGAT	19800
Db	84060	GCGACCCCAATAAAAATCTGATACGTATAGCCGCCCAAAATGAGATCTGTGTCGAT	84119
OY	19801	GCGGTGTGCAACCGTGCACACCTGGCGGCTGTGCATATACGACCGCGCGACCGT	19860
Db	84120	GCGGTGTGCAACCGTGCACACCTGGCGGCTGTGCATATACGACCGCGCGACCGT	84179
OY	19861	CAGGCTCGCGCGGAGCGGAGGAGGAGGGGCGTCCCTGGCTCAAGCCCATGAGCGCAG	19920
Db	84180	CAGGCTCGCGCGGAGCGGAGGAGGAGGGGCGTCCCTGGCTCAAGCCCATGAGCGCAG	84239
OY	19921	CCGCTCTTAAGTAAATTAGAGCAGGTCTCCGAATGACTATCTAAGATGACGGCATTAACA	19980
Db	84240	CCGCTCTTAAGTAAATTAGAGCAGGTCTCCGAATGACTATCTAAGATGACGGCATTAACA	84299
OY	19981	GCGGATCCACGGCGGCTCTCAAGTAAAAAAATCTTTCTCCGCCAAAACGCGTTGTGTTG	20040
Db	84300	GCGGATCCACGGCGGCTCTCAAGTAAAAAAATCTTTCTCCGCCAAAACGCGTTGTGTTG	84359
OY	20041	CCCGGGCATGTCCTGTGTCAAACCGACGTTTTCCCGAAGCACACCTTACACTCTTTTCC	20100
Db	84360	CCCGGGCATGTCCTGTGTCAAACCGACGTTTTCCCGAAGCACACCTTACACTCTTTTCC	84419
OY	20101	GGCACTTCGACAGTGTGCTGTGCGCTCCACATTCAGATCCCATTCAGGAGGTACGCA	20160
Db	84420	GGCACTTCGACAGTGTGCTGTGCGCTCCACATTCAGATTCCTATTCAGGAGGTACGCA	84479
OY	20161	CCACAGGTTGCATGCCACTCATACCTCGGTGCCATGATTCCTTAAAGCTCTCTTTTCT	20220
Db	84480	CCACAGGTTGCATGCCACTCATACCTCGGTGCCATGATTCCTTAAAGCTCTCTTTTCT	84539
OY	20221	CGTGCACCAACACAAAGTGTGCGGGAACAGTGTGCTTCCAAATTTGAAATATATCATC	20280
Db	84540	CGTGCACCAACACAAAGTGTGCGGGAACAGTGTGCTTCCAAATTTGAAATATATCATC	84599
OY	20281	TTGCGCAGTATTGTGATGATTTTCATCTCAGGTCATTTGGAACCTTGGTCCACGAAACT	20340
Db	84600	TTGCGCAGTATTGTGATGATTTTCATCTCAGGTCATTTGGAACCTTGGTCCACGAAACT	84659
OY	20341	AACGTCAAAAGCCCTGCACATCTCCCTTAAACTGATAGCTGAATTTTATGTCCACCTTATAG	20400

Db	84660	AACTCAAAAGCCCTACACACTCCCTAACTGAGTGAATTTATGTCCACCTTATAG		847150
QY	20401	GTGCACGGTACGTATATGACCCCGGTGAAAACCTGCGACTTCATATAATATATCCCCAA		20460
Db	84720	GTGCACGTGTACGTATATGCCCCGTGAAAACCTGCGACTTCATATAATATATCCCCAA		84779
QY	20461	GC GTTTCGGGTGCGTCACTAACTAACTCGAGCATTCACGGTTGATATGTGCCGGT		20520
Db	84780	GC GTTTCGGGTGCGTCACTAACTAACTCGAGCATTCACGGTTGATATGTGCCGGT		84833
QY	20521	TTTCGCACCTCCCCACCGCGACAGAAACGAAACGTTCATTTAAAGGACACAAAGCTC		20580
Db	84840	TTTCGCACCTCCCCACCGCGACAGAAACGAAACGTTCATTTAAAGGACACAAAGCTC		84893
QY	20581	AAC TTATATTTAAGAGAAAAAAAACACCGGCATCAGAAAGTTTCCGAGGACACACACCC		20640
Db	84900	AAC TTATATTTAAGAGAAAAAAAACACCGGCATCAGAAAGTTTCCGAGGACACACACCC		84955
QY	20641	CAAGACTATTCCTGGCAGATTCCGGCAGCGCTGATTTTCTGATTAATTTGTAATTC		20700
Db	84960	CAAGACTATTCCTGGCAGATTCCGGCAGCGCTGATTTTCTGATTAATTTGTAATTC		85019
QY	20701	GCATTCATTCGCCCCCAACATAGTCATATAAAAAACCGGTAAACACACACACTGTGTGA		20760
Db	85020	GCATTCATTCGCCCCCAACATAGTCATATAAAAAACCGGTAAACACACACACTGTGTGA		85079
QY	20761	CAAA TTATGCTTCTGTGGCCCAAGACGTGCGTAGGGTCAAGACACACCGGCTCTAA		20820
Db	85080	CAAA TTATGCTTCTGTGGCCCAAGACGTGCGTAGGGTCAAGACACACCGGCTCTAA		85133
QY	20821	AACATAAACACGAGGCTAAACAGTTTGACCCGAACACAGTCCGAGGCAACAAAAAGCCC		20880
Db	85140	AACATAAACACGAGGCTAAACAGTTTGACCCGAACACAGTCCGAGGCAACAAAAAGCCC		85199
QY	20881	AACGTGGAAGCAAAAAAATATGTGTACAGTCCGAGAGACAGAGCGTGTCAAGCCAAC		20940
Db	85200	AACGTGGAAGCAAAAAAATATGTGTACAGTCCGAGAGAGAGAGCGTGTCAAGCCAAC		85253
QY	20941	AGACAGGTTACCGCGGGCGCGCCCTCCCAATCAAAACAGTACAGATTAATAAGTCCCATCC		21000
Db	85260	AGACAGGTTACCGCGGGCGCGCCCTCCCAATCAAAACAGTACAGATTAATAAGTCCCATCC		85319
QY	21001	ACACAGCTCAAGCGCTTGCTTTATAGAGTATGTATGATACCGGCTTAGAGGTGAGCGAAAA		21060
Db	85320	ACACAGCTCAAGCGCTTGCTTTATAGAGTATGTATGATACCGGCTTAGAGGTGAGCGAAAA		85379
QY	21061	AATTGCATGGCGTGTGCTGACAGGCCCGCTCATTAAGCGATGTGACCGACAGCGTGTGAG		21120
Db	85380	AATTGCATGGCGTGTGCTGACAGGCCCGCTCATTAAGCGATGTGACCGACAGCGTGTGAG		85439
QY	21121	TGAACAAACGCGACCTCTCTATTAAGGACACAGGGGAGCAAAAACACGGGGCTTAAAA		21180
Db	85440	TGAACAAACGCGACCTCTCTATTAAGGACACAGGGGAGCAAAAACACGGGGCTTAAAA		85493
QY	21181	AAGGTTCTTAAAGAACTAAAAAATATATACACCGAAGACGCTGTAAAAATCCAAAGTTCGTA		21240
Db	85500	AAGGTTCTTAAAGAACTAAAAAATATATACACCGAAGACGCTGTAAAAATCCAAAGTTCGTA		85559
QY	21241	GTATCTGTGGCAATGCTGTGGGACAAATATATACCGATCTTTCGCCGAACAACACAGAG		21300
Db	85560	GTATCTGTGGCAATGCTGTGGGACAAATATATACCGATCTTTCGCCGAACAACACAGAG		85619
QY	21301	CAGAGGACACAGCGACGACCGCCCAAAAAATGGAAGGTGAACCCATGGAAGGTGCAAGCGC		21360
Db	85620	CAGAGGACACAGCGACGACCGCCCAAAAAATGGAAGGTGAACCCATGGAAGGTGCAAGCGC		85679
QY	21361	GAGGTGATGATGCCATTAACACCGCGGTAATTAACAAAGCGCGAGATGTTACAGTACATC		21420
Db	85680	GAGGTGATGATGCCATTAACACCGCGGTAATTAACAAAGCGCGAGATGTTACAGTACATC		85739
QY	21421	CACCTGCGGAGAGCCAGGCGCGTATGCCCCAATATATACAGAAATAGCAAAAAGACCCATG		21480

D	b	90120	ACAGCCACCCTCATTAACATCTGGGCCACGCTTTCAAAAATGGGTGAAGAACCTGGGTT	90179
Q	y	25861	CTCAGCAGCTAGCATCTGTAACCTTAAGGCGAGAGAGTGGCGGCTTAACGAATTT	25920
D	b	90180	CTAGACGCTAGCTATCTGTAACCTTAAGGCGAGAGAGTGGCGGCTTAACGAATTT	90239
Q	y	25921	GTGTATGGCTTGGCTTGGCTTAAGATCCTGTAAGAACGCTCAAGGGCGGCTTGGT	25980
D	b	90240	GTGTATGGCTTGGCTTGGCTTAAGATCCTGTAAGAACGCTCAAGGGCGGCTTGGT	90299
Q	y	25981	GACATTAAGCGCGGAGAACCTGCTGGCTTAAGCTTCCCGGAATACCGGAGATAGTCTGC	26040
D	b	90300	GACATTAAGCGCGGAGAACCTGCTGGCTTAAGCTTCCCGGAATACCGGAGATAGTCTGC	90359
Q	y	26041	ACCGTAACGAGGACCGTCTGCATTAATCTGGCCAAAGAGACCGGTTAGGAGTTG	26100
D	b	90360	ACCGTAACGAGGACCGTCTGCATTAATCTGGCCAAAGAGACCGGTTAGGAGTTG	90419
Q	y	26101	GCCTCTATGCTCCATCCAAAGTGTGGCTTTAAAGAAATTCACGAGTATCGGCGCATCT	26160
D	b	90420	GCCTCTATGCTCCATCCAAAGTGTGGCTTTAAAGAAATTCACGAGTATCGGCGCATCT	90479
Q	y	26161	TCAGGCTCAAGGCTTGAGCTACACCCCGGCTCCCGGCTGGTACTAGGTTAAAGT	26220
D	b	90480	TCAGGCTCAAGGCTTGAGCTACACCCCGGCTCCCGGCTGGTACTAGGTTAAAGT	90539
Q	y	26221	TTGAGCAGATTTTGGCGGAGAGAAAGATTGGTGTTCATTTGTTAAAGAAATAGCTTCC	26280
D	b	90540	TTGAGCAGATTTTGGCGGAGAGAAAGATTGGTGTTCATTTGTTAAAGAAATAGCTTCC	90599
Q	y	26281	AAGACCCCGGATTGGAAACAACTCCGTAATTTTAAACACCGGTTAAAGACGCGCTTTAA	26340
D	b	90600	AAGACCCCGGATTGGAAACAACTCCGTAATTTTAAACACCGGTTAAAGACGCGCTTTAA	90659
Q	y	26341	AGTGAAGCTTTGAAAGATGTTGTAAACCGGAGAGCAGCTTCCAAAGTCTGCAACTA	26400
D	b	90660	AGTGAAGCTTTGAAAGATGTTGTAAACCGGAGAGCAGCTTCCAAAGTCTGCAACTA	90719
Q	y	26401	CGCGAAGCAGAGCTTATTAATATACAGTCTCAGCTGATTAATTTGGTGGAA	26460
D	b	90720	CGCGAAGCAGAGCTTATTAATATACAGTCTCAGCTGATTAATTTGGTGGAA	90779
Q	y	26461	TCACGCGCTGTAAAAATCCCTCAATTTGGGAGCTATTTCACAATATCTTTACAGACT	26520
D	b	90780	TCACGCGCTGTAAAAATCCCTCAATTTGGGAGCTATTTCACAATATCTTTACAGACT	90839
Q	y	26521	TAAAAAACCAAGCTTCAAGGCGGCTATTTATTTACCTTAATAGTTAAGCAACAT	26580
D	b	90840	TAAAAAACCAAGCTTCAAGGCGGCTATTTATTTACCTTAATAGTTAAGCAACAT	90899
Q	y	26581	AAATAGCAGTGGGCGGAGAAAGGCTGTCGCGCAGGCTGGAGGGGATGAGTCACTA	26640
D	b	90900	AAATAGCAGTGGGCGGAGAAAGGCTGTCGCGCAGGCTGGAGGGGATGAGTCACTA	90959
Q	y	26641	AATCCAAACATGTCTACTAGGAAGCTGAAGGCCAATATGTGAACAACGGGCTCTGG	26700
D	b	90960	AATCCAAACATGTCTACTAGGAAGCTGAAGGCCAATATGTGAACAACGGGCTCTGG	91019
Q	y	26701	CGACTACGTTGCCCTTTAAGCGAGAGTCACTTTGGTGAACAAGTACTGTGACCGTTT	26760
D	b	91020	CGACTACGTTGCCCTTTAAGCGAGAGTCACTTTGGTGAACAAGTACTGTGACCGTTT	91079
Q	y	26761	GAACCAACGCGCGAGCGGCGCAAGAAAGTGAAGGAGGAGCGGTTTCCAAACAATCTT	26820
D	b	91080	GAACCAACGCGCGAGCGGCGCAAGAAAGTGAAGGAGGAGCGGTTTCCAAACAATCTT	91139
Q	y	26821	CAAAATTTGGTATGCGCTCAAGTGAAGCGCTCTGCGGCTTACCAACAACGCTATTC	26880
D	b	91140	CAAAATTTGGTATGCGCTCAAGTGAAGCGCTCTGCGGCTTACCAACAACGCTATTC	91199
Q	y	26881	TGTTGGTCTGGGGGCGAGAGTCCGCGTCTCAATCTGAAGACAGTCCGCGCAGGACGTTAGGCG	26940
D	b	91200	TGTTGGTCTGGGGGCGAGAGTCCGCGTCTCAATCTGAAGACAGTCCGCGCAGGACGTTAGGCG	91259

Q	y	26941	TGAATACATGTCAATGAGAGACCCAGTGTCACTGTTTAAAGAAACAGTAGGTGC	27000
D	b	91260	TGAATACATGTCAATGAGAGACCCAGTGTCACTGTTTAAAGAAACAGTAGGTGC	91319
Q	y	27001	CCGAGGTTCTGTGAACATCATGTGTGAGAAATAATCAAAAAATCTCATCTTTGAC	27060
D	b	91320	CCGAGGTTCTGTGAACATCATGTGTGAGAAATAATCAAAAAATCTCATCTTTGAC	91379
Q	y	27061	ATGTAGCGAGACAGATTAATAATTCATCTTTGATGCGCTCCACCGAGTGGTCCACA	27120
D	b	91380	ATGTAGCGAGACAGATTAATAATTCATCTTTGATGCGCTCCACCGAGTGGTCCACA	91439
Q	y	27121	CCACATTTTGAAGAGAGATATCAAGAACCCCTTAGAAAAAGTCCGACCGGAGATTAAG	27180
D	b	91440	CCACATTTTGAAGAGAGATATCAAGAACCCCTTAGAAAAAGTCCGACCGGAGATTAAG	91499
Q	y	27181	AAACCCGCTGAGAGGCGGCGAGTAGAGCATCAACTATCTACGCTTGTTCAGCT	27240
D	b	91500	AAACCCGCTGAGAGGCGGCGAGTAGAGCATCAACTATCTACGCTTGTTCAGCT	91559
Q	y	27241	TTGGCTCCCTGTCTTATGCGCTGTCAATCTCTGCGGACGGGCTGATTAAGGTTACG	27300
D	b	91560	TTGGCTCCCTGTCTTATGCGCTGTCAATCTCTGCGGACGGGCTGATTAAGGTTACG	91619
Q	y	27301	AGAACACGGCGGCTTTACAAATTAAGTCAACACTCTTAAGCTGACCGGATCGCTAC	27360
D	b	91620	AGAACACGGCGGCTTTACAAATTAAGTCAACACTCTTAAGCTGACCGGATCGCTAC	91679
Q	y	27361	AACAGCTTAAATCTCTGATGAGTTCACAACTAAACAGCAACCGCACCTTTTAA	27420
D	b	91680	AACAGCTTAAATCTCTGATGAGTTCACAACTAAACAGCAACCGCACCTTTTAA	91739
Q	y	27421	GCATGCCACCGGTGACCGGTTTAAATCTGATTCAAATTAAGCAACCCCGTGGTT	27480
D	b	91740	GCATGCCACCGGTGACCGGTTTAAATCTGATTCAAATTAAGCAACCCCGTGGTT	91799
Q	y	27481	CATTATTTCAAAAAACACCTGTGTTTTTTTAAATGAAGTCCGAGGCTTCCGAGGCGAG	27540
D	b	91800	CATTATTTCAAAAAACACCTGTGTTTTTTTAAATGAAGTCCGAGGCTTCCGAGGCGAG	91859
Q	y	27541	TCATTACAGACACCAAGCGCGAGAACGTCACAGGATATCTCCGAGGTTGAAATG	27600
D	b	91860	TCATTACAGACACCAAGCGCGAGAACGTCACAGGATATCTCCGAGGTTGAAATG	91919
Q	y	27601	TTCTTAATPACAGATTTGAAACACACAGGATCCGAGGCGTAAAGACAGATATC	27660
D	b	91920	TTCTTAATPACAGATTTGAAACACACAGGATCCGAGGCGTAAAGACAGATATC	91979
Q	y	27661	TCGACAAACCGTGCATATTTGGCATGATTAAGATACATACATCAGCTTAACCTTACGTA	27720
D	b	91980	TCGACAAACCGTGCATATTTGGCATGATTAAGATACATACATCAGCTTAACCTTACGTA	92039
Q	y	27721	CGCCCTCGGGGATCCACACGACACCAATGSGTATACGCCATTCACGCTGAGAGC	27780
D	b	92040	CGCCCTCGGGGATCCACACGACACCAATGSGTATACGCCATTCACGCTGAGAGC	92099
Q	y	27781	AAATTTTACAGAAACCCACCGGCAATATGGAACCTAACCCCTCCGAGTGGCTATTTA	27840
D	b	92100	AAATTTTACAGAAACCCACCGGCAATATGGAACCTAACCCCTCCGAGTGGCTATTTA	92159
Q	y	27841	TCGACATCGGGGAATGCGGCTCTCGGCTTCAGAGGTGGCTTAATCTATCGAATGTAA	27900
D	b	92160	TCGACATCGGGGAATGCGGCTCTCGGCTTCAGAGGTGGCTTAATCTATCGAATGTAA	92219
Q	y	27901	AACGTCAACTGGCACCAACCGCCCTATTCACACTGTGAGAACTGGCCGCTGCG	27960
D	b	92220	AACGTCAACTGGCACCAACCGCCCTATTCACACTGTGAGAACTGGCCGCTGCG	92279
Q	y	27961	TTACCGGCGACACGAATTTGTTTCCGCTATGAGGTGACGTGGAACGTAATCACCA	28020
D	b	92280	TTACCGGCGACACGAATTTGTTTCCGCTATGAGGTGACGTGGAACGTAATCACCA	92339

QY	2802	TTGCAGATATCAAAACACGCGCGCTTTGAGATATACAGCGCTTTGGCAATCAAAAAACA	28080
Db	92340	TGCCAGATATCAAAACACGCGCGCTTTGAGATATACAGCGCTTTGGCAATCAAAAAACA	92399
QY	28081	TAGTTGACGGCACACCAATTTTAGCGCTTCACGACACAGAACTTACAAAGTTACACCCCG	28140
Db	92400	TAGTTGACGGCACACCAATTTTAGCGCTTCACGACACAGAACTTACAAAGTTACACCCCG	92459
QY	28141	AACTGTTATTCCTGTACGACTTCGTATTCGATGCCCTGTGCAAAAACAGGATACGGGT	28200
Db	92460	AACTGTTATTCCTGTACGACTTCGTATTCGATGCCCTGTGCAAAAACAGGATACGGGT	92519
QY	28201	GTTCGGCACAACGCAATTAGCAATTTATTAAGAAAGATATCGATTTTATGGCGGAGTTGG	28260
Db	92520	GTTCGGCACAACGCAATTAGCAATTTATTAAGAAAGATATCGATTTTATGGCGGAGTTGG	92579
QY	28361	GGGCGTTCATTTGAAAAAACCTGTGGGCTATCGATGATCAACCCCTAAGCCGTGCACAGTAGAG	28320
Db	92580	GGGCGTTCATTTGAAAAAACCTGTGGGCTATCGATGATCAACCCCTAAGCCGTGCACAGTAGAG	92639
QY	28321	CCGTTAAGGCGCAGGCTCGCGAGCTGTGGCCTATCCAAAGAGCGGTGTGAAGATTTCCGCG	28380
Db	92640	CCGTTAAGGCGCAGGCTCGCGAGCTGTGGCCTATCCAAAGAGCGGTGTGAAGATTTCCGCG	92699
QY	28381	CAATGATATCTGATGACACCGCGACGAGACAGCAGCCAAAGTGGAAAAATTTTACGACTTTT	28440
Db	92700	CAATGATATCTGATGACACCGCGACGAGACAGCAGCCAAAGTGGAAAAATTTTACGACTTTT	92759
QY	28441	TAGAAATGATTAACCAATTATACACTATACGGGGTTCATTTTACGAGTGTCTTACACAGT	28500
Db	92760	TAGAAATGATTAACCAATTATACACTATACGGGGTTCATTTTACGAGTGTCTTACACAGT	92819
QY	28501	ACAAGCCCACTAGCATATGCGTGGCCAAATTCAAATATCTTAAACCGCATGTGCGG	28560
Db	92820	ACAAGCCCACTAGCATATGCGTGGCCAAATTCAAATATCTTAAACCGCATGTGCGG	92879
QY	28561	AACAGAGCGATCGCGCCCTGTGGCGGACATTCATTAATCGGGTCTTTCCGTTCCCTGGA	28620
Db	92880	AACAGAGCGATCGCGCCCTGTGGCGGACATTCATTAATCGGGTCTTTCCGTTCCCTGGA	92939
QY	28621	AATTGAACAACGTCGTGGGCTTTTATACCTTAGCACCCCGCTGGCAACGCTACAAAAA	28680
Db	92940	AATTGAACAACGTCGTGGGCTTTTATACCTTAGCACCCCGCTGGCAACGCTACAAAAA	92999
QY	28681	TCTACAAAGCAATACCGTGTGTACCTATAGAGCTTTTGTTCGAAATATAGCGGCCAACAT	28740
Db	93000	TCTACAAAGCAATACCGTGTGTACCTATAGAGCTTTTGTTCGAAATATAGCGGCCAACAT	93059
QY	28741	CGTGGGGTAAACATCGCGGCTTCGACAGAGAGCGCCCGCTAACCGACATACAGACCGCGAAC	28800
Db	93060	CGTGGGGTAAACATCGCGGCTTCGACAGAGAGCGCCCGCTAACCGACATACAGACCGCGAAC	93119
QY	28801	CACACCAAGGTCCTCGTGTCCGCGCAGGTTATGCGAAAAATATGCAAGCGCTTCCAAATA	28860
Db	93120	CACACCAAGGTCCTCGTGTCCGCGCAGGTTATGCGAAAAATATGCAAGCGCTTCCAAATA	93179
QY	28861	GGCGGACAGATTATGACGAGGCATGTCTCCAGCCCGGAGTTGCGCGCGAGTTCATTTA	28920
Db	93180	GGCGGACAGATTATGACGAGGCATGTCTCCAGCCCGGAGTTGCGCGCGAGTTCATTTA	93239
QY	28921	AAACAAAACTGTATCCGATCTTTAGCGAGGTGCTCCGAAACAGCTTCCAAAAAATGCGAT	28980
Db	93240	AAACAAAACTGTATCCGATCTTTAGCGAGGTGCTCCGAAACAGCTTCCAAAAAATGCGAT	93299
QY	28981	CGGTATTTCCAAATTTAGATGGCTCATATGTCTTGGCGGACAGAGACCCAGAGACTAGGCC	29040
Db	93300	CGGTATTTCCAAATTTAGATGGCTCATATGTCTTGGCGGACAGAGACCCAGAGACTAGGCC	93359
QY	29041	CTATACAGAGCTGCTGGCGCTCGGCGCTATTTTCAATATATGACATTTTGGAAAAAGC	29100
Db	93360	CTATACAGAGCTGCTGGCGCTCGGCGCTATTTTCAATATATGACATTTTGGAAAAAGC	93419
QY	29101	ATTCTCTCGGAGTCTTTTACAACTCTGAGCATCTTCAGGAAACATTTAGTGCATATC	29160

Db	93420	ATTCTCCGGAGTCGTTTACAAACCTGCTGGACTATCTTAGGAAACATTAGGTGATAC	93479
OY	29161	GACAGGTGATATACCGGAAGCAGAGTGGCCACAAAGATTTCTAGAAATCTTGTTACTTTTC	29220
Db	93480	GACAGGTGATATACCGGAAGCAGAGTGGCCACAAAGATTTCTAGAAATCTTGTTACTTTTC	93539
OY	29221	AAACATTTCCAAATAGACGAGCTTCATTCAAAATCCATCCATGACCTTTGTAGACAGCTGA	29280
Db	93540	AAACATTTCCAAATAGACGAGCTTCATTCAAAACATCCATGACCTTTGTAGACAGCTGA	93599
OY	29281	AAAGGGCATCCCGGTATACGGACCTGTCCCTAGTGGCCGGCTTTTAAATGTA	29340
Db	93600	AAAGGGCATCCCGGTATACGGACCTGTCCCTAGTGGCCGGCTTTTAAATGTA	93659
OY	29341	AACACTGTAGATTTCAACGCTAGACACCGCTGAGATTTCCAAAGGAAGGGCAACCCA	29400
Db	93660	AACACTGTAGATTTCAACGCTAGACACCGCTGAGATTTCCAAAGGAAGGGCAACCCA	93719
OY	29401	TCGTGCTGAGCATGTTTCGTATTCAAAATCCAGATTCGCTCTCGAGAAAGCTTTACAG	29460
Db	93720	TCGTGCTGAGCATGTTTCGTATTCAAAATCCAGATTCGCTCTCGAGAAAGCTTTACAG	93779
OY	29461	AAGCGGTTATCGCGTTTAACTCAAAAGTCCGAACCGATGTAGCAGGCGACATCCGCTGA	29520
Db	93780	AAGCGGTTATCGCGTTTAACTCAAAAGTCCGAACCGATGTAGCAGGCGACATCCGCTGA	93839
OY	29521	TGCAACACCTCAGTACATATGCAAAAGATGCGCGAGACAGAAATATGACACACAATTC	29580
Db	93840	TGCAACACCTCAGTACATATGCAAAAGATGCGCGAGACAGAAATATGACACACAATTC	93899
OY	29581	CATCCGTTTTCAGAAATATACAGAGGATATTTGACGTGTTTAAAGCGTTTAAACGTC	29640
Db	93900	CATCCGTTTTCAGAAATATACAGAGGATATTTGACGTGTTTAAAGCGTTTAAACGTC	93959
OY	29641	TCATGTTACAGTTACGGGAAGCTGCTGTACTCATGACGCGATATCTTGATTCCTAT	29700
Db	93960	TCATGTTACAGTTACGGGAAGCTGCTGTACTCATGACGCGATATCTTGATTCCTAT	94019
OY	29701	ATCAACCCCCCTATATACCCGTACCATATGTCATAAAAAATTTTAACTTAAACGACAAA	29760
Db	94020	ATCAACCCCCCTATATACCCGTACCATATGTCATAAAAAATTTTAACTTAAACGACAAA	94079
OY	29761	CGGACACAACCGACGACATCTTTAAAGCGCTGTACAGCCGCTGAGACAGACGCTCTAT	29820
Db	94080	CGGACACAACCGACGACATCTTTAAAGCGCTGTACAGCCGCTGAGACAGACGCTCTAT	94139
OY	29821	CGCGTGAAGCAAGTAGCAGTGCAGTCTCAAAAAACAGTTTAGCGCTTCAAAAAAC	29880
Db	94140	CGCGTGAAGCAAGTAGCAGTGCAGTCTCAAAAAACAGTTTAGCGCTTCAAAAAAC	94199
OY	29881	TGTACGAGACATTTTGGACACCGCGCTCACAAACAAATTAACCCCACTATTAACCTGAAAT	29940
Db	94200	TGTACGAGACATTTTGGACACCGCGCTCACAAACAAATTAACCCCACTATTAACCTGAAAT	94259
OY	29941	ATTGCGGTAAATTATACGAAGCAAGTGTGCTGATTTGAGACACATATAACCTGGTGA	30000
Db	94260	ATTGCGGTAAATTATACGAAGCAAGTGTGCTGATTTGAGACACATATAACCTGGTGA	94319
OY	30001	CATACACCGCACCGACATACGTTAAATTTACCCCGGTTTAACACGGAAGGACACTAGATC	30060
Db	94320	CATACACCGCACCGACATACGTTAAATTTACCCCGGTTTAACACGGAAGGACACTAGATC	94379
OY	30061	GCATGTTTGGCAATTAAGCAATGGAATTTGCCGCCAAATTTTTCGAAATTTTAAATAGAGG	30120
Db	94380	GCATGTTTGGCAATTAAGCAATGGAATTTGCCGCCAAATTTTTCGAAATTTTAAATAGAGG	94439
OY	30121	GCGTGGCAACGACGACGACGACGCTAGGTTTGGACAATATACCCGCGCTGCAGTGT	30180
Db	94440	GCGTGGCAACGACGACGACGACGCTAGGTTTGGACAATATACCCGCGCTGCAGTGT	94499
OY	30181	TAAAGCACTGCGTTATCTACTCGCACAAAGTTATTTCAATAGAGAGTCCCGCTGACGG	30240

Dh 94500 TAAAGCACTGCTTATCTACCTTCGCAACAAATTATTCTAATAGAGTCCCGGTCAGCG 94559
Qy 30241 ACACATAAGACCTCGAGAGAGCTTTTACGGCAAGGGGAGCTTGAGCTTATATCTGAGC 30300
Dh 94560 ACACATAAGACCTCGAGAGAGCTTTTACGGCAAGGGGAGCTTGAGCTTATATCTGAGC 94619
Qy 30301 GGTCCGGGAGCGTGGCTATTAACCAATATGCCCCAACTGCACACATACCAGCTTTATCA 30360
Dh 94620 GGTCCGGGAGCGTGGCTATTAACCAATATGCCCCAACTGCACACATACCAGCTTTATCA 94679
Qy 30361 AGACCAACGAGTGGACCGCGCCCATCTTTCATCTCAGAGTACTTTGGACTAATTGGAC 30420
Dh 94680 AGACCAACGAGTGGACCGCGCCCATCTTTCATCTCAGAGTACTTTGGACTAATTGGAC 94739
Qy 30421 TTGACCGCGGCATCCGCGAACCTTTCATCTCAGAGTACTTTGGACTAATTGGAC 30480
Dh 94740 TTGACCGCGGCATCCGCGAACCTTTCATCTCAGAGTACTTTGGACTAATTGGAC 94799
Qy 30481 AGCGCGGACCGCTTCAATACCTTTCATCTCAGAGTACTTTGGACTAATTGGAC 30540
Dh 94800 AGCGCGGACCGCTTCAATACCTTTCATCTCAGAGTACTTTGGACTAATTGGAC 94859
Qy 30541 TCATAAACAAGGTTTACCTTTCATCTCAGAGTACTTTGGACTAATTGGAC 30600
Dh 94860 TCATAAACAAGGTTTACCTTTCATCTCAGAGTACTTTGGACTAATTGGAC 94919
Qy 30601 CGGACACGTAATCAGTTCGTGACAGCCGCGCATCTACTAGATAGTACGTGACCGGCGAG 30660
Dh 94920 CGGACACGTAATCAGTTCGTGACAGCCGCGCATCTACTAGATAGTACGTGACCGGCGAG 94979
Qy 30661 ACAGAGATACCTGCGAGTTCCTATACATTAATGCGCAGCGAATATGTCATTCAGAGC 30720
Dh 94980 ACAGAGATACCTGCGAGTTCCTATACATTAATGCGCAGCGAATATGTCATTCAGAGC 95039
Qy 30721 ACATCATACCAACCACTATAGAACTATACGTTCCGCAAGTAACAGCGCCGCGACTAG 30780
Dh 95040 ACATCATACCAACCACTATAGAACTATACGTTCCGCAAGTAACAGCGCCGCGACTAG 95099
Qy 30781 ATATATTCACCGGCTATAGACCGCTGCACATCGAAGACATCCCAAGCGCGCGGATCGC 30840
Dh 95100 ATATATTCACCGGCTATAGACCGCTGCACATCGAAGACATCCCAAGCGCGCGGATCGC 95159
Qy 30841 CGGATGTGACGTAATAATCATCCACCTGCGACGCGTCCGGAACACACCGACACGAT 30900
Dh 95160 CGGATGTGACGTAATAATCATCCACCTGCGACGCGTCCGGAACACACCGACACGAT 95219
Qy 30901 CGAGCGCCAAACCCCAACCGCGGACGCTATCCGCTTACCGGGCGCGGAACACCGCA 30960
Dh 95220 CGAGCGCCAAACCCCAACCGCGGACGCTATCCGCTTACCGGGCGCGGAACACCGCA 95279
Qy 30961 GCTACCCAGACCGGCAACCAAGACGCGGACCAAACTTAACTCCGCTCCAGCGC 31020
Dh 95280 GCTACCCAGACCGGCAACCAAGACGCGGACCAAACTTAACTCCGCTCCAGCGC 95339
Qy 31021 AAAACCGCGTGCACACCCCGAAATTCACAAACACACCTGAGGACGCTACTTTTCAG 31080
Dh 95340 AAAACCGCGTGCACACCCCGAAATTCACAAACACACCTGAGGACGCTACTTTTCAG 95399
Qy 31081 AACTGTGCGATCCAGGGGTTCGGAAGCGCAAGCTTTCACGCTTCACGCTATTCGATTT 31140
Dh 95400 AACTGTGCGATCCAGGGGTTCGGAAGCGCAAGCTTTCACGCTTCACGCTATTCGATTT 95459
Qy 31141 CGAGCAAGCGTGTCTGAGAGCAAGGGGCCAGCTAGGCGGTACAGAGAGATTCGA 31200
Dh 95460 CGAGCAAGCGTGTCTGAGAGCAAGGGGCCAGCTAGGCGGTACAGAGAGATTCGA 95519
Qy 31201 TATCCGCGAGGTATCTGGATGAGAGAGATATCTCTATATATTCACGCTCCGCGA 31260
Dh 95520 TATCCGCGAGGTATCTGGATGAGAGAGATATCTCTATATATTCACGCTCCGCGA 95579
Qy 31261 CTCATCTGTTGACGAGCTGTTCGACAGCCCCCAATGAGCCGCGAGTTTACATGAGAG 31320
Dh 95580 CTCATCTGTTGACGAGCTGTTCGACAGCCCCCAATGAGCCGCGAGTTTACATGAGAG 95639

Qy 31321 ACGGACAGAGACAGGATGGCGCTTTCTAGAACAGATCGCTCGAGACGGGAAACGC 31380
Dh 95640 ACGGACAGAGACAGGATGGCGCTTTCTAGAACAGATCGCTCGAGACGGGAAACGC 95699
Qy 31381 CGTTCTGCGCTTCGACGACCTTATTAACGACACGACTTTTCTTCCCTTGATTAACAAA 31440
Dh 95700 CGTTCTGCGCTTCGACGACCTTATTAACGACACGACTTTTCTTCCCTTGATTAACAAA 95759
Qy 31441 TAGAACGTTAATCAAGTACGAAGCGCCCTCGAGACCTGCGCAACATCTCGGACAAAC 31500
Dh 95760 TAGAACGTTAATCAAGTACGAAGCGCCCTCGAGACCTGCGCAACATCTCGGACAAAC 95819
Qy 31501 AAAACGGGCGAGCGCTTCGGAAGAGCGCGCCCTCGAGCGATGAGCAAAATTTATGATTA 31560
Dh 95820 AAAACGGGCGAGCGCTTCGGAAGAGCGCGCCCTCGAGCGATGAGCAAAATTTATGATTA 95879
Qy 31561 ATATCATCTTGAACACGGTCTAATTAACAGACGCGAGCCCGGGACCGTCCGCTGCA 31620
Dh 95880 ATATCATCTTGAACACGGTCTAATTAACAGACGCGAGCCCGGGACCGTCCGCTGCA 95939
Qy 31621 AAAACGTTCTCAATTTTTCATCCTGTTGGGAGAAAACATCAATTAAGGACG 31680
Dh 95940 AAAACGTTCTCAATTTTTCATCCTGTTGGGAGAAAACATCAATTAAGGACG 95999
Qy 31681 CCAAGCAGTCTTAAGTCAATCTGATCTGCAATGATACGCTTATACGCTATCAGCGAG 31740
Dh 96000 CCAAGCAGTCTTAAGTCAATCTGATCTGCAATGATACGCTTATACGCTATCAGCGAG 96059
Qy 31741 GAAATTTCAACAGGGGGCGTTCAAAAACACCTAACACTAATAACCGGTCTGCG 31800
Dh 96060 GAAATTTCAACAGGGGGCGTTCAAAAACACCTAATAACACTAATAACCGGTCTGCG 96119
Qy 31801 CGTCATAGAGGGCGACCGACGAGTGGGCAAAAAACGCGGTGGCTTCAACGTCG 31860
Dh 96120 CGTCATAGAGGGCGACCGACGAGTGGGCAAAAAACGCGGTGGCTTCAACGTCG 96179
Qy 31861 AAGGCTCAGATTTCTCCAGGAGACGAAATATGATGTCGCGGCTGTAAGAGACAGA 31920
Dh 96180 AAGGCTCAGATTTCTCCAGGAGACGAAATATGATGTCGCGGCTGTAAGAGACAGA 96239
Qy 31921 TCGCCAAACACCTGATGCTAGGCTTTTTCAGCGGTCTACCTCGCGGACGAGATAAACATC 31980
Dh 96240 TCGCCAAACACCTGATGCTAGGCTTTTTCAGCGGTCTACCTCGCGGACGAGATAAACATC 96299
Qy 31981 TACGGGATAAATTCAGGACCTAATAACAGGACATCGAGCGGCAACAAAGAAATTCGAC 32040
Dh 96300 TACGGGATAAATTCAGGACCTAATAACAGGACATCGAGCGGCAACAAAGAAATTCGAC 96359
Qy 32041 AGGAAGAACTGTTTTTTCATGCTCAGAGCTTCAGAGCCCTGAGACGCTTCCAAACCCCTCGA 32100
Dh 96360 AGGAAGAACTGTTTTTTCATGCTCAGAGCTTCAGAGCCCTGAGACGCTTCCAAACCCCTCGA 96419
Qy 32101 AAAAGCATTTTCCATGAGATCTTTCGCAACGCTTAAACCGAAGTTATGCTGACACAC 32160
Dh 96420 AAAAGCATTTTCCATGAGATCTTTCGCAACGCTTAAACCGAAGTTATGCTGACACAC 96479
Qy 32161 TGGCGTCCATTAACACAGGTTAAACGAGACGCAACGGAAGCCCTCAACAAATTAACCTGG 32220
Dh 96480 TGGCGTCCATTAACACAGGTTAAACGAGACGCAACGGAAGCCCTCAACAAATTAACCTGG 96539
Qy 32221 AGACCCCGCGGACCAAGAAAGCACATTCACAAATTCACAACTTTTCATCATCGTGG 32280
Dh 96540 AGACCCCGCGGACCAAGAAAGCACATTCACAAATTCACAACTTTTCATCATCGTGG 96599
Qy 32281 CAATATCATATTCAGCTTAAATACTTAAGTACGAGAGAAAAGCATCAATTAACG 32340
Dh 96600 CAATATCATATTCAGCTTAAATACTTAAGTACGAGAGAAAAGCATCAATTAACG 96659
Qy 32341 TAAGCCCATAGGCAAGCTTAAGCGCTGAGTGTGTAACCTCGGAGGGAATTAAGAACCA 32400
Dh 96660 TAAGCCCATAGGCAAGCTTAAGCGCTGAGTGTGTAACCTCGGAGGGAATTAAGAACCA 96719

Db	97800	TCATCGACGGTTGGATTGGCAAGAGATGGCATATGAAATATCCAGACACGGCTGTCC	97859
OY	33541	TTCTGGTACGATTGGACAAAGCTGTGGCTTCATGAGAGCATCTCAAAACCCCTGG	33600
Db	97860	TTCTCGGTACGGTTGGACCAAAAGCTGTGGCTTCATGAGAGCATCTCAAAACCCCTGG	97919
OY	33601	ACGACATCTCTACGCGAGAACGTGGCATCTCTGCTTCCAAAGGGGCCGCTTTCAGACCCC	33660
Db	97920	ACGACATCTCTACGCGAGAACGTGGCATCTCTGCTTCCAAAGGGGCCGCTTTCAGACCCC	97979
OY	33661	CACGCTTTGACTGGATGCGGCCCTATATAACACGCGGTAAAGCGCTTTCTAAAAACCAATG	33720
Db	97980	CACGCTTTGACTGGATGCGGCCCTATATAACACGCGGTAAAGCGCTTTCTAAAAACCAATG	98039
OY	33721	GCTTGCCCAATGGTGGCAACCTTGAGGAGACAAGATCATTCACCAATGCGCAAACTGCAATC	33780
Db	98040	GCTTGCCCAATGGTGGCAACCTTGAGGAGACAAGATCATTCACCAATGCGCAAACTGCAATC	98099
OY	33781	ACGCGGTGCATCTCGGACAGACCTTCTACAGGCCACGGTGGGAACAAGTTTAGAACGACCG	33840
Db	98100	ACGCGGTGCATCTCGGACAGACCTTCTACAGGCCACGGTGGGAACAAGTTTAGAACGACCG	98159
OY	33841	CGCGCCGAATCTGTCCGAATCTCTCTACATGCAAGTCCGGTTAAAGACCAACGGAATCG	33900
Db	98160	CGCGCCGAATCTGTCCGAATCTCTCTACATGCAAGTCCGGTTAAAGACCAACGGAATCG	98219
OY	33901	CGCTAAGATGGAGGCGCGCGCGCTACACGAGCAATCACTCCCGCCCAACCTCGGA	33960
Db	98220	CGCTAAGATGGAGGCGCGCGCGCTACACGAGCAATCACTCCCGCCCAACCTCGGA	98279
OY	33961	CTCCCGCGAAACCAACCTAGAAAGCCCGCAAGAGCTAATACGGCAACTGACGCCCTTAA	34020
Db	98280	CTCCCGCGAAACCAACCTAGAAAGCCCGCAAGAGCTAATACGGCAACTGACGCCCTTAA	98339
OY	34021	CGCTCGAGGCTTTCAGATTCTCTTAAACGTCATCTTCAACAGAGACGAGGACTCA	34080
Db	98340	CGCTCGAGGCTTTCAGATTCTCTTAAACGTCATCTTCAACAGAGACGAGGACTCA	98399
OY	34081	TTTCGCTCCAGAGGCGGAATTTTCAGCAATAGAGGCAAGATCTCCGGCGCCCAAGCGC	34140
Db	98400	TTTCGCTCCAGAGGCGGAATTTTCAGCAATAGAGGCAAGATCTCCGGCGCCCAAGCGC	98459
OY	34141	TCGCGCAATCCACCCGCTGACGAGATGCGAGGCAAGATGCGACCCGCTATCACGCACTCT	34200
Db	98460	TCGCGCAATCCACCCGCTGACGAGATGCGAGGCAAGATGCGACCCGCTATCACGCACTCT	98519
OY	34201	TACCCGCGCGCGCGCTGCGAAATTCATACGAGACCGTTGAATCTTCAAAACCTTATAGCT	34260
Db	98520	TACCCGCGCGCGCGCTGCGAAATTCATACGAGACCGTTGAATCTTCAAAACCTTATAGCT	98579
OY	34261	TTTTGAGTTCAACGGGTATACGACAAAATCTGGAACAAGACCTTACGAGACACCCATAG	34320
Db	98580	TTTTGAGTTCAACGGGTATACGACAAAATCTGGAACAAGACCTTACGAGACACCCATAG	98639
OY	34321	CGGATTCGCGTGGGAAATGCGCAAAAATCCGTAATGCTTACAGTCAACAAAACG	34380
Db	98640	CGGATTCGCGTGGGAAATGCGCAAAAATCCGTAATGCTTACAGTCAACAAAACG	98699
OY	34381	AAACGCAACGTTAAACGTAATCTGTGAGCGAGGTAGAAAACAGACGACCGTCCGCAGC	34440
Db	98700	AAACGCAACGTTAAACGTAATCTGTGAGCGAGGTAGAAAACAGACGACCGTCCGCAGC	98759
OY	34441	GTCCTACAGCTTGGAACTGTGGGCAAAAACAGCGACGATGAAGTCTGTGAAGCAGG	34500
Db	98760	GTCCTACAGCTTGGAACTGTGGGCAAAAACAGCGACGATGAAGTCTGTGAAGCAGG	98819
OY	34501	CGCTACACGAACCTCGCGCCCTCTAGGGTTAAAGGCGGAAAAACACCGCTAGACGCGTGA	34560
Db	98820	CGCTACACGAACCTCGCGCCCTCTAGGGTTAAAGGCGGAAAAACACCGCTAGACGCGTGA	98879
OY	34561	AACAAAACCTGGAAGCATAGAAATCCCTGCTTCCGCGCACGAGACGGCAGCGAAATAT	34620

Db 98880 AACAAAACTGGAAGCATGAAATCCCTGCTTGGCCGACGAGACGGCGGAATAT 98939
 QY 34621 CATCGAGCTTGAACGATCGGACACAGCGGTTGGCCACCATCAGCTCGGATTTAG 34680
 Db 98940 CATCGAGCTTGAACGATCGGACACAGCGGTTGGCCACCATCAGCTCGGATTTAG 98999
 QY 34681 GAACGCTCTCCGATCAATGCGGGAAGCCGCAATTTTCTCAGACAGGCGAGTTCACCG 34740
 Db 99000 GAACGCTCTCCGATCAATGCGGGAAGCCGCAATTTTCTCAGACAGGCGAGTTCACCG 99059
 QY 34741 AAGGCTTCTGGACATAGGCAACAAACTCAGCGGCTTACGCGCTACATTAAAGTACAAA 34800
 Db 99060 AAGGCTTCTGGACATAGGCAACAAACTCAGCGGCTTACGCGCTACATTAAAGTACAAA 99119
 QY 34801 AAGGCTTCTGGACATAGGCAACAAACTCAGCGGCTTACGCGCTTACGCGCTAT 34860
 Db 99120 AAGGCTTCTGGACATAGGCAACAAACTCAGCGGCTTACGCGCTTACGCGCTAT 99179
 QY 34861 CCCAAACATACCGAAAGCTTCCGCGCGCGCGCGGATGAGCTCGGTGGCGAGACTGA 34920
 Db 99180 CCCAAACATACCGAAAGCTTCCGCGCGCGCGCGGATGAGCTCGGTGGCGAGACTGA 99239
 QY 34921 CCATACCTTACGCTGCGGCGGCGCGCGCGCGCTTACAGCTGATAGAAAGCTTAC 34980
 Db 99240 CCATACCTTACGCTGCGGCGGCGCGCGCGCGCTTACAGCTGATAGAAAGCTTAC 99299
 QY 34981 CGACCGTCTGATCGGAAACCAACTCAGCTCCGCGCGCGAGGAGAGCCCTTGGACG 35040
 Db 99300 CGACCGTCTGATCGGAAACCAACTCAGCTCCGCGCGCGAGGAGAGCCCTTGGACG 99359
 QY 35041 GCCAGATCAGTACTCAAAAGCTCTAGAGCGGTTGTTTATATATGTTCCAGCAGCTAA 35100
 Db 99360 GCCAGATCAGTACTCAAAAGCTCTAGAGCGGTTGTTTATATATGTTCCAGCAGCTAA 99419
 QY 35101 C 35101
 Db 99420 C 99420

RESULT 2

AAC64754 standard; DNA: 133719 BP.

AAC64754;

28-FEB-2001 (first entry)

Macaca mulatta rhadinovirus 17577 (RRV) genome sequence SEQ ID NO:1.

Macaca mulatta rhadinovirus 17577; RRV; rhesus macaque rhadinovirus;
 genome: Kaposi's sarcoma-associated herpesvirus; KSHV; Interleukin 6;
 IL-6; macrophage inflammatory protein; MIP; diagnosis: vaccine;
 cytotoxic; anti-HIV; gene therapy; infection: Kaposi's sarcoma;
 lymphoproliferative disorder; B-cell hyperplasia; lymphadenopathy;
 splenomegaly; hypergammaglobulinemia; autoimmune haemolytic anaemia;
 ds.

Macaca mulatta rhadinovirus 17577.

MO200028040-A2.

18-MAY-2000.

05-NOV-1999; 99MO-US26260.

06-NOV-1998; 98US-0107507.

20-NOV-1998; 98US-0109409.

(UNIV-) UNIV OREGON HEALTH SCI.

Mong SW, Axthelm MK, Searles RP;

WPI; 2000-376552/32.

XX New rhesus rhadino virus for producing non-human primate model useful
 PT for testing potential treatments and efficacy of the candidate vaccine
 PT for conditions associated with RRV infection
 PS Claim 2; Page 83-122; 141pp; English.
 XX The present invention describes a novel rhesus macaque rhadinovirus
 CC called macaca mulatta rhadinovirus 17577 (RRV). AAC64754 represents the
 CC RRV genome sequence, and AAB53123 to AAB53204 represent the proteins
 CC encoded by the genome sequence. The present invention also specifically
 CC claims the individual open reading frame (ORF) nucleotide sequences from
 CC the genome which encode the individual proteins, but these sequences are
 CC not given. A non-human animal infected with RRV can be used for testing
 CC the efficacy of drug in the treatment of condition associated with
 CC infection with RRV such as Kaposi's sarcoma, lymphoproliferative
 CC disorders, B-cell hyperplasia, lymphadenopathy, splenomegaly,
 CC hypergammaglobulinemia or autoimmune haemolytic anaemia, by
 CC administering the drug to an immuno-compromised non-human primate
 CC preferably Rhesus macaque monkey obtained by as a result of infection
 CC by Simian Immunodeficiency Virus (SIV). RRV is useful for producing
 CC non-human primate model for testing potential treatments for conditions
 CC associated with RRV infection. It is also useful for testing the
 CC efficacy of the candidate vaccine against RRV infection or conditions
 CC associated with its infection by administering the vaccine to the
 CC subject capable of infection with RRV, inoculating the subject with RRV
 CC and observing the effect of vaccine. AAC64755 to AAC64765 and AAB53205
 CC to AAB53213 represent sequence used in the exemplification of the
 CC present invention.
 XX Sequence 133719 BP; 32746 A; 35648 C; 34521 G; 30804 T; 0 other;
 SQ
 Query Match 100.0%; Score 35101; DB 21; Length 133719;
 Best Local Similarity 100.0%; Mismatches 0; Indels 0; Gaps 0;
 Matches 35101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CGACATGCTAGCGGCTCTCTACAGAGCTGTATGAGTACAGTCCCGCGGCATCGA 60
 Db 69900 CGACATGCTAGCGGCTCTCTACAGAGCTGTATGAGTACAGTCCCGCGGCATCGA 69959
 QY 61 TTCCCTCCAGCACTCGGACATGAGAGATTTTTCAGAGTTAGTCCGCTATAG 120
 Db 69960 TTCCCTCCAGCACTCGGACATGAGAGATTTTTCAGAGTTAGTCCGCTATAG 70019
 QY 121 CGGCGACGATCGGCTTGAAGATGATGACCGCAAGATGACACACGAGAGAGTTC 180
 Db 70020 CGGCGACGATCGGCTTGAAGATGATGACCGCAAGATGACACACGAGAGAGTTC 70079
 QY 181 CCACGCAACCGCGGATGCTTACCGTAAATATATACCGGTTGAAAGTCCCTGGTG 240
 Db 70080 CCACGCAACCGCGGATGCTTACCGTAAATATATACCGGTTGAAAGTCCCTGGTG 70139
 QY 241 CGACAAATATGAGCTTAAACTTACCATTTTCTGTCTATTTGGGACACTAAATTT 300
 Db 70140 CGACAAATATGAGCTTAAACTTACCATTTTCTGTCTATTTGGGACACTAAATTT 70199
 QY 301 GTGCGCAGTGGCGCAATTTTAAAGTCTGTAAATGCACTCTTTCGAAGTTCTGTC 360
 Db 70200 GTGCGCAGTGGCGCAATTTTAAAGTCTGTAAATGCACTCTTTCGAAGTTCTGTC 70259
 QY 361 CTAGAAATTTTACATCCAGTTTCAATATATATTAAGACACCTGTTTGTCTGATC 420
 Db 70260 CTAGAAATTTTACATCCAGTTTCAATATATATTAAGACACCTGTTTGTCTGATC 70319
 QY 421 TGGCGTGTATTTATCTTGAGAGGCGCCCTTAAATATGCTCTGTGTAACACACCA 480
 Db 70320 TGGCGTGTATTTATCTTGAGAGGCGCCCTTAAATATGCTCTGTGTAACACACCA 70379
 QY 481 AGAGACCCCAAGTCTGAATTTATGCAATATATGATGCAAGGGAACACACGCGGA 540
 Db 70380 AGAGACCCCAAGTCTGAATTTATGCAATATATGATGCAAGGGAACACACGCGGA 70439
 QY 541 TGAATCTCAAAACCTGTGCTGACGCGCAGATCTGCTGGGCTTATATCTATACGG 600

Db 70440 TGGATTCCTCAAAACCTGTGTCTGACGGCCAGGATCTGCTGGGCTTATATCTATACGG 70499
QY AGATAACGGCCCGTTTCCCAATATATGACAAATGACAGACAAATACCGGACAGTGC 660
Db 70500 AGAATAACGGCCCGTTTCCCAATATATGACAAATGACAGACAAATACCGGACAGTGC 70559
QY 661 AAAGCTTCGGACACTACGCTCCGGCGACGGTTTCTGGCGGTTCTGTCTCAGGATGT 720
Db 70560 AAAGCTTCGGACACTACGCTCCGGCGACGGTTTCTGGCGGTTCTGTCTCAGGATGT 70619
QY 721 ATGGAACAACACCGGAGAGGGCGGTGTTCTAAAGACCGTCCGGTCCGGAACGGCT 780
Db 70620 ATGGAACAACACCGGAGAGGGCGGTGTTCTAAAGACCGTCCGGTCCGGAACGGCT 70679
QY 781 CGGCTCAGCTAATTTACGGGCGCTCCGAGCGCTCTGTGGCCGAGCAAGGACCTCAGAG 840
Db 70680 CGGCTCAGCTAATTTACGGGCGGTCCGAGCGCTCTGTGGCCGAGCAAGGACCTCAGAG 70739
QY 841 GGGCACATGCGCTATCTGACCGGATAGGACAGAGCGGTGGCGCTGACAAATAGACTACTA 900
Db 70740 GGGCACATGCGCTATCTGACCGGATAGGACAGAGCGGTGGCGCTGACAAATAGACTACTA 70799
QY 901 AGGTGATGGGGGCTGTGGGACAAAACAAGAGCGCCCTTGACACCAATCCTTGGTTCG 960
Db 70800 AGGTGATGGGGGCTGTGGGACAAAACAAGAGCGCCCTTGACACCAATCCTTGGTTCG 70859
QY 961 GTTGCTATTCCTTTGATGTTTAAACAGTAAATGTCTGTTTATATTAACCTTGCCATAGCCG 1020
Db 70860 GTTGCTATTCCTTTGATGTTTAAACAGTAAATGTCTGTTTATATTAACCTTGCCATAGCCG 70919
QY 1021 AACCGAACACTGTGGCATCGGATTAATAACGACACACTGGACAGTCAAGTGAACGG 1080
Db 70920 AACCGAACACTGTGGCATCGGATTAATAACGACACACTGGACAGTCAAGTGAACGG 70979
QY 1081 CAAAACGGCGGGCGAGTGCAGAGACCTCGAAGAAAATAAGCCCAACAGTGCACACAG 1140
Db 70980 CAAAACGGCGGGCGAGTGCAGAGACCTCGAAGAAAATAAGCCCAACAGTGCACACAG 71039
QY 1141 TACAAATAGCAAAATTTAGTAATTTGTAATTTTAACTTCCGAGTTTCCGCTGGCT 1200
Db 71040 TACAAATAGCAAAATTTAGTAATTTGTAATTTTAACTTCCGAGTTTCCGCTGGCT 71099
QY 1201 GGGGACCGCTGTCCGCTTTAGTGTGAATACCTCTCTCAACAGCAGTATTCACAG 1260
Db 71100 GGGGACCGCTGTCCGCTTTAGTGTGAATACCTCTCTCAACAGCAGTATTCACAG 71159
QY 1261 GAGCTGGAAGTAAACAACGCAACTGACCGTCTCACCGCTCAACGAGAGCCCTCAA 1320
Db 71160 GAGCTGGAAGTAAACAACGCAACTGACCGTCTCACCGCTCAACGAGAGCCCTCAA 71219
QY 1321 AAGCAGCATCATTTTTCAGAGAGATGATATTTGATGTCAAAAAGGGAACAGTAA 1380
Db 71220 AAGCAGCATCATTTTTCAGAGAGATGATATTTGATGTCAAAAAGGGAACAGTAA 71279
QY 1381 AAAAGCAGCATGATTTTAAAGCCACCTGGGTACTAGTTTAAACTCCCTAATTTGAT 1440
Db 71280 AAAAGCAGCATGATTTTAAAGCCACCTGGGTACTAGTTTAAACTCCCTAATTTGAT 71339
QY 1441 CTATTCACCTTCATTAATAATTTTAAATACGTTTGCGGTTTGCATTTCCGTC 1500
Db 71340 CTATTCACCTTCATTAATAATTTTAAATACGTTTGCGGTTTGCATTTCCGTC 71399
QY 1501 TAAAACTATTAACAATTCATTTGGGAATAGGATTTATGAGTTTAAAGGATTAATTT 1560
Db 71400 TAAAACTATTAACAATTCATTTGGGAATAGGATTTATGAGTTTAAAGGATTAATTT 71459
QY 1561 TTTGATCATGAGATTTGGGAACATACGCTGGGATGAGGTTTATGCTCATGCTGGG 1620
Db 71460 TTTGATCATGAGATTTGGGAACATACGCTGGGATGAGGTTTATGCTCATGCTGGG 71519
QY 1621 TGGCGGATGTCAGGGGAGGTGGTGGTGCACACCTGGGACCTGACAGATGGAAT 1680

Db 71520 TGGCTGATTTGACGGGGAGGTCGGTGTGTGCCCAACCTGGGACCTGACAGATGGGAAT 71579
QY 1681 ACGAGCGGATATACAGGCACTACCTGGAAGAGTGGCCGAACAACATGAAGGCTCGGGAGCC 1740
Db 71580 ACGAGCGGATATACAGGCACTACCTGGAAGAGTGGCCGAACAACATGAAGGCTCGGGAGCC 71639
QY 1741 TGGAGGTTTCGGACAGACAAAGGGTCTGGAAACCAAGCAACACCGAAGCTAATATAT 1800
Db 71640 TGGAGGTTTCGGACAGACAAAGGGTCTGGAAACCAAGCAACACCGAAGCTAATATAT 71699
QY 1801 CGATAGACCTTAAGTTTGCATCTACAGTCAAGTCAAAATTAAGAGCCGCTGGGACAGCCGA 1860
Db 71700 CGATAGACCTTAAGTTTGCATCTACAGTCAAGTCAAAATTAAGAGCCGCTGGGACAGCCGA 71759
QY 1861 GGGCCGAATCATCACAGCACTTGCACAGCATCAGGATCAAGCAGGTTAAGCTCTCCGATTATCAA 1920
Db 71760 GGGCCGAATCATCACAGCACTTGCACAGCATCAGGATCAAGCAGGTTAAGCTCTCCGATTATCAA 71819
QY 1921 CCCCGAATTTGGCGCAACCACTCCGGTATGTAATATGACCTCCGGCGAGTCAAGTCAAG 1980
Db 71820 CCCCGAATTTGGCGCAACCACTCCGGTATGTAATATGACCTCCGGCGAGTCAAGTCAAG 71879
QY 1981 GTGGGACACCCCTGGAGAGGGCGCCCGACGGCTTATATGACACAAAGCAGATCTCA 2040
Db 71880 GTGGGACACCCCTGGAGAGGGCGCCCGACGGCTTATATGACACAAAGCAGATCTCA 71939
QY 2041 ACCCATCTGTGTCTGTCTTTCAGAGCCATCCGTCGGGCTCCACACGCGATACCGAGC 2100
Db 71940 ACCCATCTGTGTGTCTGTCTTTCAGAGCCATCCGTCGGGCTCCACACGCGATACCGAGC 71999
QY 2101 AGTCGTTGGCGATCGGAACAGGGTACAGCAACGATATGTACCCCTGGCGCCCTTCCC 2160
Db 72000 AGTCGTTGGCGATCGGAACAGGGTACAGCAACGATATGTACCCCTGGCGCCCTTCCC 72059
QY 2161 TCTTTCAAGCGAGACCTCTGTCTACAGGTGGCGGTACCCCTTGCCCGCAAGCATG 2220
Db 72060 TCTTTCAAGCGAGACCTCTGTCTACAGGTGGCGGTACCCCTTGCCCGCAAGCATG 72119
QY 2221 CAAGATACGCGAGTGCAGAACATATGCGACCAAAATTTGACCGCAAAAGATACAGGCC 2280
Db 72120 CAAGATACGCGAGTGCAGAACATATGCGACCAAAATTTGACCGCAAAAGATACAGGCC 72179
QY 2281 GTCCGTTTCAGCAGAGTCCCGGTATGAGACCTGACGGGACCTCAAGCGTCCGTGTACAG 2340
Db 72180 GTCCGTTTCAGCAGAGTCCCGGTATGAGACCTGACGGGACCTCAAGCGTCCGTGTACAG 72239
QY 2341 CCATTCCTCCTTTCGCGAGCGCGTGTGACACCTGTACCCCTTGCGGCTATAGCGGGA 2400
Db 72240 CCATTCCTCCTTTCGCGAGCGCGTGTGACACCTGTGTACCCCTTGCGGCTATAGCGGGA 72299
QY 2401 ATATTGGGCTTCAGATGCGCTTGTACAGATATATCAAAATATATGACATGAAAACTAC 2460
Db 72300 ATATTGGGCTTCAGATGCGCTTGTGTACAGATATATCAAAATATATGACATGAAAACTAC 72359
QY 2461 ACGAGCTTCATCTGGGAATTAAGGTTTATTTATTTTGCACACTAGTCCGCGCTTATTT 2520
Db 72360 ACGAGCTTCATCTGGGAATTAAGGTTTATTTATTTTGCACACTAGTCCGCGCTTATTT 72419
QY 2521 CTGTCCTGAGCTGGGGCGCGCTCCCTGCTGAGAGCGCCGCTGGGCTGGACAGATTCGG 2580
Db 72420 CTGTCCTGAGCTGGGGCGCGCTCCCTGCTGAGAGCGCCGCTGGGCTGGACAGATTCGG 72479
QY 2581 CCTGTGTGTCTGTCTCATTTGACAGCTGCACGCGGATACTAATTTCCGGCGAGGCGTCT 2640
Db 72480 CCTGTGTGTCTGTCTCATTTGACAGCTGCACGCGGATACTAATTTCCGGCGAGGCGTCT 72539
QY 2641 TCCATCTGCGCGCGGTCAAGGCTTGGCGCGTGGCGCGCTTACCTTACCTTCAATCTTA 2700
Db 72540 TCCATCTGCGCGCGGTCAAGGCTTGGCGCGTGGCGCGCTTACCTTACCTTCAATCTTA 72599
QY 2701 CGGGTTGACAGTTCATTAAGCGAAAGCGAGTGGGATTTGGCCCTCTTTCCGGG 2760
Db 72600 CGGGTTGACAGTTCATTAAGCGAAAGCGAGTGGGATTTGGCCCTCTTTCCGGG 72659

QY	2761	TTAGAGATGACGGGGTGGAGCCGGACCTGGTGGATCCCGCAAAATTATACAGCTTTTGG	2820
Db	72660	TTAGAGATGACGGGGTGGAGCCGGACCTGGTGGATCCCGCAAAATTATACAGCTTTTGG	72719
QY	2821	AGCTGCTTTGTTTTAACGGACAATTTTTCACCTGAGCGGCTTACTCTCCATTTGTCACG	2880
Db	72720	AGCTGCTTTGTTTTAACGGACAATTTTTCACCTGAGCGGCTTAACCTCCCATTTGTCACG	72779
QY	2881	TCCTTTTGGGGGGCGCTCTTGGGACGGGTGGAAGACAATGGCACTCTACTACGCAATTAC	2940
Db	72780	TCCTTTTGGGGGGCGCGCTCTTGGGACGGGTGGAAGACAATGGCACTCTACTACGCAATTAC	72839
QY	2941	AGAGTACAGCGCGAGCTTTAAATACCTTTCAGGGCGCCCTGAGAGTCACTCTGCGCCACG	3000
Db	72840	AGAGTACAGCGCGAGCTTTAAATACCTTTCAGGGCGCCCTGAGAGTCACTCTGCGCCACG	72899
QY	3001	GTTTCAACAAATTTAAAAAGCACATATATGTTTAGGTACAGAAATGTTGCAACCGCGAC	3060
Db	72900	GTTTCAACAAATTTAAAAAGCACATATATGTTTAGGTACAGAAATGTTGCAACCGCGAC	72959
QY	3061	AGAACAGAGTTGATCACCGCCCATATCTGAAAACTAGACAGCAGCGGCTGTATCGTG	3120
Db	72960	AGAACAGAGTTGATCACCGCCCATATCTGAAAACTAGACAGCAGCGGCTGTATCGTG	73019
QY	3121	TCGCCGAGCAATCATATGTCATAAAAAAGAGCGGCTTACGAGGGAGCCCGGAGGGGTTT	3180
Db	73020	TCGCCGAGCAATCATATGTCATAAAAAAGAGGGGCTTACGAGGGAGCCCGGAGGGGTTT	73079
QY	3181	GTAAGTACAGGAGCGTGGCCGTTCCGTAGTGGAGGAGTGGTGACGGGTGGCGACACC	3240
Db	73080	GTAAGTACAGGAGCGTGGCCGTTCCGTAGTGGAGGAGTGGTGACGGGTGGCGACACC	73139
QY	3241	GGCAGACAGATATTAAGACAGCCACAGGGGCTAACGCGACAAATTGACCTGTCTATT	3300
Db	73140	GGCAGACAGATATTAAGACAGCCACAGGGGCTAACGCGACAAATTGACCTGTCTATT	73199
QY	3301	TTTCAAGCCGGGCTTCGGCAGGCAACCTCCACTTTGGACAGCGCGCTCTCTTATTACT	3360
Db	73200	TTTCAAGCCGGGCTTCGGCAGGCAACCTCCACTTTGGCAGCGCGCTCTCTCTTATTACT	73259
QY	3361	ACCAATTAAACATTATGSGAGAAAGTGCAGCCCATACGGTTCGCTAGCGCTTTGACTCTCT	3420
Db	73260	ACCAATTAAACATTATGSGAGAAAGTGCAGCCCATACGGTTCGCTAGCGCTTTGACTCTCT	73319
QY	3421	GTTAAGTTGAATTAATACCAAAAAACAATCTCATCTGTATAGCGTTACGCAACAAATTC	3480
Db	73320	GTTAAGTTGAATTAATACCAAAAAACAATCTCATCTGTATAGCGTTACGCAACAAATTC	73379
QY	3481	CCGTCGTGTCAAACCGGGAGAAACCTTACTGCGTGGCCCTGGGACATAAAATATATCCGG	3540
Db	73380	CCGTCGTGTCAAACCGGGAGAAACCTTACTGCGTGGCCCTGGGACATAAAATATATCCGG	73439
QY	3541	CGCCCCAGTGCGCATCTTCTCTCAGCGGAGCGCGGAGAGTGAAGTATTACACACCG	3600
Db	73440	CGCCCCAGTGCGCATCTTCTCTCAGCGGAGCGCGGAGAGTGAAGTATTACACACCG	73499
QY	3601	GACTTATATAGATCAAGGCTATCTGTGAGAAATTAATACTCATCTGTTCTCATATAGACTTAAC	3660
Db	73500	GACTTATATAGATCAAGGCTATCTGTGAGAAATTAATACTCATCTGTTCTCATATAGACTTAAC	73559
QY	3661	AGGTGTCACACTTTTACCGGGGAGAAAGTCAACGTCACATCGGGTTTATGTAGCGCT	3720
Db	73560	AGGTGTCACACTTTTACCGGGGAGAAAGTCAACGTCACATCGGGTTTATGTAGCGCT	73619
QY	3721	CGCCCGGGCCCTTAAAAATGCCGATACTGAACCTTACACATTTACTCTTGAGAGCTGAT	3780
Db	73620	CGCCCGGGCCCTTAAAAATGCCGATACTGAACCTTACACATTTACTCTTGAGAGCTGAT	73679
QY	3781	TTGATGTTAGTGCCTCAGATGCCATGACCATACCCCAACGACAGAACCCGTTTACGT	3840
Db	73680	TTGATGTTAGTGCCTCAGATGCCATGACCATACCCCAACGACAGAACCCGTTTACGT	73739

```
|||||
Db 74820 AACGAACCGGCGCGCCATTGCCAACAATAATGATGAAATTTAGGGCAATTTTCTC 74879
Oy 4981 TACTAGTGAAGATATGCGCGAAGTAATTACGATATCTACTGTGAACGCAACGACGCG 5040
|||||
Db 74880 TACTAGTGAAGATATGCGCGAAGTAATTACGATATCTACTGTGAACGCAACGACGCG 74939
Oy 5041 GTTCCTTCTCTCGGTCTCCACGATCGGGGCGACGCGCTTAATAATCTCCACATGCGCT 5100
|||||
Db 74940 GTCCCTTCTCTCGGTCTCCACGATCGGGGCGACGCGCTTAATAATCTCCACATGCGCT 74999
Oy 5101 AATTAACTCTGCGCGCGCAAGCGCCAGCGCGCGCGCAAGGTGTTTACCGTGTAT 5160
|||||
Db 75000 AATTAACTCTGCGCGCGCAAGCGCCAGCGCGCGCGCAAGGTGTTTACCGTGTAT 75039
Oy 5161 GGTGCTGAACCTTACCGCGCGTGGCAGGTTAATCTATTTCTTACAGGTGACGACCAATTGAC 5220
|||||
Db 75060 GGTGCTGAACCTTACCGCGCGTGGCAGGTTAATCTATTTCTTACAGGTGACGACCAATTGAC 75119
Oy 5221 CTCGGATTAACATTTAAAGACCGCATTTGACCTGGCTCAGACCGAGAAATCTCGAACCCAT 5280
|||||
Db 75120 CTCGGATTAACATTTAAAGACCGCATTTGACCTGGCTCAGACCGAGAAATCTCGAACCCAT 75179
Oy 5281 AATTAGCGTACTGGCATGCAACGGGTCGCGGAGGACGACCAACATGATCGTTTAAATC 5340
|||||
Db 75180 AATTAGCGTACTGGCATGCAACGGGTCGCGGAGGACGACCAACATGATCGTTTAAATC 75239
Oy 5341 TAAAGTGCCCTGTTTACAGGCGCAAGATCTCTCGGCGCTTAAAGAAAGTGTACAAATGAC 5400
Db 75240 TAAAGTGCCCTGTTTACAGGCGCAAGATCTCTCGGCGCTTAAAGAAAGTGTACAAATGAC 75299
Oy 5401 CCCATCCCCCTATTTGGATGATATAACGCTGCTGGGCTGCTTCGAGGCATCGTTTACTGCGC 5460
Db 75300 CCCATCCCCCTATTTGGATGATATAACGCTGCTGGGCTGCTTCGAGGCATCGTTTACTGCGC 75359
Oy 5461 CGGACGTTTTTATTTTTCACATCTCATATATGACAGGCGGAGAGCGCTGTCATCTAAC 5520
|||||
Db 75360 CGGACGTTTTTATTTTTCACATCTCATATATGACAGGCGGAGAGCGCTGTCATCTAAC 75419
Oy 5521 GAGTTTATTCAGCTCCAGTCAGGCGCAGAGCTTGGTCACCGTAAACACCTATGACGAAT 5580
|||||
Db 75420 GAGTTTATTCAGCTCCAGTCAGGCGCAGAGCTTGGTCACCGTAAACACCTATGACGAAT 75479
Oy 5581 AGGGGCGCTATTCGGGCGCTCAGATTTCTTGGGAATGTTTCCAAATTTTGGGCGTATCT 5640
Db 75480 AGGGGCGCTATTCGGGCGCTCAGATTTCTTGGGAATGTTTCCAAATTTTGGGCGTATCT 75539
Oy 5641 AAAATACAAAATGCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5700
|||||
Db 75540 AAAATACAAAATGCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 75599
Oy 5701 CATACGTGGGGGTTGATGCTGTCACTCAGGACCTCGTACACTTCATCTACCTGTCAAT 5760
Db 75600 CATACGTGGGGGTTGATGCTGTCACTCAGGACCTCGTACACTTCATCTACCTGTCAAT 75659
Oy 5761 TTACAGTGCATGACGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5820
Db 75660 TTACAGTGCATGACGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 75719
Oy 5821 GACCCCGCAAGGTTAAACCTCCGACAGTGTGTGGGCGTTAGAACGCGATTTTAAAGA 5880
Db 75720 GACCCCGCAAGGTTAAACCTCCGACAGTGTGTGGGCGTTAGAACGCGATTTTAAAGA 75779
Oy 5881 GCACGTGATGGCATATTAACAATAAAGCAAGCTACCTGATCTACTTACATAACCATTTTAA 5940
Db 75780 GCACGTGATGGCATATTAACAATAAAGCAAGCTACCTGATCTACTTACATAACCATTTTAA 75839
Oy 5941 CGTACCGGCTCTCTCCCGGAGAGAGATAGAAAACCTTTAGAGAACAGATGTCATCTG 6000
Db 75840 CGTACCGGCTCTCTCTCCCGGAGAGATAGAAAACCTTTAGAGAACAGATGTCATCTG 75899
Oy 6001 GTGTGCAATCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 6060
|||||
```

```
Db 75900 GTGTGCAATCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 75959
Oy 6061 GCTGAATCTAACAAAAGATTTATCCGCTCTCTGACCTAGCGGCGCTAGATCACTATTC 6120
|||||
Db 75960 GCTGAATCTAACAAAAGATTTATCCGCTCTCTGACCTAGCGGCGCTAGATCACTATTC 76019
Oy 6121 CGGAGGCCCAAGGAAACCTTTTACGGTGGCTTCGAGAAATTTCCACATACAGTGGCA 6180
|||||
Db 76020 CGGAGGCCCAAGGAAACCTTTTACGGTGGCTTCGAGAAATTTCCACATACAGTGGCA 76079
Oy 6181 GTTTTGAATTAACAGTATTTTGTCTAATGACAGCAGCTATAGACGCTACTGGAA 6240
Db 76080 GTTTTGAATTAACAGTATTTTGTCTAATGACAGCAGCTATAGACGCTACTGGAA 76139
Oy 6241 ACAAAACATTTATCGTCCGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 6300
Db 76140 ACAAAACATTTATCGTCCGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 76199
Oy 6301 CTCAGAGATTTTACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 6360
Db 76200 CTCAGAGATTTTACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 76259
Oy 6361 AGTTTACGCGCAGAGATTTTCAACCCAGAGCTCCAGTTTATAGATGGGTGTTGATTT 6420
Db 76260 AGTTTACGCGCAGAGATTTTCAACCCAGAGCTCCAGTTTATAGATGGGTGTTGATTT 76319
Oy 6421 TGATCTAAAGGTAAACGGAAGGTAGACGAGCTCTAAACGATATCTAACATATGCGTAA 6480
Db 76320 TGATCTAAAGGTAAACGGAAGGTAGACGAGCTCTAAACGATATCTAACATATGCGTAA 76379
Oy 6481 GCTGCGGAGGTCATATTAAGAAAGCTGTCAGTTATAGTTCACATTAACGAAACGACCC 6540
Db 76380 GCTGCGGAGGTCATATTAAGAAAGCTGTCAGTTATAGTTCACATTAACGAAACGACCC 76439
Oy 6541 CGTGTATTTTAAAGTGGGCGCTGTCAGAGCCGTAACCTGCGGAGAGATCTCAGACAC 6600
Db 76440 CGTGTATTTTAAAGTGGGCGCTGTCAGAGCCGTAACCTGCGGAGAGATCTCAGACAC 76499
Oy 6601 CGCGTTCTGTCACTGTGACGCAAAATAATAGGATGAGAAATTTGAAACCCGCTTCCAGCG 6660
Db 76500 CGCGTTCTGTCACTGTGACGCAAAATAATAGGATGAGAAATTTGAAACCCGCTTCCAGCG 76559
Oy 6661 ATACTGTTTGGGGGTCGCGCTCACTGCTGTCGAGCGGATTTTAAACCCGCTGCT 6720
Db 76560 ATACTGTTTGGGGGTCGCGCTCACTGCTGTCGAGCGGATTTTAAACCCGCTGCT 76619
Oy 6721 TAACTGACACGCGGCTAGGCTCAGAGATTCCTGGGATCTTAAAGATTAAGACCAAT 6780
Db 76620 TAACTGACACGCGGCTAGGCTCAGAGATTCCTGGGATCTTAAAGATTAAGACCAAT 76679
Oy 6781 TGACTCTGGCATTTACGCCAAGGGGAGATGCGTGGCGCTACTGCTATAGGTTGG 6840
Db 76680 TGACTCTGGCATTTACGCCAAGGGGAGATGCGTGGCGCTACTGCTATAGGTTGG 76739
Oy 6841 CCGGGGGGCGAGCTGTACGCGCTCTTAAATTTTATCTGTACCCGGAAGAGTTCGA 6900
Db 76740 CCGGGGGGCGAGCTGTACGCGCTCTTAAATTTTATCTGTGTACCCGGAAGAGTTCGA 76799
Oy 6901 TAAATCGCGATTTTGAAGAAACGCGTTTAAAGTTTCTAATCTGTATACACGCGCTG 6960
Db 76800 TAAATCGCGATTTTGAAGAAACGCGTTTAAAGTTTCTAATCTGTATACACGCGCTG 76859
Oy 6961 AGACTCTGTACACAAAACGCGCACCTGTGTACGCGATCTGACGAGAAAGAGGCTT 7020
Db 76860 AGACTCTGTACACAAAACGCGCACCTGTGTACGCGATCTGACGAGAAAGAGGCTT 76919
Oy 7021 TCTAGAAAGCAAAACAGAAATTAATCTCCAAAACATTCAGGAGCGCGGCAAAAAT 7080
Db 76920 TCTAGAAAGCAAAACAGAAATTAATCTCCAAAACATTCAGGAGCGCGGCAAAAAT 76979
Oy 7081 TGAGGGAACCAAGAAAACCACTAATTTGATTTGGGACGAGCGAGTGTGGCAAAAAT 7140
Db 76980 TGAGGGAACCAAGAAAACCACTAATTTGATTTGGGACGAGCGAGTGTGGCAAAAAT 77039
```


Oy	7141	ACAGCATACCATACACCGTTTCTTCCGGATACCGCATCGGCCAAATTGGATCTGTGAG	7200
Db	77040	ACACGATACCATACACCGTTTCTTCCGGATACCGCATCGGCCAAATTGGATCTGTGAG	77099
Oy	7201	CTTCATGACACTCCGGAGACAACTTATACAAATTAAACCAACAAAAGAAACAACTTTT	7260
Db	77100	CTTCATGACACTCCGGAGACAACTTATACAAATTAAACCAACAAAAGAAACAACTTTT	77159
Oy	7261	CTGTATTTAATCATTAAGCACCGAAACACACTGACAGACAGTCCGTGTATTTTAAACCTTACA	7320
Db	77160	CTGTATTTAATCATTAAGCACCGAAACACACTGACAGACAGTCCGTGTATTTTAAACCTTACA	77219
Oy	7321	TTCCACAAAAGAAAGGAGGTGTCGGGTGACCTTTTATGATCAGTGTCTTGGTGGCAAAATG	7380
Db	77220	TTCCACAAAAGAAAGGAGGTGTCGGGTGACCTTTTATGATCAGTGTCTTGGTGGCAAAATG	77279
Oy	7381	TAAATCATTAATAGGCCCAACTGTCACATTTTTCATTTATGTATACCATAACCGGACGTAGA	7440
Db	77280	TAAATCATTAATAGGCCCAACTGTCACATTTTTCATTTATGTATACCATAACCGGACGTAGA	77339
Oy	7441	GACACGATTAATAATTCATCCGTGATGGGCCAGCTCTCCGGCTACTTGTATTTTAAACAC	7500
Db	77340	GACACGATTAATAATTCATCCGTGATGGGCCAGCTCTCCGGCTACTTGTATTTTAAACAC	77399
Oy	7501	CGCGTACCCCAAAAACATCTGGACGAGTTTGTTCGGACAGTGACATGCGACAG	7560
Db	77400	CGCGTACCCCAAAAACATCTGGACGAGTTTGTTCGGACAGTGACATGCGACAG	77459
Oy	7561	GCAATGGTGAAGCTGTGATACATGAGAGATATTTTGGACGTAAAGACACCCCTGTGGC	7620
Db	77460	GCAATGGTGAAGCTGTGATACATGAGAGATATTTTGGACGTAAAGACACCCCTGTGTGC	77519
Oy	7621	TCTTACGACTGCCATTTTAAAAACCGCACTTATCAACGGCTCTTTTATAGATTTTACAT	7680
Db	77520	TCTTACGACTGCCATTTTAAAAACCGCACTTATCAACGGCTCTTTTATAGATTTTACAT	77579
Oy	7681	GGCGTATGTGTTTCACGACACTAATTTGTTTATAGGGGGCATATCATGTGCGGAATTGGA	7740
Db	77580	GGCGTATGTGTTTCACGACACTAATTTGTTTATAGGGGGCATATCATGTGCGGAATTGGA	77639
Oy	7741	CGACTCGTCTCGSAGAAATGAGACACCTGTCCCAACGCCGGAGCCAGAACCGTCCAC	7800
Db	77640	CGACTCGTCTCGSAGAAATGAGACACCTGTCCCAACGCCGGAGCCAGAACCGTCCAC	77699
Oy	7801	AAGCCCGAAGACGTTTCCGGAGGGGCCCAATACACAGTGTGTGGCTTACTTAAATCCG	7860
Db	77700	AAGCCCGAAGACGTTTCCGGAGGGGCCCAATACACAGTGTGTGGCTTACTTAAATCCG	77759
Oy	7861	TAAAGATCTCGATCTGAGACGGCCGCTTAAAAATGTGACACACATCTCCACTTAACCGTCC	7920
Db	77760	TAAAGATCTCGATCTGAGACGGCCGCTTAAAAATGTGACACACATCTCCACTTAACCGTCC	77819
Oy	7921	GCATCTCGATCTCGAAGACGGGTCCGGGTCCGGTCAACAGTAAACACAGTCAAGCAGATA	7980
Db	77820	GCATCTCGATCTCGAAGACGGGTCCGGGTCCGGTCAACAGTAAACACAGTCAAGCAGATA	77879
Oy	7981	CGTCAAGAGATTCAAACCAACGGTGTATGCACCCCGTCAATCGAAGAACCGTGGCACAGGG	8040
Db	77880	CGTCAAGAGATTCAAACCAACGGTGTATGCACCCCGTCAATCGAAGAACCGTGGCACAGGG	77939
Oy	8041	CGGTAAAGGAAAGGCCCGTTTATCCGAGAGACGCAATGGCTGGCGCGGGTCCGACGCAC	8100
Db	77940	CGGTAAAGGAAAGGCCCGTTTATCCGAGAGACGCAATGGCTGGCGCGGGTCCGACGCAC	77999
Oy	8101	ATACGGCCACGACTATTCGCGGAAACACCGCTTTTAAACGCGAGCATTTAAAGATCTATTAA	8160
Db	78000	ATACGGCCACGACTATTCGCGGAAACACCGCTTTTAAACGCGAGCATTTAAAGATCTATTAA	78059
Oy	8161	AAAGATGCACCTTTCATCCACCATGTCTCTCTGTGTCGCAACGATAAAAAGTATTCAGAGG	8220
Db	78060	AAAGATGCACCTTTCATCCACCATGTCTCTCTGTGTCGCAACGATAAAAAGTATTCAGAGG	78119

QY	8221	ACTGTTGGCAGCAGACACTCTGGGACAGTGTCTTTCAAGTGTGTGCTCTCCGGCGCCGACCCGCT	8280
Db	78120	ACTGTTGGCCACACACACTCTGGGACAGTGTCTTTCAAGTGTGTGCTCTCCGGCGCCGACCCGCT	78179
QY	8281	GCAACCCGAGGGTTCACGGATCGAACAGCTTACCGCTATAGTCAAGTCTGGCGGCAG	8340
Db	78180	GCAACCCGAGGGTTCACGGATCGAACAGCTTACCGCTATAGTCAAGTCTGGCGGCAG	78239
QY	8341	AGACGCGTGTGGCCAAAAGTTAGCTTGCGTTAACTAACAGGCTATACAAACCCCT	8400
Db	78240	AGACGCGGTGTGGCCAAAAGTTAGCTTGCGTTAACTAACAGGCTATACAAACCCCT	78299
QY	8401	GCTCACGTTTGTGAGCGGGAGAAACACACAGCCCACTGTTGGCGACGCGCAAAAAC	8460
Db	78300	GCTCACGTTTGTGAGCGGGAGAAACACACAGCCCACTGTTGGCGACGCGCAAAAAC	78359
QY	8461	GCTAGCGTGTGGGGGACTCGAGGCTCTCGCGGCTTTATTCGAGGAAGTCTGGCGTGGG	8520
Db	78360	GCTAGCGTGTGGGGGACTCGAGGCTCTCGCGGCTTTATTCGAGGAAGTCTGGCGTGGG	78419
QY	8521	CCAGGTGTGCGATATCTCAAAACAGATCGTTGAACGACAGCCACCTAGATATCTTCAGA	8580
Db	78420	CCAGGTGTGCGATATCTCAAAACAGATCGTTGAACGACAGCCACCTAGATATCTTCAGA	78479
QY	8581	CAGTAGTCAGAGCGTGTGCACCTGGTTTCATCTCCAAATTCAGGCAATTTGCACATACGTG	8640
Db	78480	CAGTAGTCAGAGCGTGTGCACCTGGTTTCATCTCCAAATTCAGGCAATTTGCACATACGTG	78539
QY	8641	CTTCTTGGAAGTACAGGTTGAGGTTTGCCGTGGTGAAGACACTTAACCTTACCTCGTGTAT	8700
Db	78540	CTTCTTGGAAGTACAGGTTGAGGTTTGCCGTGGTGAAGACACTTAACCTTACCTCGTGTAT	78599
QY	8701	AAATAACCGCTTGCGCGAGGCGCGCAACCTTGCGGGAGAGGTGAACGTAAATTTTAACT	8760
Db	78600	AAATAACCGCTTGCGCGAGGCGCGCAACCTTGCGGGAGAGGTGAACGTAAATTTTAACT	78659
QY	8761	CGGAATGCTGATTTGGGTTTGCCTTAACCTTGGCGGCTCTCTGCAGAGCATAGTGTGTC	8820
Db	78660	CGGAATGCTGATTTGGGTTTGCCTTAACCTTGGCGGCTCTCTGCAGAGCATAGTGTGTGTC	78719
QY	8821	TGGCGAGACGCTGTACTCTGTTTAGTGTCTTCCGTGAGAAATATAGACCGGAGATGTGCAT	8880
Db	78720	TGGCGAGACGCTGTACTCTGTTTAGTGTCTTCCGTGAGAAATATAGACCGGAGATGTGCAT	78779
QY	8881	GGGACTCTTAAATTCATAGTGTGTGAGACATACACCAATGTCTGAGCGGAGTGTGT	8940
Db	78780	GGGACTCTTAAATTCATAGTGTGTGAGACATACACCAATGTCTGAGCGGAGTGTGT	78839
QY	8941	CATTACACCCACGCCATGTGTAGATCTGGCGAAAACACAGGACTTTTTTCTTTC	9000
Db	78840	CATTACACCCACGCCATGTGTAGATCTGGCGAAAACACAGGACTTTTTTCTTTC	78899
QY	9001	ACTGTAAATATTAACCATGTGTGTAGTAAAGTAAATTCACGGCGGTTTAAA	9060
Db	78900	ACTGTAAATATTAACCATGTGTGTAGTAAAGTAAATTCACGGCGGTTTAAA	78959
QY	9061	TGCAATTAACCCACATTAACAAAATTAATTAATGTGTAAACCAACACGCGTAAGCTTTTC	9120
Db	78960	TGCAATTAACCCACATTAACAAAATTAATTAATGTGTAAACCAACACGCGTCAAGCTTTTC	79019
QY	9121	TGCAAGGTTTGTGTGTCGGAACAAATTAGGACAGTTCGCCACCTAGCGGACGTTCTCT	9180
Db	79020	TGCAAGGTTTGTGTGTCGGAACAAATTAGGACAGTTCGCCACCTAGCGGACGTTCTCT	79079
QY	9181	ATAGCGTGTGTATACAGGGAGTGTATTTTAACGGAAGTCCCAACMGAAACGCTGGCGGGT	9240
Db	79080	ATAGCGTGTGTATACAGGGAGTGTATTTTAACGGAAGTCCCAACMGAAACGCTGGCGGGT	79139
QY	9241	GGGTAAACAGTAACCGGTCATCCGACAGTGTAAACAACACATATAAATAGGCGACCGT	9300
Db	79140	GGGTAAACAGTAACCGGTCATCCGACAGTGTAAACAACACATATAAATAGGCGACCGT	79199
QY	9301	TTATAGCGGTTTATTTGAACATACACACATTTTCAGGAGTTTCGCTTTTATATAAAT	9360

Db 79200 TTTATACGGTTTATTTGAACATACACACATTGAGGAGTTTCGCTTTTATAAAAT 79259
QY 9361 CTTCATTCAATTCAGATATATTTTACAGCTGGTGAGCAACATATATATCGGCG 9420
Db 79260 CTTCATTCAATTCAGATATATTTTACAGCTGGTGAGCAACATATATCGGCG 79319
QY 9421 CTCTGATGATCTCTCTCTCTGATAGGACAGGACACCCAAATCTGTGCAAAACG 9480
Db 79320 CTCTGATGATCTCTCTCTCTCTGATAGGACAGGACACCCAAATCTGTGCAAAACG 79379
QY 9481 ATCCGGTGGCCCGGAGATCAGAGGCTGGTGTACTGGGCTAACTTTTAACATGATTCATC 9540
Db 79380 ATCCGGTGGCCCGGAGATCAGAGGCTGGTGTACTGGGCTAACTTTTAACATGATTCATC 79439
QY 9541 GGATATCAAAAACGCGATGTCACCCAGATGGACGCGCTTGTTCAGAGGTGTTGA 9600
Db 79440 GGATATCAAAAACGCGATGTCACCCAGATGGACGCGCTTGTTCAGAGGTGTTGA 79499
QY 9601 GGATATGCGACGAGACCATTAATTAAGAAATCCATAGCCATTCATATCCCATATC 9660
Db 79500 GGATATGCGACGAGACCATTAATTAAGAAATCCATAGCCATTCATATCCCATATC 79559
QY 9661 ACAACGCAACAAAGACATGCGCTCTCCAGAGGCTGTAAAGCTTACAAAGTGTGCTCA 9720
Db 79560 ACAACGCAACAAAGACATGCGCTCTCCAGAGGCTGTAAAGCTTACAAAGTGTGCTCA 79619
QY 9721 CATAAATGCGTATCCATATAGGCGCGGCGGCAACCAACTGAAGGCGCCGAGAG 9780
Db 79620 CATAAATGCGTATCCATATAGGCGCGGCGGCAACCAACTGAAGGCGCCGAGAG 79679
QY 9781 CATGCAAGAGCTGTTCATTTTATCCGTTGGTCTCGTGATTAAGCAAGCCCATCC 9840
Db 79680 CATGCAAGAGCTGTTCATTTTATCCGTTGGTCTCGTGATTAAGCAAGCCCATCC 79739
QY 9841 AGAATGGTAAAGTGTGCTTGAAGGACCCCATATATTAACCTGAAATGATGATAA 9900
Db 79740 AGAATGGTAAAGTGTGCTTGAAGGACCCCATATATTAACCTGAAATGATGATAA 79799
QY 9901 TCCCAACGGGTCGTCAACAGATGCGCAACACGAGAAAGACCCCTGATGACAGATG 9960
Db 79800 TCCCAACGGGTCGTCAACAGATGCGCAACACGAGAAAGACCCCTGATGACAGATG 79859
QY 9961 CGGAGAGGCTGTTCGCCGCGGCAACGACGCGCCCTTGAATTTTCTCTGCTTAC 10020
Db 79860 CGGAGAGGCTGTTCGCCGCGGCAACGACGCGCCCTTGAATTTTCTCTGCTTAC 79919
QY 10021 GTCTTACCGAGAGGCTGTGCGGTTGCAAGCGCTGGTGGCGGGCGGTCAATGTA 10080
Db 79920 GTCTTACCGAGAGGCTGTGCGGTTGCAAGCGCTGGTGGCGGGCGGTCAATGTA 79979
QY 10081 GGTACCGGCGGAGCGGGTACGAATGACCCGAGACGCTGTACCGTATTCAGATAC 10140
Db 79980 GGTACCGGCGGAGCGGGTACGAATGACCCGAGACGCTGTACCGTATTCAGATAC 80039
QY 10141 CCGTCCCGCTGCTGGCGGCGCTTGGGCTTAAACATCCGAAACCTTAACCCCGGAGTTC 10200
Db 80040 CCGTCCCGCTGCTGGCGGCGCTTGGGCTTAAACATCCGAAACCTTAACCCCGGAGTTC 80099
QY 10201 TGCCTGTACCCAGAGAGCCGAGGCAACCTGATTAACATCTTTCATTCGAGGCA 10260
Db 80100 TGCCTGTACCCAGAGAGCCGAGGCAACCTGATTAACATCTTTCATTCGAGGCA 80159
QY 10261 CCTGAAGACCAAGTTGCAATGAAATGAAATCTCCGCTCAAAAGCTCTTCTTCTATGA 10320
Db 80160 CCTGAAGACCAAGTTGCAATGAAATGAAATCTCCGCTCAAAAGCTCTTCTTCTATGA 80219
QY 10321 AATAGGACTCTTCTTATGCAACCCATAGGCGGCTTGGCTGGCCCAAGCTTACACT 10380
Db 80220 AATAGGACTCTTCTTATGCAACCCATAGGCGGCTTGGCTGGCCCAAGCTTACACT 80279
QY 10381 CCGGAGCGAGAGGAGTGTCTCTGATGAGTGTCTGCTGATCTCCATCCGCG 10440
|||||

Db 80280 CCGGAGCGAGAGGAGTGTCTCTGATGAGTGTCTGATGAGTGTCTGATGAGTGTCT 80339
QY 10441 AAGTATATCAATATCCACAGAGACCGAGGCTGATGCGCAGAGACCACTGGTCTTTC 10500
Db 80340 AAGTATATCAATATCCACAGAGACCGAGGCTGATGCGCAGAGACCACTGGTCTTTC 80399
QY 10501 GTCTGTGCGCAAAACAGTCCCGAATAGCTTGCAGAGATTTGGTGAATGATTCATTC 10560
Db 80400 GTCTGTGCGCAAAACAGTCCCGAATAGCTTGCAGAGATTTGGTGAATGATTCATTC 80459
QY 10561 TCGAATGCCATGGCGGAGGAGACCGGCTGAGGTTGGGCGGAGTGGCTGTG 10620
Db 80460 TCGAATGCCATGGCGGAGGAGACCGGCTGAGGTTGGGCGGAGTGGCTGTG 80519
QY 10621 ATATGCCAGGTTGATCTACTACCGCTTTCAGTTGCTTAAATTAACCAATCTCCGCAT 10680
Db 80520 ATATGCCAGGTTGATCTACTACCGCTTTCAGTTGCTTAAATTAACCAATCTCCGCAT 80579
QY 10681 GCGGCTACCGCGCTGGGCGAGATGTTGTGACGCGCTACAAAGAAATCCCACTGCGCA 10740
Db 80580 GCGGCTACCGCGCGCTGGGCGAGATGTTGTGACGCGCTACAAAGAAATCCCACTGCGCA 80639
QY 10741 ACTAATTCCTCAGCGCCAGTACGCTGAGTACGCTGATTCATTCACACAGAGACGCA 10800
Db 80640 ACTAATTCCTCAGCGCCAGTACGCTGAGTACGCTGATTCATTCACACAGAGACGCA 80699
QY 10801 CCCCATCATCTTACACGCTGTTCGCCGCTCGGATGCTCATTTGAATGATGATCGCGAGT 10860
Db 80700 CCCCATCATCTTACACGCTGTTCGCCGCTCGGATGCTCATTTGAATGATGATCGCGAGT 80759
QY 10861 CGCCAGCTCTACTGCGGCTGATGCGATGCGTCTCCCTCTCTGATCTTCATCT 10920
Db 80760 CGCCAGCTCTACTGCGGCTGATGCGATGCGTCTCCCTCTCTGATCTTCATCT 80819
QY 10921 GGAATGAACAGTGGTGGGACCCCTGATGTTACATGCTCCGCGGCTTAAACCAACCT 10980
Db 80820 GGAATGAACAGTGGTGGGACCCCTGATGTTACATGCTCCGCGGCTTAAACCAACCT 80879
QY 10981 CTGTACCGATACAGAGAGGTTTCGACACAGTAAACGAGTCTCATGGAGTGGCGCAT 11040
Db 80880 CTGTACCGATACAGAGAGGTTTCGACACAGTAAACGAGTCTCATGGAGTGGCGCAT 80939
QY 11041 CGAGCGGATTTGGCGGCTGAGCGAGACAGACAGGCGGATCTGTGATATCTCTAGG 11100
Db 80940 CGAGCGGATTTGGCGGCTGAGCGAGACAGACAGGCGGATCTGTGATATCTCTAGG 80999
QY 11101 GTTCGTCTCAGAGGTTGCGGAGCTTTCGAAGAGCTTAAGATATCCACATATCAAAA 11160
Db 81000 GTTCGTCTCAGAGGTTGCGGAGCTTTCGAAGAGCTTAAGATATCCACATATCAAAA 81059
QY 11161 CCTGAACGGGTTCTGTGATGCGAGGCTCTTACTCTCTCTCATTTGTAAGCACT 11220
Db 81060 CCTGAACGGGTTCTGTGATGCGAGGCTCTTACTCTCTCATTTGTAAGCACT 81119
QY 11221 TCATTTCCCGGTTCTCCAGGTTCTTACGCAATATGCGCATATCCGTAAGGTAACAA 11280
Db 81120 TCATTTCCCGGTTCTCCAGGTTCTTACGCAATATGCGCATATCCGTAAGGTAACAA 81179
QY 11281 CACCTTCTCAGACTTTTGTGATTAACCTTATAGTCTTCTGTGCAAACTGACATCAA 11340
Db 81180 CACCTTCTCAGACTTTTGTGATTAACCTTATAGTCTTCTGTGCAAACTGACATCAA 81239
QY 11341 CGACCCCGGTGAGGTAACAAAGCTCTCATCTTGTGAACAAACAGCGTGGCGCA 11400
Db 81240 CGACCCCGGTGAGGTAACAAAGCTCTCATCTTGTGAACAAACAGCGTGGCGCA 81299
QY 11401 CGAGGAGGAGATGTTGACATGCGACAGCCGATTCACATGAACAGCTTGGAGGCGCA 11460
Db 81300 CGAGGAGGAGATGTTGACATGCGACAGCCGATTCACATGAACAGCTTGGAGGCGCA 81359
QY 11461 CGGCTCTCCAAATTTAAGAAAGTTAATGATGCGCCCTGGACGAGCTCTGCGCA 11520
Db 81360 CGGCTCTCCAAATTTAAGAAAGTTAATGATGCGCCCTGGACGAGCTCTGCGCA 81419
|||||

Qy	11521	CACGCTGTTTTTGTCCATCCGACTCCGAGCCAAATACCGTTGCGGTAAAAAACCCTCTTC	11580	Qy	12601	GATTCGAGCTTCCCTTGAACGAACGCCAGGGAATGCCCAACATCTAATGTAATAGCCG	12660
Db	81420	CACGCTGTTTTTGTCCATCCGACTCCGAGCCAAATACCGTTGCGGTAAAAAACCCTCTTC	81479	Db	82500	GATTCGAGCTTCCCTTGAACGAACGCCAGGGAATGCCCAACATCTAATGTAATAGCCG	82559
Qy	11581	TTTACGCTCAGACCCACCCCTGCTGTAATGGAACTCACTGATTAACCAAGGCACT	11640	Qy	12661	GAGGGGTGGCCCAAAAGCCCAACCCGCGCAAAATCTTTATCCAGGAAGGCAACGCC	12720
Db	81480	TTTACGCTCAGACCCACCCCTGCTGTAATGGAACTCACTGATTAACCAAGGCACT	81539	Db	82560	GAGGGGTGGCCCAAAAGCCCAACCCGCGCAAAATCTTTATCCAGGAAGGCAACGCC	82619
Qy	11641	GAGTTTGGTGGAGACATCAGATTAACATTTGCAACCTTACCGCGGTTCCGGCAACA	11700	Qy	12721	TCGGCTGAACCTGCTGAAGTGGCTGGAATCTCGGAACCGAGTGCCTGCTCGCGATTC	12780
Db	81540	GAGTTTGGTGGAGACATCAGATTAACATTTGCAACCTTACCGCGGTTCCGGCAACA	81599	Db	82620	TCGGCTGAACCTGCTGAAGTGGCTGGAATCTCGGAACCGAGTGCCTGCTCGCGATTC	82679
Qy	11701	GCGCAACAGTCTATATCAGACACCCGGTCCGCCATAGGCGCTTATTAATTAATTTAGCT	11760	Qy	12781	GGTGGGCGCATATGTGCCCTTGAAGGCGAGCTTGCAACATGGAGCAACAGATAGCCG	12840
Db	81600	GCGCAACAGTCTATATCAGACACCCGGTCCGCCATAGGCGCTTATTAATTAATTTAGCT	81659	Db	82680	GGTGGGCGCATATGTGCCCTTGAAGGCGAGCTTGCAACATGGAGCAACAGATAGCCG	82739
Qy	11761	CTCGATATCTTTTGTGGTGTCTCATGTGTACAGAAATCTCATTTTCTGAAATCTGCAT	11820	Qy	12841	TTGAGCAATTCAGTACCACTTACCAACTCTGTGCCATATATATAAACAATTAATGCT	12900
Db	81660	CTCGATATCTTTTGTGGTGTCTCATGTGTACAGAAATCTCATTTTCTGAAATCTGCAT	81719	Db	82740	TTGAGCAATTCAGTACCACTTACCAACTCTGTGCCATATATATAAACAATTAATGCT	82799
Qy	11821	AGTGGAGCGTTTTTCCGCTGACATATATCCCGCATGTGCAAGTATCATCAAAAACCT	11880	Qy	12901	AGCATCCAAACCTGTTCAACCCCGGCTCCACCGGACAGTGTACCGAACACCGGCGCA	12960
Db	81720	AGTGGAGCGTTTTTCCGCTGACATATATCCCGCATGTGCAAGTATCATCAAAAACCT	81779	Db	82800	AGCATCCAAACCTGTTCAACCCCGGCTCCACCGGACAGTGTACCGAACACCGGCGCA	82859
Qy	11881	TCCTGCTATTCATACGAGACCGATCTGCAAGTACTTTGTTCCACGCGAACCGGACACGG	11940	Qy	12961	ACCGGACCAAACTTATTCAGGCGCTCTCGGCAACCCCGCTAATAGCACTAGTGCCTG	13020
Db	81780	TCCTGCTATTCATACGAGACCGATCTGCAAGTACTTTGTTCCACGCGAACCGGACACGG	81839	Db	82860	ACCGGACCAAACTTATTCAGGCGCTCTCTCGGCAACCCCGCTAATAGCACTAGTGCCTG	82919
Qy	11941	TCCTGTCTCTCATTTCTCCCAAAACAATCCGCGGTACTCCCGCATTCGACCGCGCAACGA	12000	Qy	13021	GAGGCTGATGCGAACGACGACACGACACTCAGCGTAATTTGGTAAGGCGAATGATTGGG	13080
Db	81840	TCCTGTCTCTCATTTCTCCCAAAACAATCCGCGGTACTCCCGCATTCGACCGCGCAACGA	81899	Db	82920	GAGGCTGATGCGAACGACGACACGACACTCAGCGTAATTTGGTAAGGCGAATGATTGGG	82979
Qy	12001	GCGAGGCGCTGATATCGACTCCAGCGCGCGCATTCGCGTATTTGGAGCTTGACGAGATC	12060	Qy	13081	CATCTGTCGGATATGAGTGCAGAAAGTTGTCCTAGTTGACACGCTCCGACCGGTTTGA	13140
Db	81900	GCGAGGCGCTGATATCGACTCCAGCGCGCGCATTCGCGTATTTGGAGCTTGACGAGATC	81959	Db	82980	CATCTGTCGGATATGAGTGCAGAAAGTTGTCCTAGTTGACACGCTCCGACCGGTTTGA	83039
Qy	12061	AGCTCTCAAGACAAATGAACCCCTTGCGTTACGCGCACAGTTCATTAATGATCTAAT	12120	Qy	13141	CTATGCGGTATGCGCTGATATGACGATTTTGTGATTCCTTAGCGGTTAATTCCTGCGCA	13200
Db	81960	AGCTCTCAAGACAAATGAACCCCTTGCGTTACGCGCACAGTTCATTAATGATCTAAT	82019	Db	83040	CTATGCGGTATGCGCTGATATGACGATTTTGTGATTCCTTAGCGGTTAATTCCTGCGCA	83099
Qy	12121	GACGAGTCAATGTGCGCTTAACATATGTGCTAAGACTACTCAAAAGTGTCTTAAGGGGAAGA	82079	Qy	13201	GCCGCTGCAAGATCCCTCGATGAGACAGTATGTAATTAATTTTTTCCGCTTC	13260
Db	82020	GACGAGTCAATGTGCGCTTAACATATGTGCTAAGACTACTCAAAAGTGTCTTAAGGGGAAGA	82079	Db	83100	GCCGCTGCAAGATCCCTCGATGAGACAGTATGTAATTAATTTTTTCCGCTTC	83159
Qy	12181	GTCACAAACACCTGGCACTCAATTAATTTGAGTGGGCAATGACCGGTCCTTCCTC	12240	Qy	13261	TCGACTCTCTGCTCCCTCTGCTGATTCACAGGTATGCGGTAATGCGGTTAATTCCTGCGCA	13320
Db	82080	GTCACAAACACCTGGCACTCAATTAATTTGAGTGGGCAATGACCGGTCCTTCCTC	82139	Db	83160	TCGACTCTCTGCTCCCTCTGCTGATTCACAGGTATGCGGTAATGCGGTTAATTCCTGCGCA	83219
Qy	12241	TGCTTATGATTAACCCCATCGCACATATTCAGAGAACAAACACTCCAGATACAAAC	12300	Qy	13321	TCAACCCACCGCATTCGCGGATGACGACTGTCTGCAAGCATTCACACGACATCTCGA	13380
Db	82140	TGCTTATGATTAACCCCATCGCACATATTCAGAGAACAAACACTCCAGATACAAAC	82139	Db	83220	TCAACCCACCGCATTCGCGGATGACGACTGTCTGCAAGCATTCACACGACATCTCGA	83279
Qy	12301	ACTTTATTAACAGATTAAGAGCGCTACACCGCTCACAAAACCGGTCGCGCACAGGTA	12360	Qy	13381	AGGCTGATGATTTGGTCACTGAGACCGGCGCTCCATATCTCTCGCGCTGACAGGCA	13440
Db	82200	ACTTTATTAACAGATTAAGAGCGCTACACCGCTCACAAAACCGGTCGCGCACAGGTA	82259	Db	83280	AGGCTGATGATTTGGTCACTGAGACCGGCGCTCCATATCTCTCGCGCTGACAGGCA	83339
Qy	12361	CATTAAACATTAGCGGCGGACAAACCGCCGACACACTGCTGACACAGCTGATTAAT	12420	Qy	13441	TCGCAAACTTGTCCAAGTTACCTCTGACAAAGCACTGCGACCTCAGACAGCTACGCG	13500
Db	82260	CATTAAACATTAGCGGCGGACAAACCGCCGACACACTGCTGACACAGCTGATTAAT	82319	Db	83340	TCGCAAACTTGTCCAAGTTACCTCTGACAAAGCACTGCGACCTCAGACAGCTACGCG	83399
Qy	12421	AGCGGTACAGTCTTGGACTCCGCCCTCGGGTGTAGGTAGCGCCCAAAATATAGGTA	12480	Qy	13501	TGGCAACGGGAATTTGTGTCTGATCTGTGCGGACAGTACTTAAGCTTAATTTATCT	13560
Db	82320	AGCGGTACAGTCTTGGACTCCGCCCTCGGGTGTAGGTAGCGCCCAAAATATAGGTA	82379	Db	83400	TGGCAACGGGAATTTGTGTCTGATCTGTGCGGACAGTACTTAAGCTTAATTTATCT	83459
Qy	12481	ACACAAGCTTGTGGAAGCGCGCTCGTCCGAGATGTTCTGGCCATGGCTGTCAATAG	12540	Qy	13561	GTTCGTGACCTCTGCGGCGGAAGTTTGTGTTTATGACACACACCGGGAAGGATTCATGT	13620
Db	82380	ACACAAGCTTGTGGAAGCGCGCTCGTCCGAGATGTTCTGGCCATGGCTGTCAATAG	82439	Db	83460	GTTCGTGACCTCTGCGGCGGAAGTTTGTGTTTATGACACACACCGGGAAGGATTCATGT	83519
Qy	12541	TCAACCAAGTTAAATGACAGACAGCGTTGGGCGACGACAGGACCGCAACCGCCCGTA	12600	Qy	13621	GTTCGTGACAGCTGCTGCTGACAGACACAGCAACAGAAATAGAACTTTGGGCTCTCTT	13680
Db	82440	TCAACCAAGTTAAATGACAGACAGCGTTGGGCGACGACAGGACCGCAACCGCCCGTA	82499	Db	83520	GTTCGTGACAGCTGCTGCTGACAGACACAGCAACAGAAATAGAACTTTGGGCTCTCTT	83579
				Qy	13681	GCGCACAGGCTGTGTGAGAGATACAGTGTTCCTCCGCTTGACAGGCGCATGCTCTCTG	13740

Db	83580	GGGACACAGGCGTGTGTGAGAGATACAGTGTTCGCCCGTTGCACGGCGCATGGCTCTCG	83639
OY	13741	GTCCCGAGAGCGGGCAGCTTTCTCATGAACCATGAAGTTAAAAATTTCTGTTAG	13800
Db	83640	GTCCCGAGAGCGGGCAGGCTTTCTCATGAACCATGAAGTTAAAAATTTCTGTTAG	83699
OY	13801	AGAGAACATGACCTCTCGTGGATATATACCATTAACAGTGTACCGCGCGCTACA	13860
Db	83700	AGAGAACATGACCTCTCGTGGATATATACCATTAACAGTGTACCGCGCGCTACA	83759
OY	13861	GCCTTTCCCTGTTCTATATACAGCTACCTCCGGTTGTTGCCGTATCGTAGATGC	13920
Db	83760	GCCTTTCCCTGTTCTATATATACAGCTACCTCCGGTTGTTGCCGTATCGTAGATGC	83819
OY	13921	CCCTGTAATPAGCGACACAGATGGTTTTTATTCGGTATATCTGTGGCGTACGTTTT	13980
Db	83820	CCCTGTAATPAGCGACACAGATGGTTTTTATTCGGTATATCTGTGGCGTACGTTTT	83879
OY	13981	CACGATCTGGAGATGAGAAACAGACAGTAGAACCCGGTGCATAGAAACACAGATGCCG	14040
Db	83880	CACGATCTGGAGATGAGAAACAGACAGTAGAACCCGGTGCATAGAAACACAGATGCCG	83939
OY	14041	GATGGGAACCGGGCGCGGATGCAAAAGAACACTCTCCGATCTTGGACGTGTATCCA	14100
Db	83940	GATGGGAACCGGGCGCGGATGCAAAAGAACACTCTCCGATCTTGGACGTGTATCCA	83999
OY	14101	GTGCGACAAGCGCCAAATATAAACACGTGAATTCACACGCCAAACGGCACAAATTGAT	14160
Db	84000	GTGCGACAAGCGCCAAATATAAACACCGTGAATTCACACGCCAAACGGCACAAATTGAT	84059
OY	14161	GAGGCACGGCGCTTCTGGGACCCCGAGACGATGTCTGGCGGTACGCTGATCTGTG	14220
Db	84060	GAGGCACGGCGCTTCTGGGACCCCGAGACGATGTCTGGCGGTACGCTGATCTGTG	84119
OY	14221	GAGGAGACAACGTGGCGAAGGGGGCGGCGACGCGATCCCGGCTTACCCGATGCCAC	14280
Db	84120	GAGGAGACAACGTGGCGAAGGGGGCGGCGACGCGATCCCGGCTTACCCGATGCCAC	84179
OY	14281	ACACCTGCTCCAAATATATTAATCCCTTCAAGAGTTCTCATCAGATACACGATACG	14340
Db	84180	ACACCTGCTCCAAATATATTAATCCCTTCAAGAGTTCTCATCAGATACACGATACG	84239
OY	14341	ATCCAGATCCATCAAAAGTTTTACCGGGAAGCGGTCCAGCGCCACCGCTGATCCGA	14400
Db	84240	ATCCAGATCCATCAAAAGTTTTACCGGGAAGCGGTCCAGCGCCACCGCTGATCCGA	84299
OY	14401	CGACCCCATGCTCCACTTCTTGAATTCACGATTCCTCTCAAAACCCCTCAAAAATCGTC	14460
Db	84300	CGACCCCATGCTCCACTTCTTGAATTCACGATTCCTCTCAAAACCCCTCAAAAATCGTC	84359
OY	14461	TCTTACACTTAGCAGGTTTCCATCTAGACCCAAACCTGACAGACTCTCTCCACGCAGTAG	14520
Db	84360	TCTTACACTTAGCAGGTTTCCATCTAGACCCAAACCTGACAGACTCTCTCCACGCAGTAG	84419
OY	14521	CGAACACGCGTGGAGTTTCCAGCTGCCGCCCTTCTTCCAAACAGACTTAAAGCTTTTTC	14580
Db	84420	CGAACACGCGTGGAGTTTCCAGCTGCCGCCCTTCTTCCAAACAGACTTAAAGCTTTTTC	84479
OY	14581	CTCATCGCACCAAGTTAGTCTGAATAGTTTTCTGCTTGAGATGGTAAAGGTCACAGA	14640
Db	84480	CTCATCGCACCAAGTTAGTCTGAATAGTTTTCTGCTTGAGATGGTAAAGGTCACAGA	84539
OY	14641	TCTGTAATGGCTGTAGTTAGAAATCTGATTCGCCATGACAGGCTACCTATACAAATAG	14700
Db	84540	TCTGTAATGGCTGTAGTTAGAAATCTGATTCGCCATGACAGGCTACCTATACAAATAG	84599
OY	14701	GCGGGAATACAGATGTAATTTTCCCTGATGATATTTTGCAGGGGCTCATCTCTCAAAAG	14760
Db	84600	GCGGGAATACAGATGTAATTTTCCCTGATGATATTTTGCAGGGGCTCATCTCTCAAAAG	84659
OY	14761	TGCACCTGGCTAAGCAAGACGCTATATTTCTGGCACTTCTCATATTAACCAATATTC	14820

Db	84660	TGCACCTGGGCTAAACCAAGCAGCTCTATTTCTGGCACTTCTCTATTTATTAACCAATATG	84719
Oy	14821	TTTCTGGCTCAGCTTTTTCGAGCTCACTCAACGACACGGGTAAATGATCCGAGTTTCG	14880
Db	84720	TTTTCTGGTCTCAGCTTTTTCGAGCTCACTCAACGACACGGGTAAATGATCCGAGTTTCG	84779
Oy	14881	CTCTCCAGTGCCTTGAACAACACTGGCCAGAGTTAAAAAGGAAGCAAAAGGCTATAC	14940
Db	84780	CTCTCCAGTGCCTTGAACAACACTGGCCAGAGTTAAAAAGGAAGCAAAAGGCTATAC	84839
Oy	14941	TTTTCGATTTTCACTCAGTCGCGCAGTGAAGTGGTGACATTAGAAGTGTTCGGCCACACATT	15000
Db	84840	TTTTCGATTTTCACTCAGTCGCGCAGTGAAGTGGTGACATTAGAAGTGTTCGGCCACACATT	84899
Oy	15001	CAGCTGTGCACCTCAAGCCGACCAATATGGCAGTGCACATTCCTCCATCACACACTAG	15060
Db	84900	CAGCTGTGCACCTCAAGCCGACCAATATGGCAGTGCACATTCCTCCATCACACACTAG	84959
Oy	15061	TACGAAAAAAGCAAAACACACGCGAGTGACATTTTCCAGGTTAGAGAAATTTATTAG	15120
Db	84960	TACGAAAAAAGCAAAACACACGCGAGTGACATTTTCCAGGTTAGAGAAATTTATTAG	85019
Oy	15121	CCGGCGAATCATTATCAAAACAGCAAAAGTTATTCAAAAGGCTATAGATTTCTGTT	15180
Db	85020	CCGGCGAATCATTATCAAAACAGCAAAAGTTATTCAAAAGGCTATAGATTTCTGTT	85079
Oy	15181	TGATTAACCAATTAATAGATAGTGGAGGCTCTGAAAGCTTTCGCTCCGCGCCAGGAAACAA	15240
Db	85080	TGATTAACCAATTAATAGATAGTGGAGGCTCTGAAAGCTTTCGCTCCGCGCCAGGAAACAA	85139
Oy	15241	CCCGAAACCCAGAGATTAAACAAAGCGCGGGGGGACCCGTGTGCGCGGGGAGGGGGAC	15300
Db	85140	CCCGAAACCCAGAGATTAAACAAAGCGCGGGGGGACCCGTGTGCGCGGGGAGGGGGAC	85199
Oy	15301	CTGGCCATATCAAGCAATTAACATCAGTGCATCAAAAGCCACACGTCGATCCCGGTGTAG	15360
Db	85200	CTGGCCATATCAAGCAATTAACATCAGTGCATCAAAAGCCACACGTCGATCCCGGTGTAG	85259
Oy	15361	GCACGATGTGGCAAACTGTACGGTTCACGGGTATTTTCCTGAAACACACGTTAGACCC	15420
Db	85360	GCACGATGTGGCAAACTGTACGGTTCACGGGTATTTTCCTGAAACACACGTTAGACCC	85319
Oy	15421	CCGGTATTCGTGAACAATTAATTCCTCGTGGTCTGACAGAAATTTTTCATCCACGAGC	15480
Db	85320	CCGGTATTCGTGAACAATTAATTCCTCGTGGTCTGACAGAAATTTTTCATCCACGAGC	85379
Oy	15481	CATTTCAAAGCGTCTCGAGTCTGTGCACACAGACGACTCAGTGTGTGGTATCGCA	15540
Db	85380	CATTTCAAAGCGTCTCGAGTCTGTGCACACAGACGACTCAGTGTGTGGTATCGCA	85439
Oy	15541	GGAACCAAGCCGTGAAGGGGTGCATCCAAACACACAGGGGTCCCGGCTTAATTTGTT	15600
Db	85440	GGAACCAAGCCGTGAAGGGGTGCATCCAAACACACAGGGGTCCCGGCTTAATTTGTT	85499
Oy	15601	GGTTTTGAATATAGCCGTGATTCCTGCTCCGGTGGTGTCAACAGCTCAGCCTGCATTTGC	15660
Db	85500	GGTTTTGAATATAGCCGTGATTCCTGCTCCGGTGGTGTCAACAGCTCAGCCTGCATTTGC	85559
Oy	15661	CCATAGTAATTAATCTTTATATGCATGTGACCCCATGTGATCGCGGCAATGGCGAGCA	15720
Db	85560	CCATAGTAATTAATCTTTATATGCATGTGACCCCATGTGATCGCGGCAATGGCGAGCA	85619
Oy	15721	CAGGCCATATGCTGGCGGCGCAAAAGGCCGGAAGATTAGCTGCGATCGTCTGCGCGG	15780
Db	85620	CAGGCCATATGCTGGCGGCGCAAAAGGCCGGAAGATTAGCTGCGATCGTCTGCGCGG	85679
Oy	15781	TCGCTGTCATCTTGATGACCTTCCGATACCGTCTCTCTTGATTCATTTAGGACGGTCC	15840
Db	85680	TCGCTGTCATCTTGATGACCTTCCGATACCGTCTCTCTTGATTCATTTAGGACGGTCC	85739
Oy	15841	GAAAGGGCGTGAAGCATTTCCGGCGCCGAGCATGGCAACCGCATTTGCGCACTCAAGG	15900
Db	85740	GAAAGGGCGTGAAGCATTTCCGGCGCCGAGCATGGCAACCGCATTTGCGCACTCAAGG	85799

OY	15901	CGGAGCGCGACACACGCGCGACACACCGGACAAGACATCTTTCCGATGAGACGCAACTA	15960
Db	85800	CGGAGCGCGACACACGCGCGGACACACCGGACAAGACATCTTTCCGATGAGACGCAACTA	85859
OY	15961	AAGACCGAGCGCGGTGAACGGAAATTGATGGTAGGGAATTCCTTATCTTCCCAAGTAC	16020
Db	85860	AAGACCGAGCGCGGTGAACGGAAATTGATGGTAGGGAATTCCTTATCTTCCCAAGTAC	85919
OY	16021	TTGCTCTTTCTTACGGCTCCGACAGCGCGCCCTGGCTTGACACAGCCTGCTCTTCCA	16080
Db	85920	TTGCTCTTTCTTACGGCTCCGACAGCGCGCCCTGGCTTGACACAGCCTGCTCTTCCA	85979
OY	16081	GAGCGGAGTGGGATGTGTCTTAACTCAGAGTAGGCATTCATTACTGTTGACACCGTGGTTGA	16140
Db	85980	GAGCGGAGTGGGATGTGTCTTAACTCAGAGTAGGCATTCATTACTGTTGACACCGTGGTTGA	86039
OY	16141	TAATCATTAATTGGGAAACGACGGTGGTGTAGTGCACACACGAGCTGCTCTTGTCTCG	16200
Db	86040	TAATCATTAATTGGGAAACGACGGTGGTGTAGTGCACACACGAGCTGCTCTTGTCTCG	86099
OY	16201	TTCTGCCAAACAGCGCCGGGTACAGACACTATGGCTTTTGAGTCAAGCATTCTTG	16260
Db	86100	TTCTGCCAAACAGCGCCGGGTACAGACACTATGGCTTTTGAGTCAAGCATTCTTG	86159
OY	16261	AGGGCCATGTGCATACAGATGGGGCCCTTCTGATTTCCCGAGCGGCCATGTATTAAGTCG	16320
Db	86160	AGGGCCATGTGCATACAGATGGGGCCCTTCTGATTTCCCGAGCGGCCATGTATTAAGTCG	86219
OY	16321	GCAACGTTTAAACCCCATGTAAAGTTTCAAGTTCAATTTAAATGACACAACTCCGCCAT	16380
Db	86220	GCAACGTTTAAACCCCATGTAAAGTTTCAAGTTCAATTTAAATGACACAACTCCGCCAT	86279
OY	16381	GCCTGTGCAACAACATTAAGAAAGTGGACACAGTGTGGCTTGGCCGTCTCTGCAATGAA	16440
Db	86280	GCCTGTGCAACAACATTAAGAAAGTGGACACAGTGTGGCTTGGCCGTCTCTGCAATGAA	86339
OY	16441	CCCCGCGGATTAACATTACTTCTCTCCCATACGGTGGAGGAGTAGATACAGATGTGCTTCC	16500
Db	86340	CCCCGCGGATTAACATTACTTCTCTCCCATACGGTGGAGGAGTAGATACAGATGTGCTTCC	86399
OY	16501	CGTTGTTCCTCCGAGACACCGACACCCGCTCCAGACGGTCCCTCTGCTCATCTTCC	16560
Db	86400	CGTTGTTCCTCCGAGACACCGACACCCGCTCCAGACGGTCCCTCTGCTCATCTTCC	86459
OY	16561	CGCGGCACTCTGCTGACATCACTATACACATCATATTTGACACAGTAGCAAGTTTACG	16620
Db	86460	CGCGGCACTCTGCTGACATCACTATACACATCATATTTGACACAGTAGCAAGTTTACG	86519
OY	16621	GGCAGTGGAGCATTCCTCATGTATTTTGGACTGATGACGGGACACATGAATCCACGC	16680
Db	86520	GGCAGTGGAGCATTCCTCATGTATTTTGGACTGATGACGGGACACATGAATCCACGC	86579
OY	16681	ACAGTTCAGGGGGGGGACATCTCTCTGGAGTGTGGCGATCTCGCGAGCTCCCTCAATTAAG	16740
Db	86580	ACAGTTCAGGGGGGGGACATCTCTCTGGAGTGTGGCGATCTCGCGAGCTCCCTCAATTAAG	86639
OY	16741	CAGAGATTCGAACGCTTGAGCGCGCTGCGAAGGCCACAGCTCATAGTAATTTTCAAGATA	16800
Db	86640	CAGAGATTCGAACGCTTGAGCGCGCTGCGAAGGCCACAGCTCATAGTAATTTTCAAGATA	86699
OY	16801	GTTGTGTCAATGCCGTCAATGTGTGGTCTTCCAGGTTTTCACACAGATTTCCAGACTCCGT	16860
Db	86700	GTTGTGTCAATGCCGTCAATGTGTGGTCTTCCAGGTTTTCACACAGATTTCCAGACTCCGT	86759
OY	16861	CATTAACACATATCAAACTCTCTCGCATTTTCTGACAGGGCTGCAATTCGCCCTGAC	16920
Db	86760	CATTAACACATATCAAACTCTCTCGCATTTTCTGACAGGGCTGCAATTCGCCCTGAC	86819
OY	16921	AAACTCCGAGGAATCACTATGGGACAGCGCAAGAAACAGTCATATGATTAATCGGACACA	16980
Db	86820	AAACTCCGAGGAATCACTATGGGACAGCGCAAGAAACAGTCATATGATTAATCGGACACA	86879

QY	16981	ACNAGAGTGTCCGGAGACGTTTGGATATCAGAAAGCCACATATATCGACACCCGAGCCGC	17040
Db	86880	ACACAGGTGTCCGGAGCGTTTGGATCTCAGAAAGCCACATATATCGACACCCGAGCCGC	86939
QY	17041	TCGCAAAATTTGAACTCCGACGTTCCTCCAAAGTAAAAAAGATATACCTCAACACGCCC	17100
Db	86940	TCGCAAAATTTGAACTCCGACGTTCCTCCAAAGTAAAAAAGATATACCTCAACACGCCC	86999
QY	17101	TAGCAGAGTTCGCGACAGAAAGTCTTGAGTCTGTTTGATTTCCGTTTAAACGGAGAC	17160
Db	87000	TAGCAGAGTTCGCGACAGAAAGTCTTGAGTCTGTTTGATTTCCGTTTAAACGGAGAC	87059
QY	17161	TCTCAGTGGCGCCTTACCCCTCGGCGCCGCTGTCTCTCGAAACATCTCTGTCAAGCA	17220
Db	87060	TCTCAGTGGCGCCTTACCCCTCGGCGCCGCTGTCTCTCGAAACATCTCTGTCAAGCA	87119
QY	17221	ACTCGCATGGAACAGTATGCAACGATGTGGTGGATGAGTTACACAGATCGAGCC	17280
Db	87120	ACTGCATGGAACAGTATGCAACGATGTGGTGGATGAGTTACACAGATCGAGCC	87179
QY	17281	CACCGTAACCTCAGAGAGCAATTTGAAAGTCTGTATCTTTTCCCGACAGACGCCCGCCG	17340
Db	87180	CACCGTAACCTCAGAGAGCAATTTGAAAGTCTGTATCTTTTCCCGACAGACGCCCGCCG	87239
QY	17341	CTTCTCGCGCGGTGTACGTCCTCAATATCTGTGAGATCTCAGTCGATATATACATCT	17400
Db	87240	CTTCTCGCGCGGTGTACGTCCTCAATATCTGTGAGATCTCAGTCGATATATACATCT	87299
QY	17401	AATTTTCTTAAATTTCTGGGCAATGTGAACCGGTTTGACACACGCCACGCGGTGAGCAAA	17460
Db	87300	AATTTTCTTAAATTTCTGGGCAATGTGAACCGGTTTGACACACGCCACGCGGTGAGCAAA	87359
QY	17461	ATCTGCAAAATATCTTGTATTAATCTTATCATGACGCGACGTCTGCGTACACGGTTCACAG	17520
Db	87360	ATCTGCAAAATATCTTGTATTAATCTTATCATGACGCGACGTCTGCGTACACGGTTCACAG	87419
QY	17521	GACACGTATATAGTCTTGTCTCTGTCATCCATATTCACATCCGGGTTATCGCTTAGACTC	17580
Db	87420	GACACGTATATAGTCTTGTCTCTGTCATCCATATTCACATCCGGGTTATCGCTTAGACTC	87479
QY	17581	CAGGCGCTCGATGAGCAAGCTTTTAAATCCATATGCGGTCCGCGCATCTCGGTAATTA	17640
Db	87480	CAGGCGCTCGATGAGCAAGCTTTTAAATCCATATGCGGTCCGCGCATCTCGGTAATTA	87539
QY	17641	ATTACCTGTGACCGACGCGCTCAGTTTAAATATCCGAGACCCCAACACCCAGCGCTCCGTA	17700
Db	87540	ATTACCTGTGACCGACGCGCTCAGTTTAAATATCCGAGACCCCAACACCCAGCGCTCCGTA	87599
QY	17701	ACAAAAGAGTCTAGATCTGAAAGAAAGCCTTACTATATACGCCACGGGAAAACTCTGTA	17760
Db	87600	ACAAAAGAGTCTAGATCTGAAAGAAAGCCTTACTATATACGCCACGGGAAAACTCTGTA	87659
QY	17761	ACAAATGAAAAAATGTCTTCAGAAAAAGAGAGAAAACTGACAGACAGCAATCTAG	17820
Db	87660	ACAAATGAAAAAATGTCTTCAGAAAAAGAGAGAAAACTGACAGACAGCAATCTAG	87719
QY	17821	TCAACACGAAACCTTAAAGGCGGTCTGACCCATATCTTTTCCGCTTCCGAGGAGTGGG	17880
Db	87720	TCAACACGAAACCTTAAAGGCGGTCTGACCCATATCTTTTCCGCTTCCGAGGAGTGGG	87779
QY	17881	GTTTCTCACAATGCGCTGAGCAAAAGCAAGATATATTAAGACAGGTGTGAGAGA	17940
Db	87780	GTTTCTCACAATGCGCTGAGCAAAAGCAAGATATATTAAGACAGGTGTGAGAGA	87839
QY	17941	AAACTTATTTGACAGGACAGGCAAAAGCAAGCTGTGACAGGTATACAGTATGTCTACTG	18000
Db	87840	AAACTTATTTGACAGGACAGGCAAAAGCAAGCTGTGACAGGTATACAGTATGTCTACTG	87899
QY	18001	GGCGCGATTCGCCGAGCGCGGCAAGACACTGTGCGCAAAATTTGAAATGACAGGGGAGT	18060
Db	87900	GGCGCGATTCGCCGAGCGCGGCAAGACACTGTGCGCAAAATTTGAAATGACAGGGGAGT	87959
QY	18061	TGTGGGACAGGGCTCGGCTTCCGGAGTGGGGAAGCCCTCTAGTGTGAGAGACGATAGCG	18120

Db 87960 TGTGGACACGGCTCCCTTCCGAGTGGAGACGCTCCTAGGTGAGAGACCATAGGC 88019
Qy 18121 GGGTGGAAATCGCGTTCGCTGTGGCGGGGTGGCTGACACCGCATCATGATATTTGGCGAG 18180
Db 88020 GGGTGGAAATCGCGTTCGCTGTGGCGGGGTGGCTGACACCGCATCATGATATTTGGCGAG 88079
Qy 18181 CGAAACACGCGCAGACACTCGCGCGTGTGTAATTAATATCCACCGGCTCCAGGACCTCC 18240
Db 88080 CGAAACACGCGCAGACACTCGCGCGTGTGTAATTAATATCCACCGGCTCCAGGACCTCC 88139
Qy 18241 GTTACCACAGAGAGGTGGAACGTAACCATATCCGAATGTAATCCAGACCGCTC 18300
Db 88140 GTTACCACAGAGAGGTGGAACGTAACCATATCCGAATGTAATCCAGACCGCTC 88199
Qy 18301 TGGTAAATCATCAACCCGATATGATCTCTCCACGCACTTTAGCATGCTCTG 18360
Db 88200 TGGTAAATCATCAACCCGATATGATCTCTCCACGCACTTTAGCATGCTCTG 88259
Qy 18361 GTGAGGAAACATATCTGTGGGGTATGCGGCAACAGGGCTGTTCGGCCGAATGCCCG 18420
Db 88260 GTGAGGAAACATATCTGTGGGGTATGCGGCAACAGGGCTGTTCGGCCGAATGCCCG 88319
Qy 18421 ACAACGTGCTTGCAGTGGTGGCTTTGGCGCGGCAACAGGCGAAGCGCTGGGGCA 18480
Db 88320 ACAACGTGCTTGCAGTGGTGGCTTTGGCGCGGCAACAGGCGAAGCGCTGGGGCA 88379
Qy 18481 CCGGACCTCCATGTTCCCAACCAACCGCCATAGTAAATAAACACAGCGCTAGCATCA 18540
Db 88380 CCGGACCTCCATGTTCCCAACCAACCGCCATAGTAAATAAACACAGCGCTAGCATCA 88439
Qy 18541 AACAGTCTCCGCTGCGCTCCCAACAGGCGCTTGTACTCTCATCCGCGCACCGAGATACG 18600
Db 88440 AACAGTCTCCGCTGCGCTCCCAACAGGCGCTTGTACTCTCATCCGCGCACCGAGATACG 88499
Qy 18601 GAATCGGGGTTTACCTGCTGGGTGACGACAGACATGCGCGCGGTGGCATCCGCTTC 18660
Db 88500 GAATCGGGGTTTACCTGCTGGGTGACGACAGACATGCGCGCGGTGGCATCCGCTTC 88559
Qy 18661 GTTACAGAGCGGGCAAGATCTAACAAGATCGGCAACAGGCGAATTAACGCGGACCTGTT 18720
Db 88560 GTTACAGAGCGGGCAAGATCTAACAAGATCGGCAACAGGCGAATTAACGCGGACCTGTT 88619
Qy 18721 AGGCGCGCGCGCGAGATGTTCTCCATGATGATATCTTGACGCGTGTGACTGGGG 18780
Db 88620 AGGCGCGCGCGCGAGATGTTCTCCATGATGATATCTTGACGCGTGTGACTGGGG 88679
Qy 18781 TATAGCGTGGCCAAACGATCTTACATTCCTGAGCGTCAATCGTCTGTTACCGGCTG 18840
Db 88680 TATAGCGTGGCCAAACGATCTTACATTCCTGAGCGTCAATCGTCTGTTACCGGCTG 88739
Qy 18841 CCGTATGCTTTAAATGACAATAGTCAGATACATGTTTCTCTCATGCTCAGAGAGCGC 18900
Db 88740 CCGTATGCTTTAAATGACAATAGTCAGATACATGTTTCTCTCATGCTCAGAGAGCGC 88799
Qy 18901 ACCCGCGCGCTTAAATGATTCGCAAGGTAAAGAACACAGTCTTTCTCATCCAGCA 18960
Db 88800 ACCCGCGCGCTTAAATGATTCGCAAGGTAAAGAACACAGTCTTTCTCATCCAGCA 88859
Qy 18961 ATGATTCAGAGATGCTTATCTATTCGCAACAATGAGCAACATGCGCTCAGGCGAGA 19020
Db 88860 ATGATTCAGAGATGCTTATCTATTCGCAACAATGAGCAACATGCGCTCAGGCGAGA 88919
Qy 19021 CGGCGGGTTTACGCGAGTACGCTGCGCTCTTCGCGCATCTGTGAGGGTCCGCTGC 19080
Db 88920 CGGCGGGTTTACGCGAGTACGCTGCGCTCTTCGCGCATCTGTGAGGGTCCGCTGC 88979
Qy 19081 AATAACTGGCTTAAAAATATATCCCGCGCGTACTTACATGACACTTGG 19140
Db 88980 AATAACTGGCTTAAAAATATATCCCGCGCGTACTTACATGACACTTGG 89039
Qy 19141 GGCACAGCGCTAGGGCTGGAGGAGCGGACACGACGCTATTTTCATCTCTAGGCGCG 19200
Db 89040 GGCACAGCGCGTAGGGCTGGAGGAGCGGACACGACGCTATTTTCATCTCTAGGCGCG 89099
Qy 19201 CCTACTAGCGGAATCTGGGCTGTACAAAATCCACCGAGCCGCGCAATGTACCATGAG 19260
Db 89100 CCTACTAGCGGAATCTGGGCTGTACAAAATCCACCGAGCCGCGCAATGTACCATGAG 89159
Qy 19261 TCAATTCATCTGACAGATCACCAGATGACAGAGGACCTGGGGTCTTTTACTGAGACCG 19320
Db 89160 TCAATTCATCTGACAGATCACCAGATGACAGAGGACCTGGGGTCTTTTACTGAGACCG 89219
Qy 19321 GCGGACCGCCCAAGGTAAAGTACTGCTGTGGGGAACAGTGTCCGGGAACGGGAG 19380
Db 89220 GCGGACCGCCCAAGGTAAAGTACTGCTGTGGGGAACAGTGTCCGGGAACGGGAG 89279
Qy 19381 ACCGGCGAGTCTGCGCAGTAGACCCATACATAGAAATTTGAGATTTGACAGAGATC 19440
Db 89280 ACCGGCGAGTCTGCGCAGTAGACCCATACATAGAAATTTGAGATTTGACAGAGATC 89339
Qy 19441 GCACAGCCCGTGTGGTGGTCCCTCTGCGCTGCTTCCCTGGCGACGACCGTGTGC 19500
Db 89340 GCACAGCCCGTGTGGTGGTCCCTCTGCGCTGCTTCCCTGGCGACGACCGTGTGC 89399
Qy 19501 TGGTCTGTATCCACATACATCCCGAGCTCATTTGCGCAAAAAGAGCGCTCTCAC 19560
Db 89400 TGGTCTGTATCCACATACATCCCGAGCTCATTTGCGCAAAAAGAGCGCTCTCAC 89459
Qy 19561 ACCCGTTTAAATCTCACACAGGTTCTCTGCTCGGCGTTAGCGGCGCATCCACT 19620
Db 89460 ACCCGTTTAAATCTCACACAGGTTCTCTGCTCGGCGTTAGCGGCGCATCCACT 89519
Qy 19621 GAGTTTGGAGCCCATCTATACGCTGCCATAGAAACATCTGTAACCGGTTGG 19680
Db 89520 GAGTTTGGAGCCCATCTATACGCTGCCATAGAAACATCTGTAACCGGTTGG 89579
Qy 19681 GGTCTTGGGCGTTATGCAATCGTACCCCTGACGCTCGGGACGCTGTTCGCTACCA 19740
Db 89580 GGTCTTGGGCGTTATGCAATCGTACCCCTGACGCTCGGGACGCTGTTCGCTACCA 89639
Qy 19741 GCGACCCAAATTAATAAATCTGTAATAGCGGCCCAAAATGAGATGATCTGTGAT 19800
Db 89640 GCGACCCAAATTAATAAATCTGTAATAGCGGCCCAAAATGAGATGATCTGTGAT 89699
Qy 19801 GGGGTGTGCAACCGTGGCAACCTGGCGGCGCTGTCATATGCGGCGCGCGCGCT 19860
Db 89700 GGGGTGTGCAACCGTGGCAACCTGGCGGCGCTGTCATATGCGGCGCGCGCGCT 89759
Qy 19861 CAGCTCTCGCGGAGCGGAGAGGAGGAGGCGCTCCCTGGCTCAAGCCCATGAGCGCAG 19920
Db 89760 CAGCTCTCGCGGAGCGGAGAGGAGGAGGCGCTCCCTGGCTCAAGCCCATGAGCGCAG 89819
Qy 19921 CCGCTCTAATTAATTTAGAGCGGTCTCCGAATGACTATCTAAGATGACAGCATACAA 19980
Db 89820 CCGCTCTAATTAATTTAGAGCGGTCTCCGAATGACTATCTAAGATGACAGCATACAA 89879
Qy 19981 GGGGATCCAGCGGCGGCTCAAGTAAATAAATCTTCTCCGCAAAACGCGTGTGTG 20040
Db 89880 GGGGATCCAGCGGCGGCTCAAGTAAATAAATCTTCTCCGCAAAACGCGTGTGTG 89939
Qy 20041 CCGGCGCATGCTCTGTTAAACCCAGCGCTTTTCCGGAAGCAACCTTACAGCTTTTCC 20100
Db 89940 CCGGCGCATGCTCTGTTAAACCCAGCGCTTTTCCGGAAGCAACCTTACAGCTTTTCC 89999
Qy 20101 GGCATCTCGACACGTTGTGCTGGCTGACATTCAGATTCATTCAGGCGATACGCA 20160
Db 90000 GGCATCTCGACACGTTGTGCTGGCTGACATTCAGATTCATTCAGGCGATACGCA 90059
Qy 20161 CCAAGGTGATGACATGACATACCTGGGTGACATGATTCCTAAAGCTCCTTTCT 20220
Db 90060 CCAAGGTGATGACATGACATACCTGGGTGACATGATTCCTAAAGCTCCTTTCT 90119
Qy 20221 CGTGACACCAACAAGTGTGGGAAAGTGTGCTTCCAAATTTGAAATATCATC 20280
Db 90120 CGTGACACCAACAAGTGTGGGAAAGTGTGCTTCCAAATTTGAAATATCATC 90179

Db	92340	CCCCGAGGCGATGGTCGTCCTACCAAACTGCGGCTTCTCTCCGGGTCCGACTGCTCCC	92399
Qy	22501	CGTGTGTGATGAGACGGCAGCTTCATTTCCGCAATGTTAACTCCAAACATCTCAGGGGTGT	22560
Db	92400	CGTGGGTGATGAGACGGCAGCTTCATTTCCGCAATGTTAACTCCAAACATCTCAGGGGTGT	92459
Qy	22561	GTGTGACGTGTGTTCCAGAGGAGGTGTTTCGAAAGCTAAAGCTAACCTGTGCTGCTATGT	22620
Db	92460	GTGTGAACTGTGTTCCAGAGGAGGTGTTTCGAAAGCTAAAGCTAACCTGTGCTGCTATGT	92519
Qy	22621	CAGAAATATACATCTCAGCGGCGCAGTGCATTTTAAAGCTGAGACCGAGACGGCCGGCT	22680
Db	92520	CAGAAATATACATCTCAGCGGCGCAGTGCATTTTAAAGCTGAGACCGAGACGGCCGGCT	92579
Qy	22681	CCCCCAGCGTGGAGAGACAGCTTAAGGACGCGGGGCCCTGCGCTGCGCGCTGATCTGTATA	22740
Db	92580	CCCCCAGCGTGGAGAGACAGCTTAAGGACGCGGGGCCCTGCGCTGCGCGCTGATCTGTATA	92639
Qy	22741	CGCCTTTCTTAACGATGCGCTTAATGTGTCGTAACCTGCTAATGCTGCGCAAGCGCAT	22800
Db	92640	CGCCTTTCTTAACGATGCGCTTAATGTGTCGTAACCTGCTAATGCTGCGCAAGCGCAT	92699
Qy	22801	CGACGTCACCCCTGGGGCGGTATGAAACGAGACAGGCGTAAAGGGAATTAACAC	22860
Db	92700	CGACGTCACCCCTGGGGCGGTATGAAACGAGACAGGCGTAAAGGGAATTAACAC	92759
Qy	22861	CCTAAAAAGAGAGAGAAATGGCAAAACAGACAGACAGCGCTTCATATGTTCAACCTTT	22920
Db	92760	CCTAAAAAGAGAGAGAAATGGCAAAACAGACAGACAGCGCTTCATATGTTCAACCTTT	92819
Qy	22921	TAAATGAGCTCTGGCCCGGAAAAATGAGTAACATGGGACACATGGGACTACAGATCAT	22980
Db	92820	TAAATGAGCTCTGGCCCGGAAAAATGAGTAACATGGGACACATGGGACTACAGATCAT	92879
Qy	22981	ATGACAGGATGTGACATATTTGAAATTTATCAGCTCAACAAAAAGTTCCACCTGTGGCACT	23040
Db	92880	ATGACAGGATGTGACATATTTGAAATTTATCAGCTCAACAAAAAGTTCCACCTGTGGCACT	92939
Qy	23041	CGTATACGACAAAGGACACGCGTTTGGGGGGCGGACCGAACAGGGGGGATGTTTAT	23100
Db	92940	CGTATACGACAAAGGACACGCGTTTGGGGGGCGGACCGAACAGGGGGGATGTTTAT	92999
Qy	23101	TGACCTTGAATCTGTCGGCCCTGGCCCTGCGCAAAAACTGCTGAGATGTCGCGACGTCCAC	23160
Db	93000	TGACCTTGAATCTGTCGGCCCTGGCCCTGCGCAAAAACTGCTGAGATGTCGCGACGTCCAC	93059
Qy	23161	CATGTCACAGTCTCGGCTCTTGAAGCAATTAACAGAGTCTCTATCTCCACGGCTTCGCG	23220
Db	93060	CATGTCACAGTCTCGGCTCTTGAAGCAATTAACAGAGTCTCTATCTCCACGGCTTCGCG	93119
Qy	23221	AAAGAGCCGCTGATGTATGCGAGCGAGGGGATTCGTCGCGGAGATCANTGGTGTGTA	23280
Db	93120	AAAGAGCCGCTGATGTATGCGAGCGAGGGGATTCGTCGCGGAGATCANTGGTGTGTA	93179
Qy	23281	CAGCAAGTGGGGGCCCTGTGTGTGTAGACAGCTGTCGCTGGAGATGTAGTCTTAGCCAG	23340
Db	93180	CAGCAAGTGGGGGCCCTGTGTGTGTGTAGACAGCTGTCGCTGGAGATGTAGTCTTAGCCAG	93239
Qy	23341	GCACACCCCGCATGATTCGCGAAGGGGAAAAAGTCCATAGAGTAAATGAACCTTAT	23400
Db	93240	GCACACCCCGCATGATTCGCGAAGGGGAAAAAGTCCATAGAGTAAATGAACCTTAT	93299
Qy	23401	AAAGTATATCCCTTGATTAACAGAGACAGACACCTTCTGCGCCGCGGTGGCCCTT	23460
Db	93300	AAAGTATATCCCTTGATTAACAGAGACAGACACCTTCTGCGCCGCGGTGGCCCTT	93359
Qy	23461	GGGCACTGGGGAATGACAGCAATCATCTTCTGCGCAGAGGTAGCGTCTGCACATATTTT	23520
Db	93360	GGGCACTGGGGAATGACAGCAATCATCTTCTGCGCAGAGGTAGCGTCTGCACATATTTT	93419
Qy	23521	TTTGSCATTAATCATTAAGTCCCGCATTAACCGCAAAAAATTAAGTTAGATATGTGGC	23580
Db	93420	TTTGSCATTAATCATTAAGTCCCGCATTAACCGCAAAAAATTAAGTTAGATATGTGGC	93479
Qy	23581	ATACACTTGGCCGTGAGTGTTCATGAGCTACCTGTCGGCGTAATAGTGGTACAGTC	23640
Db	93480	ATACACTTGGCCGTGAGTGTTCATGAGCTACCTGTCGGCGTAATAGTGGTACAGTC	93539
Qy	23641	GTGATTTGCAACTCTTTTAACATAGGCTTCGATGTTAAAGTTTACAGACTCTGCGCAT	23700
Db	93540	GTGATTTGCAACTCTTTTAACATAGGCTTCGATGTTAAAGTTTACAGACTCTGCGCAT	93599
Qy	23701	ACCCAAAAATGTGAAGAGAAATGTTAAACCTCCATGCGGGAGCTCAATAGTCGAC	23760
Db	93600	ACCCAAAAATGTGAAGAGAAATGTTAAACCTCCATGCGGGAGCTCAATAGTCGAC	93659
Qy	23761	CTCATGAGAGCTCTGCTGACAGGAAATTTGACTGGGGAACCATCTGTTCTGCATGCTC	23820
Db	93660	CTCATGAGAGCTCTGCTGACAGGAAATTTGACTGGGGAACCATCTGTTCTGCATGCTC	93719
Qy	23821	CTGGGTGAGTGTCTAAAAACCCAGGGTGTGCGCTCCGCTACAGAAACCGATCTGGGACTC	23880
Db	93720	CTGGGTGAGTGTCTAAAAACCCAGGGTGTGCGCTCCGCTACAGAAACCGATCTGGGACTC	93779
Qy	23881	CATGGGGCGGTTACTATGACAGGCAAAACATACCTTGTGCGCTCACCGCTGCGCTTT	23940
Db	93780	CATGGGGCGGTTACTATGACAGGCAAAACATACCTTGTGCGCTCACCGCTGCGCTTT	93839
Qy	23941	TGTACGAGTATGACTCGGCCCTCTGTGAAGAGATGTGTACCAACAGCATGATCTAAG	24000
Db	93840	TGTACGAGTATGACTCGGCCCTCTGTGAAGAGATGTGTACCAACAGCATGATCTAAG	93899
Qy	24001	CACCTGAGGGCAATTAAGTTTCTGCTTCTCAATTCGACATTAATACGATGATGTTT	24060
Db	93900	CACCTGAGGGCAATTAAGTTTCTGCTTCTCAATTCGACATTAATACGATGATGTTT	93959
Qy	24061	AACTAGGCTGTATCCGGTCCAGAGCAAGTCTCAATTAACCTGCGCCGCTGCGCTGEC	24120
Db	93960	AACTAGGCTGTATCCGGTCCAGAGCAAGTCTCAATTAACCTGCGCCGCTGCGCTGEC	94019
Qy	24121	TCCTCCTTTAAAAAGAAATTAAGCGACTGACTGTGTCTACAAATGAGGCCCGCACCG	24180
Db	94020	TCCTCCTTTAAAAAGAAATTAAGCGACTGACTGTGTCTACAAATGAGGCCCGCACCG	94079
Qy	24181	GGCGGCTCCACTGTATATGGGAGTAAATGAAGGCCGTCAAAAAATCTGTATGTCG	24240
Db	94080	GGCGGCTCCACTGTATATGGGAGTAAATGAAGGCCGTCAAAAAATCTGTATGTCG	94139
Qy	24241	TCCTTCAGGGGTTCTGGAATTAAGCAACAGTCCGCTAACAGGCGCACCGTTGCAAG	24300
Db	94140	TCCTTCAGGGGTTCTGGAATTAAGCAACAGTCCGCTAACAGGCGCACCGTTGCAAG	94199
Qy	24301	TCACAGGCTTCATCTCTTTAAAAAAGTACGCTTGGCTTCAAGATCTCTTCTGCTG	24360
Db	94200	TCACAGGCTTCATCTCTTTAAAAAAGTACGCTTGGCTTCAAGATCTCTTCTGCTG	94259
Qy	24361	GTGACCTTCGATGATATGTCGCAAAAGCAAGGATTAATGCTTGGGTGATCCCGTAAGC	24420
Db	94260	GTGACCTTCGATGATATGTCGCAAAAGCAAGGATTAATGCTTGGGTGATCCCGTAAGC	94319
Qy	24421	TGAGAGGTTCCGGCCGTTGGGATCAGCGCCAAAAAAGTGGTGTAAAAATTCATGCTGG	24480
Db	94320	TGAGAGGTTCCGGCCGTTGGGATCAGCGCCAAAAAAGTGGTGTAAAAATTCATGCTGG	94379
Qy	24481	GCAATGCTGCGCCCGCATGCTCTCCATCTCTCAAGAGGAGGTGGAGCGCTTAACGCCG	24540
Db	94380	GCAATGCTGCGCCCGCATGCTCTCCATCTCTCAAGAGGAGGTGGAGCGCTTAACGCCG	94439
Qy	24541	TCACAGTTCGCAAGTGAACACACCTGAGGCAATTCACCTCCCATCCAGAGAAC	24600
Db	94440	TCACAGTTCGCAAGTGAACACACCTGAGGCAATTCACCTCCCATCCAGAGAAC	94499
Qy	24601	GGAGTCCCTCGCCAGTAAAAACAATCTCATGCTGTTTGGACCGCGGTAAAAATACATT	24660
Db	94500	GGAGTCCCTCGCCAGTAAAAACAATCTCATGCTGTTTGGACCGCGGTAAAAATACATT	94559

QY	24661	GCCTGAAAAATCTCCACGTCACGCTTGCGGCGTCTCGGCGCTCAAGGTAGCCAAAGCCCACT	247120
Db	94560	GCCTGAAAAATCTCCACGTCACGCTTGCGGCGTCTCGGCGCTCAAGGTAGCCAAAGCCCACT	94619
QY	24721	TTCCGCAAAACGTCGCGGCGCAGTCCTTGAGAGCCAAATCCCATTTGATCGTTCCCTCGGCGC	24780
Db	94620	TTCCGCAAAACGTCGCGGCGCAGTCCTTGAGAGCCAAATCCCATTTGATCGTTCCCTCGGCGC	94679
QY	24781	CGCCTTAACGCTCTCGTAGGCGGCGCTCCGCCCAAAATCAGACGATTTGACATGATTACT	24840
Db	94680	CGCCTTAACGCTCTCGTAGGCGGCGCTCCGCCCAAAATCAGACGATTTGACATGATTACT	94739
QY	24841	GGCGGCTTCACAGGCATCTAGAGACGTTCAAACCAATGTTACATCCCCCTCCAGGC	24900
Db	94740	GGCGGCTTCACAGGCATCTAGAGACGTTCAAACCAATGTTACATCCCCCTCCAGGC	94799
QY	24901	TTCCACACCAACCTCCCGCTGTGAGGCGTAGAGCACTTTGGTAGGCTATGTTTGCCAAAG	24960
Db	94800	TTCCACACCAACCTCCCGCTGTGAGGCGTAGAGCACTTTGGTAGGCTATGTTTGCCAAAG	94859
QY	24961	TTTACACAGGAAGCCTGACCCCTGCGGGTTGCTGCACATTTCCGCACAGAGATTTAAGACAG	25020
Db	94860	TTTACACAGGAAGCCTGACCCCTGCGGGTTGCTGCACATTTCCGCACAGAGATTTAAGACAG	94919
QY	25021	TTTATGCGCGTGCCTTGCGTCTCAACACAGTGTGTTGTTGAGCGCCTCTTTAGCAGG	25080
Db	94920	TTTATGCGCGTGCCTTGCGTCTCAACACAGTGTGTTGTTGAGCGCCTCTTTAGCAGG	94979
QY	25081	ACGTAGGGAGCTGGCGGCTTAAATAGACAGTGTAAATAAAGGCAATCATCATGATTTTAC	25140
Db	94980	ACGTAGGGAGCTGGCGGCTTAAATAGACAGTGTAAATAAAGGCAATCATCATGATTTTAC	95039
QY	25141	GGCAAGAGGTAGAGTGTGTTGCCAGCGGCCACTAGTCTGTGATTAATCTCAAAATTCG	25200
Db	95040	GGCAAGAGGTAGAGTGTGTTGCCAGCGGCCACTAGTCTGTGATTAATCTCAAAATTCG	95089
QY	25201	GCACCGTAGAGTTTAAAGAAATTTGGCGCACCTCTGGGCGCAAAAGGCGCACGCGCA	25260
Db	95100	GCACCGTAGAGTTTAAAGAAATTTGGCGCACCTCTGGGCGCAAAAGGCGCACGCGCA	95159
QY	25261	TCCTGGGTTTATCTGTCACATCCGAAAAAAGCTCCGGCACACACAGCGCCTCGAAACAGG	25320
Db	95160	TCCTGGGTTTATCTGTCACATCCGAAAAAAGCTCCGGCACACACAGCGCCTCGAAACAGG	95219
QY	25321	TTGTGACACCGCTCTGATTTCTCCGGCATCTTCGGGTTCAAAAATCACAATCTGATGA	25380
Db	95320	TTGTGACACCGCTCTGATTTCTCCGGCATCTTCGGGTTCAAAAATCACAATCTGATGA	95379
QY	25381	TTGCCATGTTCATGTAGAGGCGGCGGACCAACAGAGAGATTTGTTATTCGTGGAATAC	25440
Db	95380	TTGCCATGTTCATGTAGAGGCGGCGGACCAACAGAGAGATTTGTTATTCGTGGAATAC	95399
QY	25441	CCAACGTAAGGCGTTTATTAATTTTAAACAGCTGGTATGTTCTGTGTTCCGCAAAAGAC	25500
Db	95340	CCAACGTAAGGCGTTTATTAATTTTAAACAGCTGGTATGTTCTGTGTTCCGCAAAAGAC	95399
QY	25501	GAGACATCTATCCCCACGCTGACTTGTAGCGAAGAGGGGACATTTCTCATGAAGT	25560
Db	95400	GAGACATCTATCCCCACGCTGACTTGTGTAGCGAAGAGGGGACATTTCTCATGAAGT	95459
QY	25561	GCCTTGAAGGTTTTGTTCTTGCGGCGCATGCGAGAGGCTTTTAAATATAACAGTACAAAGC	25620
Db	95460	GCCTTGAAGGTTTTGTTCTTGCGGCGCATGCGAGAGGCTTTTAAATATAACAGTACAAAGC	95519
QY	25621	TGACCTCCGGGAAGCCCGGCTGACTTAATATACAGGCTTGGCAGCACACAATCTGTGAC	25680
Db	95520	TGACCTCCGGGAAGCCCGGCTGACTTAATATACAGGCTTGGCAGCACACAATCTGTGAC	95579
QY	25681	GAGATGTAATGGAACGCGTAAACCAACAGGTACATCTCATCCAGCTCCGTTTCGGCTTCC	25740
Db	95580	GAGATGTAATGGAACGCGTAAACCAACAGGTACATCTCATCCAGCTCCGTTTCGGCTTCC	95639

QY	25741	ACACAGGTGCTGAGGGCTCTCCCGCAACACGGAATTTTATATACACTGACAGGCCACAAAA	25800
Db	95640	ACCGAGGTGTGAGGGCTCTCCCGCAACACGGAATTTTATACACTGACAGGCCACAAAA	95659
QY	25801	ACACCAACCCMCATAAACATCTGGGACGCTTTCAAAAATGGGTGAACACCCAGGGTT	25860
Db	95700	ACACCAACCCCTCATTAACATCTGGGACGCTTTCAAAAATGGGTGAACACCCCTGGGTT	95759
QY	25861	CTCAGCAGTACGTATCTGTAACCACTAACGGCAGACAGGTAGCCGCACTTAACGAATTT	25920
Db	95760	CTCAGCAGCAGTACGTATCTGTAACCACTAACGGCAGACAGGTAGCCGCACTTAACGAATTT	95819
QY	25921	GTGTATGCTCTTGCTCTCTCTTAAAGTCCGTGTAAAGACCGTCAAGGGCCGCTTGCTTTT	25980
Db	95820	GTGTATGCTCTTGCTCTCTCTTAAAGTCCGTGTAAAGACCGTCAAGGGCCGCTTGCTTTT	95879
QY	25981	GACATTAACGGGCGCAACCTGCTGGCTTAGGCTTCCCGCAATACCGCGAGATAGTCTGC	26040
Db	95880	GACATTAACGGGCGCAACCTGCTGGCTTAGGCTTCCCGCAATACCGCGAGATAGTCTGC	95939
QY	26041	ACCGTAAACCAAGCACCTGTCTCCATTTATCTGTGCCAAAGAGACCGGTTAGTAAATTG	26100
Db	95940	ACCGTAAACCAAGCACCTGTCTCCATTTATCTGTGCCAAAGAGACCGGTTAGTAAATTG	95999
QY	26101	GCCCTCTATGTGCCATCCAACTGTTCCTTTAAAGATTCACGAGTATTTGGCGCATCGT	26160
Db	96000	GCCCTCTATGTGCCATCCAACTGTTCCTTTAAAGATTCACGAGTATTTGGCGCATCGT	96059
QY	26161	TCAGGGTCAAGGGCTGAGCTACACCCCGCATTCGCGGCGGTACTGAGGGTTAAAGT	26220
Db	96060	TCAGGGTCAAGGGCTGAGCTACACCCCGCATTCGCGGCGGTACTGAGGGTTAAAGT	96119
QY	26221	TTGGCAATTTTGGCCGAGAGAAAGATTCGCTGTCAATTGTAAAGAAATAGCTTCC	26280
Db	96120	TTGGCAATTTTGGCCGAGAGAAAGATTCGCTGTCAATTGTAAAGAAATAGCTTCC	96179
QY	26281	AAGACCCCGGATTGGAAACAACTCCGTAAATTTTAAACACCGGTAAAGCAGCGCTTTAA	26340
Db	96180	AAGACCCCGGATTGGAAACAACTCCGTAAATTTTAAACACCGGTAAAGCAGCGCTTTAA	96239
QY	26341	AGTAAAGGCTTTGAAAAGATGGTTGTAAACCGGAAGCAGCGCTCCAACTGTGCAACATA	26400
Db	96240	AGTAAAGGCTTTGAAAAGATGGTTGTAAACCGGAAGCAGCGCTCCAACTGTGCAACATA	96299
QY	26401	CGCGGAACGCAAGCCCTATTTATATACAGGTATCTGACAGCTGAATGTATTTGGTCCGA	26460
Db	96300	CGCGGAACGCAAGCCCTATTTATATACAGGTATCTGACAGCTGAATGTATTTGGTCCGA	96359
QY	26461	TCAGCGCGCTGTAAAAATCCCTCAATTTGGCAGCTATTTACAAATTCCTTTACAGACT	26520
Db	96360	TCAGCGCGCTGTAAAAATCCCTCAATTTGGCAGCTATTTACAAATTCCTTTACAGACT	96419
QY	26521	TAAAAAACCCCAAGTCCTAAGGGCCGGTCTATTTTACCCTAAATGTAGTTAAGCAAACT	26580
Db	96420	TAAAAAACCCCAAGTCCTAAGGGCCGGTCTATTTTACCCTAAATGTAGTTAAGCAAACT	96479
QY	26581	AAATAGACAGATGGGCGGGGAAAAGGCTCGTCCGCGAGCGTGAAGGGCATGAGTCTCTA	26640
Db	96480	AAATAGACAGATGGGCGGGGAAAAGGCTCGTCCGCGAGCGTGAAGGGCATGAGTCTCTA	96539
QY	26641	AATCCACAAACATGTCTACTAGGAAGCGCTAAGGCCAATATGTGTAAACACGGGCTCTTGG	26700
Db	96540	AATCCACAAACATGTCTACTAGGAAGCGCTAAGGCCAATATGTGTAAACACGGGCTCTTGG	96599
QY	26701	CGACTAGCTGGCCCTTTAACGCAGAGGTACCTTTGGTGAACAAACGTACTGTGGACGCTT	26760
Db	96600	CGACTAGCTGGCCCTTTAACGCAGAGGTACCTTTGGTGAACAAACGTACTGTGGACGCTT	96659
QY	26761	GAACCAAGGGCCGACCGGGGCAAGAAACGTATGAAGCGAGCGCGTTTCCACAAATCTT	26820
Db	96660	GAACCAAGGGCCGACCGGGGCAAGAAACGTATGAAGCGAGCGCGTTTCCACAAATCTT	96719
QY	26821	CAAAATGGGTATGGCTCAAGTAGACCCGCTCTGTTGGCCGTACCAAAACACACGCTATTTC	26880

Db 96720 CAAAATTTGGGTATGGGTCTCAAGTAGACCGCTCTGCGCGGTACCAAAACACAGCTATTTC 96779
Qy 26881 TGTGGTCTGGGGGAGAGATCCGCGTCCATCTTAGACAGTCCGGCAGAGAGTATGGCG 26940
Db 96780 TGTGGTCTGGGGGAGAGATCCGCGTCCATCTTAGACAGTCCGGCAGAGAGTATGGCG 96839
Qy 26941 TGAATAACATGTCATATGAGAGACCCAGATGTCAGTCTGTTTAAAGAAACAGGTAGGTGC 27000
Db 96840 TGAATAACATGTCATATGAGAGACCCAGATGTCAGTCTGTTTAAAGAAACAGGTAGGTGC 96899
Qy 27001 CCGAGGTTCTGTGTAACATGTCATATGAGAGACCCAGATGTCAGTCTGTTTAAAGAAACAGGTAGGTGC 27060
Db 96900 CCGAGGTTCTGTGTAACATGTCATATGAGAGACCCAGATGTCAGTCTGTTTAAAGAAACAGGTAGGTGC 96959
Qy 27061 ATGTAGCGAGACAGATATAAAATCCATCTTGTGAGCTCCACCCAGTGGTGTGACA 27120
Db 96960 ATGTAGCGAGACAGATATAAAATCCATCTTGTGAGCTCCACCCAGTGGTGTGACA 97019
Qy 27121 CCACATATTTAGAGACAGATCAAGAACACCTTAGAAAAATGCGCAGCGAGATACG 27180
Db 97020 CCACATATTTAGAGACAGATCAAGAACACCTTAGAAAAATGCGCAGCGAGATACG 97079
Qy 27181 AAACCGGTGAGAGGCGGGGCGAGTAGAGCGATCAAACTATTCAGTTGTACGT 27240
Db 97080 AAACCGGTGAGAGGCGGGGCGAGTAGAGCGATCAAACTATTCAGTTGTACGT 97139
Qy 27241 TTGCGTCCGTGCTTTCATGCGCTGCTCAATTCCTCCGACGCGGTGATTAACGTAGAC 27300
Db 97140 TTGCGTCCGTGCTTTCATGCGCTGCTCAATTCCTCCGACGCGGTGATTAACGTAGAC 97199
Qy 27301 AAGAACCGGGGCGGCTTTACAAATTAACGACAACTCTAGTGCACCGGATCCCTAC 27360
Db 97200 AAGAACCGGGGCGGCTTTACAAATTAACGACAACTCTAGTGCACCGGATCCCTAC 97259
Qy 27361 AACAGCTTAAACCTCGATGAGATTCACACTAAACACCTACCAACCGCAGACCTTTAA 27420
Db 97260 AACAGCTTAAACCTCGATGAGATTCACACTAAACACCTACCAACCGCAGACCTTTAA 97319
Qy 27421 GCATGCCAACCGTGACCGGGTTTTTAATTAATGATTCATTAATAATGACAAACCCCGTGGTTT 27480
Db 97320 GCATGCCAACCGTGACCGGGTTTTTAATTAATGATTCATTAATAATGACAAACCCCGTGGTTT 97379
Qy 27481 CATTATTCAAAAACCGCTGTGTTTTTTTAAATGAGATGCGCAGAGCTTCGCGAACCG 27540
Db 97380 CATTATTCAAAAACCGCTGTGTTTTTTTAAATGAGATGCGCAGAGCTTCGCGAACCG 97439
Qy 27541 TCATTACAGACCAACCAAGCAGAAAGCTCAACAGGATCTACTGAGGTTGTGAATG 27600
Db 97440 TCATTACAGACCAACCAAGCAGAAAGCTCAACAGGATCTACTGAGGTTGTGAATG 97499
Qy 27601 TTCTTAATACAGCTATTGCAAAAACACAGAGTCCCGAGCGGCTAAAGAACAGATTATC 27660
Db 97500 TTCTTAATACAGCTATTGCAAAAACACAGAGTCCCGAGCGGCTAAAGAACAGATTATC 97559
Qy 27661 TCGACAAACGCTGCATATTGGGCATGATTAACAGAAATACATCCATCCGTAACCTCAGTA 27720
Db 97560 TCGACAAACGCTGCATATTGGGCATGATTAACAGAAATACATCCATCCGTAACCTCAGTA 97619
Qy 27721 CGCGCTCGGGGATCCCGACCGACCAACCAATGGGTATCAGCACTTACCGTGGGTAGAC 27780
Db 97620 CGCGCTCGGGGATCCCGACCGACCAACCAATGGGTATCAGCACTTACCGTGGGTAGAC 97679
Qy 27781 AAATTTTACAGAAACCAACCGGCAATTAAGTAACCTAACCCTCCGAGTGGCTATTTA 27840
Db 97680 AAATTTTACAGAAACCAACCGGCAATTAAGTAACCTAACCCTCCGAGTGGCTATTTA 97739
Qy 27841 TCGACATGGGGAAGTGGGTCTCCGCTTCAGACGCGGTATTCCTATGATGTAATA 27900
Db 97740 TCGACATGGGGAAGTGGGTCTCCGCTTCAGACGCGGTATTCCTATGATGTAATA 97799
Qy 27901 AACTGCAACTGGCAGCAGCGGCTTATCCACCTGTCAGCAAGTGGCGCGGTG 27960
Db 97800 AACTGCAACTGGCAGCAGCGGCTTATCCACCTGTCAGCAAGTGGCGCGGTGCTG 97859
Qy 27961 TTACCGGCAACCAAGATTTGTTGTCCCGCTATCGACGTCTAGTGAAGATATCATCACA 28020
Db 97860 TTACCGGCAACCAAGATTTGTTGTCCCGCTATCGACGTCTAGTGAAGATATCATCACA 97919
Qy 28021 TGGCAGTATCAAAACAGCGAGCTTTGAGATATACAGCGTCTTTGCCAATCAAAAACA 28080
Db 97920 TGGCAGTATCAAAACAGCGAGCTTTGAGATATACAGCGCTTTGCCAATCAAAAACA 97979
Qy 28081 TAGTTACGCGCAACCAATTTAGGTTACCGCAGACAGAACTTACAGCTTACAGCTTACCGCG 28140
Db 97980 TAGTTACGCGCAACCAATTTAGGTTACCGCAGACAGAACTTACAGCTTACAGCTTACCGCG 98039
Qy 28141 AACTGTTATTCCTGTACGACTTCTGTAATGAGTCCCTGTGCAAAAACCAAGGATACGAGT 28200
Db 98040 AACTGTTATTCCTGTACGACTTCTGTAATGAGTCCCTGTGCAAAAACCAAGGATACGAGT 98099
Qy 28201 GTTCGCGCAACCAATTTAGACATTTTATTAAGAAAGTATCCATTTTATGGCGAGTTGG 28260
Db 98100 GTTCGCGCAACCAATTTAGACATTTTATTAAGAAAGTATCCATTTTATGGCGAGTTGG 98159
Qy 28261 GGGCGTTCAATTGAAAAAAGGTGTGCTATCGATCAACCGTAAGCCTGTCCAAGTGAAG 28320
Db 98160 GGGCGTTCAATTGAAAAAAGGTGTGCTATCGATCAACCGTAAGCCTGTCCAAGTGAAG 98219
Qy 28321 CCGTTAAGCCAGCGCTCGGAGCTGTGCGCTATCCAAAGCGCTGTGAAGATTTCGCG 28380
Db 98220 CCGTTAAGCCAGCGCTCGGAGCTGTGCGCTATCCAAAGCGCTGTGAAGATTTCGCG 98279
Qy 28381 CAATGATACGATGACACCGGACAGACAGCGCAAGGAGGAAATTTTACGAGATTTT 28440
Db 98280 CAATGATACGATGACACCGGACAGACAGCGCAAGGAGGAAATTTTACGAGATTTT 98339
Qy 28441 TAGAAATGGTAAACCAATTAACACTATACGAGGTTCTATTTTTACGAGTCTTAACACT 28500
Db 98340 TAGAAATGGTAAACCAATTAACACTATACGAGGTTCTATTTTTACGAGTCTTAACACT 98399
Qy 28501 ACAGCCCACTAGACATATGCTGTGCGCAAAATTAATTAATTAACGAGTGTGATGCGG 28560
Db 98400 ACAGCCCACTAGACATATGCTGTGCGCAAAATTAATTAATTAACGAGTGTGATGCGG 98459
Qy 28561 AACAGAGCATGCGCGCTGTGCGGACATCAATTAATGCGGCTTCCGCTTCCCTGGA 28620
Db 98460 AACAGAGCATGCGCGCTGTGCGGACATCAATTAATGCGGCTTCCGCTTCCCTGGA 98519
Qy 28621 AATGGAACAACGCTGCGGTTTTTTTAAAGCCTAAGCACCCCGTGGCAACGCTACAAAAA 28680
Db 98520 AATGGAACAACGCTGCGGTTTTTTTAAAGCCTAAGCACCCCGTGGCAACGCTACAAAAA 98579
Qy 28681 TCTACAAAGCAATTAACCGTGTACCTATATAGGTTCTTTGTCGAATATGCGGCAACAAAT 28740
Db 98580 TCTACAAAGCAATTAACCGTGTACCTATATAGGTTCTTTGTCGAATATGCGGCAACAAAT 98639
Qy 28741 CGTGGGTTAAACATGCGGCTCGCAGAGAGGCGCCGCTAACCGACATACAGACCGCGAAC 28800
Db 98640 CGTGGGTTAAACATGCGGCTCGCAGAGAGGCGCCGCTAACCGACATACAGACCGCGAAC 98699
Qy 28801 CAGACCAAGGTCCTCGTCCGCCAGCTATATGCAAAATATTGACGCGTCTCCAAATTA 28860
Db 98700 CAGACCAAGGTCCTCGTCCGCCAGCTATATGCAAAATATTGACGCGTCTCCAAATTA 98759
Qy 28861 GCGCGACAGATTAATGACGACGCAATGCTCCAGCCCGGAGATTGCGCGCGAGTTCAATTA 28920
Db 98760 GCGCGACAGATTAATGACGACGCAATGCTCCAGCCCGGAGATTGCGCGCGAGTTCAATTA 98819
Qy 28921 AAACAAACCTGTATCGATCTTAAAGGAGTGTCTCGAAACAGTCCAAAAAATTCGAT 28980
Db 98820 AAACAAACCTGTATCGATCTTAAAGGAGTGTCTCGAAACAGTCCAAAAAATTCGAT 98879
Qy 28981 CGCTATTCCAAAATTTAGATGCTATAGTCTTTCGCGGACAGAGACCGCAGAGACTTAGGCC 29040
Db 98880 CGCTATTCCAAAATTTAGATGCTATAGTCTTTCGCGGACAGAGACCGCAGAGACTTAGGCC 98939

Db 97800 AACTGCAACTGGCAGCACCGCCCTTATTCACCTGTCAGACAACTGGCCCGCTGCTG 97859
Qy 27961 TTACCGGCAACCAAGATTTGTTGTCCCGCTATCGACGTCTAGTGAAGATATCATCACA 28020
Db 97860 TTACCGGCAACCAAGATTTGTTGTCCCGCTATCGACGTCTAGTGAAGATATCATCACA 97919
Qy 28021 TGGCAGTATCAAAACAGCGAGCTTTGAGATATACAGCGTCTTTGCCAATCAAAAACA 28080
Db 97920 TGGCAGTATCAAAACAGCGAGCTTTGAGATATACAGCGCTTTGCCAATCAAAAACA 97979
Qy 28081 TAGTTACGCGCAACCAATTTAGGTTACCGCAGACAGAACTTACAGCTTACAGCTTACCGCG 28140
Db 97980 TAGTTACGCGCAACCAATTTAGGTTACCGCAGACAGAACTTACAGCTTACAGCTTACCGCG 98039
Qy 28141 AACTGTTATTCCTGTACGACTTCTGTAATGAGTCCCTGTGCAAAAACCAAGGATACGAGT 28200
Db 98040 AACTGTTATTCCTGTACGACTTCTGTAATGAGTCCCTGTGCAAAAACCAAGGATACGAGT 98099
Qy 28201 GTTCGCGCAACCAATTTAGACATTTTATTAAGAAAGTATCCATTTTATGGCGAGTTGG 28260
Db 98100 GTTCGCGCAACCAATTTAGACATTTTATTAAGAAAGTATCCATTTTATGGCGAGTTGG 98159
Qy 28261 GGGCGTTCAATTGAAAAAAGGTGTGCTATCGATCAACCGTAAGCCTGTCCAAGTGAAG 28320
Db 98160 GGGCGTTCAATTGAAAAAAGGTGTGCTATCGATCAACCGTAAGCCTGTCCAAGTGAAG 98219
Qy 28321 CCGTTAAGCCAGCGCTCGGAGCTGTGCGCTATCCAAAGCGCTGTGAAGATTTCGCG 28380
Db 98220 CCGTTAAGCCAGCGCTCGGAGCTGTGCGCTATCCAAAGCGCTGTGAAGATTTCGCG 98279
Qy 28381 CAATGATACGATGACACCGGACAGACAGCGCAAGGAGGAAATTTTACGAGATTTT 28440
Db 98280 CAATGATACGATGACACCGGACAGACAGCGCAAGGAGGAAATTTTACGAGATTTT 98339
Qy 28441 TAGAAATGGTAAACCAATTAACACTATACGAGGTTCTATTTTTACGAGTCTTAACACT 28500
Db 98340 TAGAAATGGTAAACCAATTAACACTATACGAGGTTCTATTTTTACGAGTCTTAACACT 98399
Qy 28501 ACAGCCCACTAGACATATGCTGTGCGCAAAATTAATTAATTAACGAGTGTGATGCGG 28560
Db 98400 ACAGCCCACTAGACATATGCTGTGCGCAAAATTAATTAATTAACGAGTGTGATGCGG 98459
Qy 28561 AACAGAGCATGCGCGCTGTGCGGACATCAATTAATGCGGCTTCCGCTTCCCTGGA 28620
Db 98460 AACAGAGCATGCGCGCTGTGCGGACATCAATTAATGCGGCTTCCGCTTCCCTGGA 98519
Qy 28621 AATGGAACAACGCTGCGGTTTTTTTAAAGCCTAAGCACCCCGTGGCAACGCTACAAAAA 28680
Db 98520 AATGGAACAACGCTGCGGTTTTTTTAAAGCCTAAGCACCCCGTGGCAACGCTACAAAAA 98579
Qy 28681 TCTACAAAGCAATTAACCGTGTACCTATATAGGTTCTTTGTCGAATATGCGGCAACAAAT 28740
Db 98580 TCTACAAAGCAATTAACCGTGTACCTATATAGGTTCTTTGTCGAATATGCGGCAACAAAT 98639
Qy 28741 CGTGGGTTAAACATGCGGCTCGCAGAGAGGCGCCGCTAACCGACATACAGACCGCGAAC 28800
Db 98640 CGTGGGTTAAACATGCGGCTCGCAGAGAGGCGCCGCTAACCGACATACAGACCGCGAAC 98699
Qy 28801 CAGACCAAGGTCCTCGTCCGCCAGCTATATGCAAAATATTGACGCGTCTCCAAATTA 28860
Db 98700 CAGACCAAGGTCCTCGTCCGCCAGCTATATGCAAAATATTGACGCGTCTCCAAATTA 98759
Qy 28861 GCGCGACAGATTAATGACGACGCAATGCTCCAGCCCGGAGATTGCGCGCGAGTTCAATTA 28920
Db 98760 GCGCGACAGATTAATGACGACGCAATGCTCCAGCCCGGAGATTGCGCGCGAGTTCAATTA 98819
Qy 28921 AAACAAACCTGTATCGATCTTAAAGGAGTGTCTCGAAACAGTCCAAAAAATTCGAT 28980
Db 98820 AAACAAACCTGTATCGATCTTAAAGGAGTGTCTCGAAACAGTCCAAAAAATTCGAT 98879
Qy 28981 CGCTATTCCAAAATTTAGATGCTATAGTCTTTCGCGGACAGAGACCGCAGAGACTTAGGCC 29040
Db 98880 CGCTATTCCAAAATTTAGATGCTATAGTCTTTCGCGGACAGAGACCGCAGAGACTTAGGCC 98939

OY	29041	CTATCAGACGCTCGCTGGCCCTGGCGTATTTTCAATAATGACATTTTGGAGAAAGC	29100
Db	98940	CTATCAGACGCTCGCTGGCCCGCGTATTTTCAATAATGACATTTTGGAGAAAGC	98999
OY	29101	ATTCTCCGAGATCGTTTTCACAACCTGCTGCACTATCTCAGGAACATTTAGTGCATAC	29160
Db	99000	ATTCTCCGAGATCGTTTTCACAACCTGCTGCACTATCTCAGGAACATTTAGTGCATAC	99059
OY	29161	GACAGGTATACCGGAAGCAGCTGCCCAAGAATTTCTACAATCTGTTTACTTTTC	29220
Db	99060	GACAGGTATACCGGAAGCAGCTGCCCAAGAATTTCTACAATCTGTTTACTTTTC	99119
OY	29221	AAAACATTCCAATAGCAGCGAGCTTCATTCAAAACATTCATGACCTTTGTAGAGACCTGA	29280
Db	99120	AAAACATTCCAATAGCAGCGAGCTTCATTCAAAACATTCATGACCTTTGTAGAGACCTGA	99179
OY	29281	AAAAGGCAATCCCGGTTACTGACCTTGTCTCCTTAGGTGCGCGTTTATACATGA	29340
Db	99180	AAAAGGCAATCCCGGTTACTGACCTTGTCTCCTTAGGTGCGCGTTTATACATGA	99239
OY	29341	AACATCTAGCATTCACAGCTAGACACCGCTGAGATTCACAACGGAAGAAAGGCAACCCA	29400
Db	99240	AACATCTAGCATTCACAGCTAGACACCGCTGAGATTCACAACGGAAGAAAGGCAACCCA	99299
OY	29401	TCGTCGTAGCATGTTTCGTATTCAATCCACGATTCGCTCCGCGAAGACTTTACAG	29460
Db	99300	TCGTCGTAGCATGTTTCGTATTCAATCCACGATTCGCTCCGCGAAGACTTTACAG	99359
OY	29461	AAGCCGTTATGCGCTTTAACTCAACGCTCCGAACCGATGTACGCAAGCAGCATCCGTCTGA	29520
Db	99360	AAGCCGTTATGCGCTTTAACTCAACGCTCCGAACCGATGTACGCAAGCAGCATCCGTCTGA	99419
OY	29521	TGCAACACCTCAGCAGTAATGCAAAAGATGCGCGGACAGCAAAATTAAGACACACCACTTC	29580
Db	99420	TGCAACACCTCAGCAGTAATGCAAAAGATGCGCGGACAGCAAAATTAAGACACCACTTC	99479
OY	29581	CATCCGTTTTCACGAATAACACGAGGGATATTTCGAGTGTTTTAAGCGTTTAAACGTC	29640
Db	99480	CATCCGTTTTCACGAATAACACGAGGGATATTTCGAGTGTTTTAAGCGTTTAAACGTC	99539
OY	29641	TCATGTTACAGTTACGGGAGCTGCTGCTACTCACTGACGGAGACTTTGGATTCCCTAT	29700
Db	99540	TCATGTTACAGTTACGGGAGCTGCTGCTACTCACTGACGGAGACTTTGGATTCCCTAT	99599
OY	29701	ATCAACCCCCCTATTAACCCGTACCATCTGTCACAAAAATTTTAACTTAAACACAAAA	29760
Db	99600	ATCAACCCCCCTATTAACCCGTACCATCTGTCACAAAAATTTTAACTTAAACACAAAA	99659
OY	29761	CGGACACAAACGAGACATCTTAAAGAGCTGTCAAGCCGCGAGACAAAGACCTCTAT	29820
Db	99660	CGGACACAAACGAGACATCTTAAAGAGCTGTCAAGCCGCGAGACAAAGACCTCTAT	99719
OY	29821	CGGCTGAAAAAGAAAGTAGCACTGTCAAAAAACAACGTTGAAGCTCTTCAAAAAC	29880
Db	99720	CGGCTGAAAAAGAAAGTAGCACTGTCAAAAAACAACGTTGAAGCTCTTCAAAAAC	99779
OY	29881	TGTACGACGACTTTGGGACCGCTCTCACAAACATTAACCCACCTTATTTAACTTGAAT	29940
Db	99780	TGTACGACGACTTTGGGACCGCTCTCACAAACATTAACCCACCTTATTTAACTTGAAT	99839
OY	29941	ATTGCGTAATATTATACGAAACACAAAGTGTCCGTAGATTGGAGACATATAACCTGGTGA	30000
Db	99840	ATTGCGTAATATTATACGAAACACAAAGTGTCCGTAGATTGGAGACATATAACCTGGTGA	99899
OY	30001	CATACACGCAACCCGACGATACGTTAAATTTCAACCCGGTTTAAACGAGAGCACTAGATC	30060
Db	99900	CATACACGCAACCCGACGATACGTTAAATTTCAACCCGGTTTAAACGAGAGCACTAGATC	99959
OY	30061	GCATGTTTGCAGAAATTAACGATGGAATTCGCGCAATTTTTCGAAATTTTAAATAGAGG	30120
Db	99960	GCATGTTTGCAGAAATTAACGATGGAATTCGCGCAATTTTTCGAAATTTTAAATAGAGG	100019

QY	30121	GCCTGGCAACGACGCACCAAGCCGACTGCAGAGTTTGGACAAATACGCCGCTGCAGTGTCT	30180
Db	1000220	GGCTGGCAACGACGCACCAAGCCGACTGCAGAGTTTGGACAAATACGCCGCTGCAGTGTCT	1000797
QY	30181	TGAGCAACGTGGCTTATCTACCTGGCAAGATTAATTCAATAGAGAGTCCCGGTGACGG	30240
Db	100080	TGAGCAACGTGGCTTATCTACCTGGCAAGATTAATTCAATAGAGAGTCCCGGTGACGG	100138
QY	30241	ACACTAACGACCTTCGACGACGTTTTTACGGCAAGGGGGGACGTTGGACTTATACTGAGAC	30300
Db	100140	ACACTAACGACCTTCGACGACGTTTTTACGGCAAGGGGGGACGTTGGACTTATACTGAGAC	100199
QY	30301	GGTCCGGGACGCTCGGCTATTAACAATATGCCACATGACACATACCAGCTTATCA	30360
Db	100200	GGTCCGGGACGCTCGGCTATTAACAATATGCCACATGACACATACCAGCTTATCA	100258
QY	30361	AGACCAACGAGTGGACCGCGGCCATCTTTCATCTCAGAGTACTTTGGACTAATGGAC	30420
Db	100260	AGACCAACGAGTGGACCGCGGCCATCTTTCATCTCAGAGTACTTTGGACTAATGGAC	100315
QY	30421	TTGACGGCGGCATTCGCGCAACCTTTTCATGGAATCCCTTAAATATGATCCTAACGGAATTT	30480
Db	100320	TTGACGGCGGCATTCGCGCAACCTTTTCATGGAATCCCTTAAATATGATCCTAACGGAATTT	100378
QY	30481	ACGCCGGACCGCTTCATACTTCTTCTTTATATGCGGCGCAAAAGCCGGGCGGTAAATTA	30540
Db	100380	ACGCCGGACCGCTTCATACTTCTTCTTTATATGCGGCGCAAAAGCCGGGCGGTAAATTA	100439
QY	30541	TCAAAAACAAACGTTTTTACCTGTGTGATCCCATTTGCGTACCCACGTAACCAATATGTC	30600
Db	100440	TCAAAAACAAACGTTTTTACCTGTGTGATCCCATTTGCGTACCCACGTAACCAATATGTC	100499
QY	30601	CGGACACGTAATCAGTTGCTGACAGCCCAACGCGCATCTAGAGTACGTCTACCCGACG	30660
Db	100500	CGGACACGTAATCAGTTGCTGACAGCCCAACGCGCATCTAGAGTACGTCTACCCGACG	100559
QY	30661	ACAGAGAATACACTGGCAGTTTTCTATACATTATGGCCAGCAATATGTCATCCAGAGC	30720
Db	100560	ACAGAGAATACACTGGCAGTTTTCTATACATTATGGCCAGCAATATGTCATCCAGAGC	100619
QY	30721	ACTACATCACAACCACTATAGACATATAAGTTTGGCAAAAGTACAGGGCCGACACTAG	30780
Db	100620	ACTACATCACAACCACTATAGACATATAAGTTTGGCAAAAGTACAGGGCCGACACTAG	100679
QY	30781	ATTATATCCACGGCATAGAGCCGTGGACCATCGAAGACATCCCAAGGCCCGGAGTACGC	30840
Db	100680	ATTATATCCACGGCATAGAGCCGTGGACCATCGAAGACATCCCAAGGCCCGGAGTACGC	100739
QY	30841	CGGATGTGACGTCAAAATCATCCAACTCGCACGCGTCCGAGAACCCACCGACACGTA	30900
Db	100740	CGGATGTGACGTCAAAATCATCCAACTCGCACGCGTCCGAGAACCCACCGACACGTA	100799
QY	30901	CGAGCGCCAAACCCCAACGGGAGCGCTATCCGGTTTACGGGGCGGGAACCAACGACAA	30960
Db	100800	CGAGCGCCAAACCCCAACGGGAGCGCTATCCGGTTTACGGGGCGGGAACCAACGACAA	100859
QY	30961	GGTACCCAGACCGCGCAACCAACGAGGGGAGCAAAACCTTAACTCCGGTCCACAGCG	31020
Db	100860	GGTACCCAGACCGCGCAACCAACGAGGGGAGCAAAACCTTAACTCCGGTCCACAGCG	100919
QY	31021	AAACGCGCCTTCGACACACCCGGAATTTCAAAACAACACTTGAGGCGACGCTACTTCTTCAG	31080
Db	100920	AAACGCGCCTTCGACACACCCGGAATTTCAAAACAACACTTGAGGCGACGCTACTTCTTCAG	100979
QY	31081	AACTGTCCGATTCAGGGGTGGAAAACGCAAGCTTTCAGCCTTCAGACGATTAATCGAATT	31140
Db	100980	AACTGTCCGATTCAGGGGTGGAAAACGCAAGCTTTCAGCCTTCAGCAGATTAATTCGATT	101039
QY	31141	CGGACGAACGTCGTCTGACGACGAAGGGGGCCCACTGAGGGCGTAACAGAGATGGCGA	31200
Db	101040	CGGACGAACGTCGTCTGACGACGAAGGGGGCCCACTGAGGGCGTAACAGAGATGGCGA	101099
QY	31201	TATCCGCGAGGTGATCTGGATGAGACGAGATATATCTCCTCTATATTCACCTCGGCGCA	31260

```
|||||
Db 101100 TATCCCGAGGAGTCTGGATGAGACGATATATCTCTCATATATCACTCGGCGA 101159
QY 31261 CTCATCGTTTGAAGCAGTGTTCGACAGCCCCCAATGAGCCGGAGTTTACATACGAAG 31320
Db 101160 CTCATCGTTTGAAGCAGTGTTCGACAGCCCCCAATGAGCCGGAGTTTACATACGAAG 101219
QY 31321 AGCGCAGAGAGACAGGATGGCGCTTTCAGACAGATGCTCGAGAGCGGGAACGC 31380
Db 101220 ACCCGCAGAGAGACAGGATGGCGCTTTCAGACAGATGCTCGAGAGCGGGAACGC 101279
QY 31381 CGTTCCTGCGTTCGAGCAGCTTATACGAGACGACATTTCTTCCCTGATATAAAAAA 31440
Db 101280 CGTTCCTGCGTTCGAGCAGCTTATACGAGACGACATTTCTTCCCTGATATAAAAAA 101339
QY 31441 TAGAACGTTTAAATCAAGTACGAAGCGCCTCGAGCAGCTGCCAAACATCTCGAGCAAC 31500
Db 101340 TAGAACGTTTAAATCAAGTACGAAGCGCCTCGAGCAGCTGCCAAACATCTCGAGCAAC 101399
QY 31501 AAAACGGGCGAGCGCTCCGAGAAAGCGGCGCTCCAGAGGATGACAAAAATTATGATTA 31560
Db 101400 AAAACGGGCGAGCGCTCCGAGAAAGCGGCGCTCCAGAGGATGACAAAAATTATGATTA 101459
QY 31561 ATATCTACTTGAACACGGTCTAATTACAGACGCGAGGCGCGGGACCGCTCGCGGCA 31620
Db 101460 ATATCTACTTGAACACGGTCTAATTACAGACGCGAGGCGCGGGACCGCTCGCGGCA 101519
QY 31621 AAAACGTTCTCAATTTTTCATCTGTGGGAGAAAAAACTCAACATACCAATTAAGGAGC 31680
Db 101520 AAAACGTTCTCAATTTTTCATCTGTGGGAGAAAAAACTCAACATACCAATTAAGGAGC 101579
QY 31681 CCAAGCAGGTCCTAGAACCTGATCTGCACTGATACCGTTACTATACGGCTATACGGAAG 31740
Db 101580 CCAAGCAGGTCCTAGAACCTGATCTGCACTGATACCGTTACTATACGGCTATACGGAAG 101639
QY 31741 GAAATTTCAACAGGCGGCGTTCAAAAAACACTTAACAATACTAACCGGCTGTCTGG 31800
Db 101640 GAAATTTCAACAGGCGGCGTTCAAAAAACACTTAACAATACTAACCGGCTGTCTGG 101699
QY 31801 CGTCAATGAGGCGCACGACGACGATGCGCAAAAAAACTGGCGCTTTCACAGCTGC 31860
Db 101700 CGTCAATGAGGCGCACGACGACGATGCGCAAAAAAACTGGCGCTTTCACAGCTGC 101759
QY 31861 AAGGCTCACAGATTCGTCAGAGAGCAAAAAATATCATGTCGGGCGCTGAAGAAACA 31920
Db 101760 AAGGCTCACAGATTCGTCAGAGAGCAAAAAATATCATGTCGGGCGCTGAAGAAACA 101819
QY 31921 TCGCCAAACCACTGAGTCCAGGCTTTTAGCGGTACTCCGGGAGAGGTAAACATC 31980
Db 101820 TCGCCAAACCACTGAGTCCAGGCTTTTAGCGGTACTCCGGGAGAGGTAAACATC 101879
QY 31981 TACGGGATTAATTCAGACCTTAATAAAGGCAATCGAGCAGCGCAAAAGAAATCAAC 32040
Db 101880 TACGGGATTAATTCAGACCTTAATAAAGGCAATCGAGCAGCGCAAAAGAAATCAAC 101939
QY 32041 AAGAAAGAACTGTTTTTATGTCATGCTACACAGCCCTGGACAGCTTCAACCCCTCGCA 32100
Db 101940 AAGAAAGAACTGTTTTTATGTCATGCTACACAGCCCTGGACAGCTTCAACCCCTCGCA 101999
QY 32101 AAACGCAATTTTCAATGAGATCTTTCCGACACGTTAAACCGAAGTTATGCTGACACAC 32160
Db 102000 AAACGCAATTTTCAATGAGATCTTTCCGACACGTTAAACCGAAGTTATGCTGACACAC 102059
QY 32161 TGGCGTCAATTAACACAGGTTAACGAGAGCGCACCGCAAGCCCTCAACAAATTAACCTG 32220
Db 102060 TGGCGTCAATTAACACAGGTTAACGAGAGCGCACCGCAAGCCCTCAACAAATTAACCTG 102119
QY 32221 AAGACCCCGCCGACCAAGAGACGACATTAACAACATTTTCAATTCATCCATGCTGG 32280
Db 102120 AAGACCCCGCCGACCAAGAGAGACGACATTAACAACATTTTCAATTCATCCATGCTGG 102179
QY 32281 CAATATCATATTCAGCTTAATAAAATCTTAAGTACGCAAAAAAGCAATGCAATTAAGC 32340
|||||
Db 102180 CAATATCATATTCAGCTTAATAAAATCTTAAGTACGCAAAAAAGCAATGCAATTAAGC 102239
QY 32341 TAAAGCCCATGAGCAAGGTACAGGCGTCAAGCTGTTTATACCTCGAGAGCGAGTTAGCAACA 32400
Db 102240 TAAAGCCCATGAGCAAGGTACAGGCGTCAAGCTGTTTATACCTCGAGAGCGAGTTAGCAACA 102299
QY 32401 TCTTTAATTTTATAGTGGCCATACGAACCGTGGCACCGGTTTCAAGAAATGCCCCCTGTGG 32460
Db 102300 TCTTTAATTTTATAGTGGCCATACGAACCGTGGCACCGGTTTCAAGAAATGCCCCCTGTGG 102359
QY 32461 CGCGGGCGAAAGCAAAATGGAATCGGTAACAAAAAATGAAAAAGCAACAGAGCTCTCG 32520
Db 102360 CGCGGGCGAAAGCAAAATGGAATCGGTAACAAAAAATGAAAAAGCAACAGAGCTCTCG 102419
QY 32521 ACCAAATACTGGGAGAGCGCGAAACGTTACTTGACACAAATTAACCGCAATCCGGAGATG 32580
Db 102420 ACCAAATACTGGGAGAGCGCGAAACGTTACTTGACACAAATTAACCGCAATCCGGAGATG 102479
QY 32581 AGAACCCGGTCCCGCCATGCTCATACCGTACTGAGAGCTCTATTACAAACGAGCGC 32640
Db 102480 AGAACCCGGTCCCGCCATGCTCATACCGTACTGAGAGCTCTATTACAAACGAGCGC 102539
QY 32641 CCTGTATAGGCAAGTCTCGAAACACGAGGTTGAAAAAACTCAAGGCGCCATCCAGAGC 32700
Db 102540 CCTGTATAGGCAAGTCTCGAAACACGAGGTTGAAAAAACTCAAGGCGCCATCCAGAGC 102599
QY 32701 TGGCATCATCGAGTCTTATATATATGCTGTAAACACACGCGGCTTGATACATAT 32760
Db 102600 TGGCATCATCGAGTCTTATATATATGCTGTAAACACACGCGGCTTGATACATAT 102659
QY 32761 CAGACATCTGGGCAAGATCGAGGAGTCTGACCAACAAACACGTTTTTCTTCAAAAC 32820
Db 102660 CAGACATCTGGGCAAGATCGAGGAGTCTGACCAACAAACACGTTTTTCTTCAAAAC 102719
QY 32821 CCAGTGTATAGCAAAAGCTCTCAAAACGCTGGGAGAGCAGCTTAATACCGAATGCGTAAAG 32880
Db 102720 CCAGTGTATAGCAAAAGCTCTCAAAACGCTGGGAGAGCAGCTTAATACCGAATGCGTAAAG 102779
QY 32881 CGCTAATAATAAGAGCCCTCTTCCCTCAACAGCGCGCTCTCTCGCGGTTCAAAACA 32940
Db 102780 CGCTAATAATAAGAGCCCTCTTCCCTCAACAGCGCGCTCTCTCGCGGTTCAAAACA 102839
QY 32941 TACTGGGGCAGCGGTCGTTCCGATCAGAGAGCGGTGACGGCAATGTTTCGGGGCTGC 33000
Db 102840 TACTGGGGCAGCGGTCGTTCCGATCAGAGAGCGGTGACGGCAATGTTTCGGGGCTGC 102899
QY 33001 CCAGCGCACAAAAAGGATCCGCTGGGAGATTCAGATAGTATAGTGGAGCGAGTAAACGCGTC 33060
Db 102900 CCAGCGCACAAAAAGGATCCGCTGGGAGATTCAGATAGTATAGTGGAGCGAGTAAACGCGTC 102959
QY 33061 ACCTTAACGAGCTGAAGCTGTGTAATACCAATCGCTGTGCAAAAGCCACAGCGCA 33120
Db 102960 ACCTTAACGAGCTGAAGCTGTGTAATACCAATCGCTGTGCAAAAGCCACAGCGCA 103019
QY 33121 AACTGTTAATGATTAATTAACCCGTAAGTCAAGAGCGGAGGTCGTCAAGAAACGCGTC 33180
Db 103020 AACTGTTAATGATTAATTAACCCGTAAGTCAAGAGCGGAGGTCGTCAAGAAACGCGTC 103079
QY 33181 TGGAAACAGGTGGGCAAGAAAGCTCTAAAGTTTCAACGCTGACGTCGCAAAAGAAATG 33240
Db 103080 TGGAAACAGGTGGGCAAGAAAGCTCTAAAGTTTCAACGCTGACGTCGCAAAAGAAATG 103139
QY 33241 AAGACTTTTACAGTGGGACCGTCAAGCAAGGCGCGAAATTCGCAAGAAAAACACTTAC 33300
Db 103140 AAGACTTTTACAGTGGGACCGTCAAGCAAGGCGCGAAATTCGCAAGAAAAACACTTAC 103199
QY 33301 GGAAGCTGATCAACCAATTCACGGGCAAGAGGAGGAGCGGCTCCAGGCGCACCGCGCTTC 33360
Db 103200 GGAAGCTGATCAACCAATTCACGGGCAAGAGGAGGAGCGGCTCCAGGCGCACCGCGCTTC 103259
QY 33361 CCATGAGCTACAGCGCGGACCATATCCACGCGCAAGGCGGTTTATAGGGCTACCGCGG 33420
Db 103260 CCATGAGCTACAGCGCGGACCATATCCACGCGCAAGGCGGTTTATAGGGCTACCGCGG 103319
```


QY 33421 AAAAGGAAAGGCGCATGGAATAAATTCACAGAGGCTTTCAGAGATTTCACTTCAACC 33480
 Db 103320 AAAAGGAAAGGCGCATGGAATAAATTCACAGAGGCTTTCAGAGATTTCACTTCAACC 103379
 QY 33481 TCATGACGCTTCGGATTTGGCAGAGATGGCATAGAAATCTCCAGACAGCGCTGCTCC 33540
 Db 103380 TCATGACGCTTCGGATTTGGCAGAGATGGCATAGAAATCTCCAGACAGCGCTGCTCC 103439
 QY 33541 TTCTGGTAGGGTTGGACCAAGGTGGCTTCATGAGAGATGCAAAACCCCTGG 33600
 Db 103440 TTCTGGTAGGGTTGGACCAAGGTGGCTTCATGAGAGATGCAAAACCCCTGG 103499
 QY 33601 ACAGATCTCTACAGCAGAGATGGCATCTGCTTCCAAAGGGGCGCGCTTCAGACCCC 33660
 Db 103500 ACAGATCTCTACAGCAGAGATGGCATCTGCTTCCAAAGGGGCGCGCTTCAGACCCC 103559
 QY 33661 CAGCGTTTGACTGGATGCGCGCTATCAACACCGCTTAACGCGTTTCTAAACCATAG 33720
 Db 103560 CAGCGTTTGACTGGATGCGCGCTATCAACACCGCTTAACGCGTTTCTAAACCATAG 103619
 QY 33721 GCGTGGCCATGCTGGGCAACCTGGGAGCAAGATCAATCAACATGCAATGCTGCTC 33780
 Db 103620 GCGTGGCCATGCTGGGCAACCTGGGAGCAAGATCAATCAACATGCAATGCTGCTC 103679
 QY 33781 ACAGGATGCAATCCGACAGACCTTCAACAGGCGCAGGTTGGAACAGTTCAGACCCG 33840
 Db 103680 ACAGGATGCAATCCGACAGACCTTCAACAGGCGCAGGTTGGAACAGTTCAGACCCG 103739
 QY 33841 CCGCGCAATCTGTCGAATCTCTCTGATGCAAGTCGCGTTCAACAGCAGCAAGATCG 33900
 Db 103740 CCGCGCAATCTGTCGAATCTCTCTGATGCAAGTCGCGTTCAACAGCAGCAAGATCG 103799
 QY 33901 CCGTAAGATGGAAGCGCGCGCGCTACACGAGCAATCACTCGCGCGCAACGCTGGA 33960
 Db 103800 CCGTAAGATGGAAGCGCGCGCGCTACACGAGCAATCACTCGCGCGCAACGCTGGA 103859
 QY 33961 CTCCCGGAAACCCCACTAGAACCCCAAGAAAGCTAATTAAGGCAATCTGACGCGCTTA 34020
 Db 103860 CTCCCGGAAACCCCACTAGAACCCCAAGAAAGCTAATTAAGGCAATCTGACGCGCTTA 103919
 QY 34021 CCGTCGAGGACTTTCAGATTTCTCTAAACAGTCAATCTTCAACAGAGACGAGCTCA 34080
 Db 103920 CCGTCGAGGACTTTCAGATTTCTCTAAACAGTCAATCTTCAACAGAGACGAGCTCA 103979
 QY 34081 TTGCGCTCCAGAGCGGAATTTACGAACCTAGAGGCGAGATCTCGCGCGCGCAAGCGC 34140
 Db 103880 TTGCGCTCCAGAGCGGAATTTACGAACCTAGAGGCGAGATCTCGCGCGCGCAAGCGC 104039
 QY 34141 TCCGCCAATCCACCCGTCAGAGATCCAGGCAAGATGGCAACGCTATCAAGCAACTCT 34200
 Db 104040 TCCGCCAATCCACCCGTCAGAGATCCAGGCAAGATGGCAACGCTATCAAGCAACTCT 104099
 QY 34201 TACCCCGCGCGCGCTGCGCAATATCATCGAGACCGCTTGAATTCATAAACCTTAGACT 34260
 Db 104100 TACCCCGCGCGCGCTGCGCAATATCATCGAGACCGCTTGAATTCATAAACCTTAGACT 104159
 QY 34261 TTTGAGTTCAAGCGTTATAGCAAAATCTGAGCAAGGAGCCTTAGACAGACAGCAATAG 34320
 Db 104160 TTTGAGTTCAAGCGTTATAGCAAAATCTGAGCAAGGAGCCTTAGACAGACAGCAATAG 104219
 QY 34321 CGGGATTGCGCTGGCTGGAATTCGACAAATCCGTAATGCTTACAGTCAACAAAACG 34380
 Db 104220 CGGGATTGCGCTGGCTGGAATTCGACAAATCCGTAATGCTTACAGTCAACAAAACG 104279
 QY 34381 AAACGCAACAGTTAAAGCTACTGCTGAGCGAGGTTAGAAAAACAGACACCGTCCGCGCAGC 34440
 Db 104280 AAACGCAACAGTTAAAGCTACTGCTGAGCGAGGTTAGAAAAACAGACACCGTCCGCGCAGC 104339
 QY 34441 GTCTACAGATTTGGAAGTCTCGGCGAAAAACAGGACGAGTAAAGGTGCTGAAGCAGG 34500
 Db 104340 GTCTACAGATTTGGAAGTCTCGGCGAAAAACAGGACGAGTAAAGGTGCTGAAGCAGG 104399

QY 34501 CGTAGACAGACTGCGGCCCTCAAGGTAAAGGGCGGAAAAACACCGCTAGACGCTGGA 34560
 Db 104400 CGTAGACAGACTGCGGCCCTCAAGGTAAAGGGCGGAAAAACACCGCTAGACGCTGGA 104459
 QY 34561 AACAAAACTGGAAGCATTAATTCCTGCTTCGGGCCACAGAGAGCGGACGCAAAATAT 34620
 Db 104460 AACAAAACTGGAAGCATTAATTCCTGCTTCGGGCCACAGAGAGCGGACGCAAAATAT 104519
 QY 34621 CATGCGAGCTTGAACGCATCGGACACAGGGGCTTGGACCATCACTCCGCGATTAG 34680
 Db 104520 CATGCGAGCTTGAACGCATCGGACACAGGGGCTTGGACCATCACTCCGCGATTAG 104579
 QY 34681 GAAAGCTCTCGCATCAATGCGGGAAGCGCAAAATTTCTAGACAGGCAAGTACCCG 34740
 Db 104580 GAAAGCTCTCGCATCAATGCGGGAAGCGCAAAATTTCTAGACAGGCAAGTACCCG 104639
 QY 34741 AAGGCTTCGGACATAGGCAACAAATCTCAGGAGCTTCAGGCGTACATTAAATCAAAA 34800
 Db 104640 AAGGCTTCGGACATAGGCAACAAATCTCAGGAGCTTCAGGCGTACATTAAATCAAAA 104699
 QY 34801 AACAGTTCTGAGCATTTTGAACACACCGACCTAACGCTCTTCAACGCTTCCGCTAT 34860
 Db 104700 AACAGTTCTGAGCATTTTGAACACACCGACCTAACGCTCTTCAACGCTTCCGCTAT 104759
 QY 34861 CCAAAACATTAACCGAAAGCTTCCGGCGCGCGCGATGGAATCGGTGGCCAGACTGA 34920
 Db 104760 CCAAAACATTAACCGAAAGCTTCCGGCGCGCGCGATGGAATCGGTGGCCAGACTGA 104819
 QY 34921 CCAATCACTTCAGCTGGCGGCGAGCGGCGCCCAATTTTACAACTGATAGAAAGCTTAC 34980
 Db 104820 CCAATCACTTCAGCTGGCGGCGAGCGGCGCCCAATTTTACAACTGATAGAAAGCTTAC 104879
 QY 34981 CGACGCTGATCCGGAACCAACTCACTACGTCGCGGCGACGAGAGAGCCCTCTGCACC 35040
 Db 104880 CGACGCTGATCCGGAACCAACTCACTACGTCGCGGCGACGAGAGAGCCCTCTGCACC 104939
 QY 35041 GCCAGATCAGTACTCAAAAGCTCTAGAGGCGGTTTTCATTTATGTTCCACACGCTAA 35100
 Db 104940 GCCAGATCAGTACTCAAAAGCTCTAGAGGCGGTTTTCATTTATGTTCCACACGCTAA 104999
 QY 35101 C 35101
 Db 105000 C 105000

RESULT 3
 AAL35004
 ID AAL35004 standard; cDNA: 370 BP.
 AC AAL35004;
 XX
 DT 08-JAN-2002 (first entry)
 XX
 DE Human musculoskeletal system related polynucleotide SEQ ID NO 346.
 XX
 KW Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
 KW antiallergic; hepatotropic; antidiabetic; antiinflammatory; antilucer;
 KW vulnerability; anticonvulsant; antibacterial; antifungal; antiparasitic;
 KW radiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
 KW neurological disease; infection; human; secreted protein;
 KW musculoskeletal system; ss.
 KM
 OS Homo sapiens.
 OS
 PN WO20015367-A1.
 XX
 PD 02-AUG-2001.
 XX
 PE 17-JAN-2001; 2001WO-US01338.
 XX
 PR 31-JAN-2000; 2000US-0179065.
 PR 04-FEB-2000; 2000US-0180628.
 PR 24-FEB-2000; 2000US-0184664.

PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226688.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.

PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251088.
PR 05-DEC-2000; 2000US-0251856.
PR 06-DEC-2000; 2000US-0251719.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251858.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 11-DEC-2000; 2000US-0251990.
PR 05-JAN-2001; 2001US-0259678.

(HUMA-) HUMAN GENOME SCI INC.
PA
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
XX WPI: 2001-451937/48.
DR P-PSDB; ABB03422.
XX
XX
XX Isolated polypeptide for treating, preventing and/or prognosing
PT disorders related to the musculoskeletal system including
PT musculoskeletal cancers and also for testing and detection e.g.
PT diagnosis -
XX

PS Claim 1; SEQ ID NO 346; 781pp + Sequence Listing; English.
XX
CC The invention relates to novel genes (AAL34669-AAL37666) and proteins
CC (AB03087-AB04109) associated with the musculoskeletal system useful
CC for preventing, treating or ameliorating medical conditions e.g. by
CC protein or gene therapy. The genes are isolated from a range of human
CC tissues disclosed in the specification. The nucleic acids, proteins,
CC antibodies and (ant)agonists are useful in the diagnosis, treatment
CC and prevention of: (a) cancer, e.g. breast and ovarian cancer and
CC other cancers of the adrenal gland, bone, bone marrow, breast,
CC gastrointestinal tract, liver, lung, or urogenital; (b) immune
CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic
CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,
CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis;
CC (c) cardiovascular disorders such as myocardial ischaemias; (d) wound
CC healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy;
CC and (f) infectious diseases such as viral, bacterial, fungal and
CC parasitic infections.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pcl_sequences.
XX
SQ Sequence 370 BP; 107 A; 71 C; 74 G; 115 T; 3 other;

Query Match 0.1%; Score 23; DB 22; Length 370;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4250 TTAAACATGCGATTATTATAA 4272
Dn 73 TTAAACATGCGATTATTATAA 95

RESULT 4
ID ABX57992 standard; cDNA: 370 BP.
XX
AC ABX57992:
XX
DT 26-FEB-2003 (first entry)
XX
DE cDNA encoding novel human musculoskeletal system antigen #336.
XX
KW Gene; ss; musculoskeletal system antigen; cancer; metastasis;
KW re-vascularisation; thrombosis; arteriosclerosis; mineral content;
KW cardiovascular condition; wound; injury; burn; angiogenesis; ulcer;
KW post-operative tissue repair; limb regeneration; neuronal growth;
KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
KW AIDS-related complex; chondrocyte growth; bone regeneration;
KW periodontal regeneration; tissue transport; bone graft; skin aging;
KW keratinocyte growth; hair loss; melanocyte growth; cell proliferation;
KW cell growth; organ transplant; cell differentiation; body height;
KW weight; hair colour; eye colour; skin; percentage of adipose tissue;
KW pigmentation; cosmetic surgery; metabolism; biorythm; cardiac rhythm;
KW depression; tendency for violence; pain; reproductive capability;
KW hormone level; endocrine level; appetite; libido; memory; stress;
KW storage capability; fat content; lipid content; protein content;
KW carbohydrate content; vitamin content; cofactor content;
KW nutritional component.
XX
XX Homo sapiens.
XX
PN US2002147140-A1.
XX
PD 10-OCT-2002.
XX
PF 17-JAN-2001; 2001US-0764877.
XX
PR 31-JAN-2000; 2000US-179065P.
PR 04-FEB-2000; 2000US-180628P.
PR 28-JUN-2000; 2000US-214886P.
PR 07-JUL-2000; 2000US-216647P.
PR 07-JUL-2000; 2000US-216880P.

PR 11-JUL-2000; 2000US-217487P.
PR 11-JUL-2000; 2000US-217496P.
PR 14-JUL-2000; 2000US-218290P.
PR 26-JUL-2000; 2000US-220963P.
PR 26-JUL-2000; 2000US-220964P.
PR 14-AUG-2000; 2000US-224518P.
PR 14-AUG-2000; 2000US-224519P.
PR 14-AUG-2000; 2000US-225267P.
PR 14-AUG-2000; 2000US-225268P.
PR 14-AUG-2000; 2000US-225270P.
PR 14-AUG-2000; 2000US-225447P.
PR 14-AUG-2000; 2000US-225757P.
PR 14-AUG-2000; 2000US-225758P.
PR 22-AUG-2000; 2000US-226688P.
PR 30-AUG-2000; 2000US-228924P.
PR 01-SEP-2000; 2000US-229287P.
PR 01-SEP-2000; 2000US-229343P.
PR 01-SEP-2000; 2000US-229344P.
PR 01-SEP-2000; 2000US-229345P.
PR 05-SEP-2000; 2000US-229509P.
PR 05-SEP-2000; 2000US-229513P.
PR 08-SEP-2000; 2000US-231413P.
PR 21-SEP-2000; 2000US-234223P.
PR 21-SEP-2000; 2000US-234274P.
PR 25-SEP-2000; 2000US-234974P.
PR 27-SEP-2000; 2000US-235834P.
PR 29-SEP-2000; 2000US-236327P.
PR 29-SEP-2000; 2000US-236367P.
PR 29-SEP-2000; 2000US-236368P.
PR 29-SEP-2000; 2000US-236369P.
PR 29-SEP-2000; 2000US-236370P.
PR 02-OCT-2000; 2000US-236802P.
PR 02-OCT-2000; 2000US-237037P.
PR 02-OCT-2000; 2000US-237038P.
PR 02-OCT-2000; 2000US-237039P.
PR 02-OCT-2000; 2000US-237040P.
PR 13-OCT-2000; 2000US-239335P.
PR 20-OCT-2000; 2000US-240960P.
PR 20-OCT-2000; 2000US-241785P.
PR 20-OCT-2000; 2000US-244809P.
PR 01-NOV-2000; 2000US-244617P.
PR 17-NOV-2000; 2000US-249299P.
PR 08-DEC-2000; 2000US-251856P.
PR 08-DEC-2000; 2000US-251868P.
PR 08-DEC-2000; 2000US-251869P.

PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
XX
PI Rosen CA, Ruben SM, Barash SC;
XX
DR WPI: 2003-128199/12.
XX P-PSDB: AB012716.
XX
PT Isolated nucleic acid molecules encoding musculoskeletal system
XX associated polypeptides, useful for detecting disorders, e.g. cancer -
PS Claim 1; SEQ ID NO 346; 321pp; English.
XX
XX The invention describes an isolated nucleic acid molecule comprising a
XX sequence encoding musculoskeletal system associated polypeptides useful
XX for detecting disorders, e.g., cancer or cancer metastases, in animals
XX or humans. The nucleic acid; stimulates re-vascularisation of ischemic
XX tissues associated with conditions such as thrombosis, arteriosclerosis,
XX and other cardiovascular conditions; treats wounds due to injuries,
XX burns, post-operative tissue repair, and ulcers; stimulates angiogenesis
XX and limb regeneration; stimulates neuronal growth; can treat and prevent
XX neuronal damage occurring in certain disorders or neurodegenerative
XX conditions, such as, Alzheimer's disease, Parkinson's disease, and
XX AIDS-related complex; stimulates chondrocyte growth, thus they can be
XX used to enhance bone and periodontal regeneration and aid in tissue
XX transports or bone grafts; prevents skin aging due to sunburn by

CC stimulating keratinocyte growth; prevents hair loss, since FGF family
CC members activate hair-forming cells and promotes melanocyte growth;
CC stimulates growth and differentiation of hematopoietic cells and bone
CC marrow cells when used in combination with other cytokines; maintains
CC organs before transplantation or for supporting cell culture of primary
CC tissues; induces tissue of mesodermal origin to differentiate in early
CC embryos; increases or decreases the differentiation or proliferation of
CC embryonic stem cells; besides, haematopoietic lineage; modulates
CC mammalian characteristics, such as, body height, weight, hair colour, eye
CC colour, skin, percentage of adipose tissue, pigmentation, size, and shape
CC (e.g., cosmetic surgery); modulates mammalian metabolism; changes
CC mammal's metal state or physical state by influencing biorhythms;
CC cardiac rhythms; depression, tendency for violence, tolerance for pain,
CC reproductive capabilities, hormonal or endocrine levels, appetite,
CC libido, memory, or stress; increases or decreases storage capabilities,
CC fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors
CC or other nutritional components. This sequence encodes a novel human
CC musculoskeletal system antigen.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from the US patent office at
CC ftp.segdata.uspto.gov/sequence.html?DocID=20020147140.
CC
XX

SO Sequence 370 BP; 107 A; 71 C; 74 G; 115 T; 3 other;

Query Match 0.1%; Score 23; DB 25; Length 370;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4250 TTAACAATGCATTATTTTTAA 4272
|||||
DB 73 TTAACAATGCATTATTTTTAA 95

RESULT 5

AAI37650/C
ID AAI37650 standard; DNA; 2004 BP.

XX AAI37650;

DT 08-JAN-2002 (first entry)

XX Human musculoskeletal system related polynucleotide SEQ ID NO 4015.

DE Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
XX antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiviral;
KM vulnary; anticonvulsant; antibacterial; antifungal; antiparasitic;
KM cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
KW neurological disease; infection; human; secreted protein;
KW musculoskeletal system; ds.

XX Homo sapiens.

OS WO20015367-A1.

PN 02-AUG-2001.

XX 17-JAN-2001; 2001WO-US01338.

PF 31-JAN-2000; 2000US-0179065.

PR 04-FEB-2000; 2000US-0180628.

PR 24-FEB-2000; 2000US-0184664.

PR 02-MAR-2000; 2000US-0186350.

PR 16-MAR-2000; 2000US-0189874.

PR 17-MAR-2000; 2000US-0190076.

PR 18-APR-2000; 2000US-0198123.

PR 19-MAY-2000; 2000US-0205515.

PR 07-JUN-2000; 2000US-0209467.

PR 28-JUN-2000; 2000US-0214886.

PR 30-JUN-2000; 2000US-0215135.

PR 07-JUL-2000; 2000US-0216647.

PR 07-JUL-2000; 2000US-0216880.

PR 11-JUL-2000; 2000US-0217487.

PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225477.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226686.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227182.
PR 30-AUG-2000; 2000US-0227009.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.

PR	01-NOV-2000;	2000US-0234617.
PR	08-NOV-2000;	2000US-0246474.
PR	08-NOV-2000;	2000US-0246475.
PR	08-NOV-2000;	2000US-0246476.
PR	08-NOV-2000;	2000US-0246477.
PR	08-NOV-2000;	2000US-0246478.
PR	08-NOV-2000;	2000US-0246523.
PR	08-NOV-2000;	2000US-0246524.
PR	08-NOV-2000;	2000US-0246525.
PR	08-NOV-2000;	2000US-0246526.
PR	08-NOV-2000;	2000US-0246527.
PR	08-NOV-2000;	2000US-0246528.
PR	08-NOV-2000;	2000US-0246532.
PR	08-NOV-2000;	2000US-0246609.
PR	08-NOV-2000;	2000US-0246610.
PR	08-NOV-2000;	2000US-0246611.
PR	08-NOV-2000;	2000US-0246613.
PR	17-NOV-2000;	2000US-0249207.
PR	17-NOV-2000;	2000US-0249208.
PR	17-NOV-2000;	2000US-0249209.
PR	17-NOV-2000;	2000US-0249210.
PR	17-NOV-2000;	2000US-0249211.
PR	17-NOV-2000;	2000US-0249212.
PR	17-NOV-2000;	2000US-0249213.
PR	17-NOV-2000;	2000US-0249214.
PR	17-NOV-2000;	2000US-0249215.
PR	17-NOV-2000;	2000US-0249216.
PR	17-NOV-2000;	2000US-0249217.
PR	17-NOV-2000;	2000US-0249218.
PR	17-NOV-2000;	2000US-0249224.
PR	17-NOV-2000;	2000US-0249245.
PR	17-NOV-2000;	2000US-0249264.
PR	17-NOV-2000;	2000US-0249265.
PR	17-NOV-2000;	2000US-0249297.
PR	17-NOV-2000;	2000US-0249299.
PR	17-NOV-2000;	2000US-0249300.
PR	01-DEC-2000;	2000US-0250160.
PR	01-DEC-2000;	2000US-0250391.
PR	05-DEC-2000;	2000US-0251030.
PR	05-DEC-2000;	2000US-0251988.
PR	05-DEC-2000;	2000US-0256719.
PR	06-DEC-2000;	2000US-0251479.
PR	08-DEC-2000;	2000US-0251856.
PR	08-DEC-2000;	2000US-0251868.
PR	08-DEC-2000;	2000US-0251869.
PR	08-DEC-2000;	2000US-0251989.
PR	08-DEC-2000;	2000US-0251990.
PR	11-DEC-2000;	2000US-0254097.
PR	05-JAN-2001;	2001US-0259678.
PA	(HUMA-) HUMAN GENOME SCI INC.	
XX		
PI	Rosen CA, Barash SC, Ruben SM;	
XX		
DR	WPI: 2001-451937/48.	
XX		
PT	Isolated polypeptide for treating, preventing and/or prognosing	
PT	disorders related to the musculoskeletal system including	
PT	musculoskeletal cancers and also for testing and detection e.g.	
PT	diagnosis -	
XX		
PS	Example 2; SEQ ID NO 4015; 781pp + Sequence Listing; English.	
XX		
CC	(ABB03087-ABB04109) associated with the musculoskeletal system useful	
CC	for preventing, treating or ameliorating medical conditions e.g. by	
CC	protein or gene therapy. The genes are isolated from a range of human	
CC	tissues disclosed in the specification. The nucleic acids, proteins,	
CC	antibodies and (ant)agonists are useful in the diagnosis, treatment	
CC	and prevention of: (a) cancer, e.g. breast and ovarian cancer and	
CC	other cancers of the adrenal gland, bone, bone marrow, breast,	
CC	gastrointestinal tract, liver, lung, or urogenital; (b) immune	
CC	disorders e.g. Addison's disease, allergies, autoimmune haemolytic	

Query Match	0.1%;	Score 23;	DB 22;	Length 2004;
Best Local Similarity	100.0%;	Pred. No. 55;		
Matches 23;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY 4250	TTAAACATGGCATTTTAA	4272		
Db 439	TTAAACATGGCATTTTAA	417		
RESULT 6				
AA137651/C				
ID AA137651	standard; DNA; 2004 BP.			
XX AA137651;				
XX AC				
XX DT				
XX 08-JAN-2002	(first entry)			
DE	Human musculoskeletal system related polynucleotide SEQ ID NO 4016.			
XX				
KW	Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;			
KW	antiallergic; hepatotropic; antidiabetic; antiinflammatory; anticancer;			
KW	vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic;			
KW	cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;			
KW	neurological disease; infection; human; secreted protein;			
KW	musculoskeletal system; ds.			
XX				
OS	Homo sapiens.			
XX				
XX				
PD	02-AUG-2001.			
PF	17-JAN-2001; 2001WO-US01338.			
XX				
PR	31-JAN-2000; 2000US-0179065.			
PR	04-FEB-2000; 2000US-0180628.			
PR	24-FEB-2000; 2000US-0184664.			
PR	02-MAR-2000; 2000US-0186350.			
PR	16-MAR-2000; 2000US-0189874.			
PR	17-MAR-2000; 2000US-0190076.			
PR	18-APR-2000; 2000US-0198123.			
PR	19-MAY-2000; 2000US-0205515.			
PR	07-JUN-2000; 2000US-0209467.			
PR	28-JUN-2000; 2000US-0214886.			
PR	30-JUN-2000; 2000US-0215135.			
PR	07-JUL-2000; 2000US-0216647.			
PR	07-JUL-2000; 2000US-0216880.			
PR	11-JUL-2000; 2000US-0217487.			
PR	11-JUL-2000; 2000US-0217496.			
PR	14-JUL-2000; 2000US-0218290.			
PR	26-JUL-2000; 2000US-0220963.			
PR	26-JUL-2000; 2000US-0220964.			
PR	14-AUG-2000; 2000US-0224518.			
PR	14-AUG-2000; 2000US-0224519.			
PR	14-AUG-2000; 2000US-0225213.			
PR	14-AUG-2000; 2000US-0225214.			
PR	14-AUG-2000; 2000US-0225266.			
PR	14-AUG-2000; 2000US-0225267.			
PR	14-AUG-2000; 2000US-0225268.			
PR	14-AUG-2000; 2000US-0225270.			
PR	14-AUG-2000; 2000US-0225270.			

Best Local Similarity 100.0%; Pred. No. 55;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4250 TTAACATGCATTTATTTAAA 4272
|||||
Db 439 TTAACATGCATTTATTTAAA 417

RESULT 7
ABX60638/c
ID ABX60638 standard; cDNA; 2004 BP.
XX
AC ABX60638;
XX
DT 26-FEB-2003 (first entry)
XX
DE cDNA encoding novel human musculoskeletal system antigen #2982.
XX
KW Gene; ss; musculoskeletal system antigen; cancer; metastasis;
KW re-vascularisation; thrombosis; arteriosclerosis; mineral content;
KW cardiovascular condition; wound; injury; burn; angiogenesis; ulcer;
KW post-operative tissue repair; limb regeneration; neuronal growth;
KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
KW AIDS-related complex; chondrocyte growth; bone regeneration;
KW periodontal regeneration; tissue transport; bone graft; skin aging;
KW keratinocyte growth; hair loss; melanocyte growth; cell proliferation;
KW cell growth; organ transplant; cell differentiation; body height;
KW weight; hair colour; eye colour; skin; percentage of adipose tissue;
KW pigmentation; cosmetic surgery; metabolism; biorhythm; circadian rhythm;
KW depression; tendency for violence; pain; reproductive capability;
KW hormone level; endocrine level; appetite; libido; memory; stress;
KW storage capability; fat content; lipid content; protein content;
KW carbohydrate content; vitamin content; cofactor content;
KW nutritional component.
XX
OS Homo sapiens.
XX
PN US2002147140-A1.
XX
PD 10-OCT-2002.
XX
PF 17-JAN-2001; 2001US-0764877.
XX
XX 31-JAN-2000; 2000US-179065P.
PR 04-FEB-2000; 2000US-180628P.
PR 28-JUN-2000; 2000US-214866P.
PR 07-JUL-2000; 2000US-216647P.
PR 07-JUL-2000; 2000US-216880P.
PR 11-JUL-2000; 2000US-217487P.
PR 11-JUL-2000; 2000US-217496P.
PR 14-JUL-2000; 2000US-218290P.
PR 26-JUL-2000; 2000US-220963P.
PR 26-JUL-2000; 2000US-220964P.
PR 14-AUG-2000; 2000US-224518P.
PR 14-AUG-2000; 2000US-224519P.
PR 14-AUG-2000; 2000US-225267P.
PR 14-AUG-2000; 2000US-225268P.
PR 14-AUG-2000; 2000US-225270P.
PR 14-AUG-2000; 2000US-225447P.
PR 14-AUG-2000; 2000US-225757P.
PR 14-AUG-2000; 2000US-225758P.
PR 22-AUG-2000; 2000US-226868P.
PR 30-AUG-2000; 2000US-228924P.
PR 01-SEP-2000; 2000US-229287P.
PR 01-SEP-2000; 2000US-229343P.
PR 01-SEP-2000; 2000US-229344P.
PR 01-SEP-2000; 2000US-229345P.
PR 05-SEP-2000; 2000US-229509P.
PR 05-SEP-2000; 2000US-229513P.
PR 08-SEP-2000; 2000US-231413P.
PR 21-SEP-2000; 2000US-234223P.
PR 21-SEP-2000; 2000US-234274P.
PR 25-SEP-2000; 2000US-234997P.

PR 27-SEP-2000; 2000US-235834P.
PR 29-SEP-2000; 2000US-236327P.
PR 29-SEP-2000; 2000US-236367P.
PR 29-SEP-2000; 2000US-236368P.
PR 29-SEP-2000; 2000US-236369P.
PR 29-SEP-2000; 2000US-236370P.
PR 02-OCT-2000; 2000US-236802P.
PR 02-OCT-2000; 2000US-237037P.
PR 02-OCT-2000; 2000US-237038P.
PR 02-OCT-2000; 2000US-237039P.
PR 02-OCT-2000; 2000US-237040P.
PR 13-OCT-2000; 2000US-239335P.
PR 20-OCT-2000; 2000US-240960P.
PR 20-OCT-2000; 2000US-241785P.
PR 20-OCT-2000; 2000US-241809P.
PR 01-NOV-2000; 2000US-244617P.
PR 17-NOV-2000; 2000US-249299P.
PR 08-DEC-2000; 2000US-251856P.
PR 08-DEC-2000; 2000US-251868P.
PR 08-DEC-2000; 2000US-251869P.

XX (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
XX
XX Rosen CA, Ruben SM, Barash SC;
XX
XX WPI; 2003-128199/12.
XX
XX Isolated nucleic acid molecules encoding musculoskeletal system
PT associated polypeptides, useful for detecting disorders, e.g. cancer -
XX
XX Disclosure; SEQ ID NO 4015; 321pp; English.

XX
CC The invention describes an isolated nucleic acid molecule comprising a
CC sequence encoding musculoskeletal system associated polypeptides useful
CC for detecting disorders, e.g., cancer or cancer metastases, in animals
CC or humans. The nucleic acid: stimulates re-vascularisation of ischaemic
CC tissues associated with conditions such as thrombosis, arteriosclerosis,
CC and other cardiovascular conditions; treats wounds due to injuries,
CC burns, post-operative tissue repair, and ulcers; stimulates angiogenesis
CC and limb regeneration; stimulates neuronal growth; can treat and prevent
CC neuronal damage occurring in certain disorders or neurodegenerative
CC conditions, such as, Alzheimer's disease, Parkinson's disease, and
CC AIDS-related complex; stimulates chondrocyte growth, thus they can be
CC used to enhance bone and periodontal regeneration and aid in tissue
CC transports or bone grafts; prevents skin aging due to sunburn by
CC stimulating keratinocyte growth; prevents hair loss, since FGF family
CC members activate hair-forming cells and promotes melanocyte growth;
CC stimulates growth and differentiation of hematopoietic cells and bone
CC marrow cells when used in combination with other cytokines; maintains
CC organs before transplantation or for supporting cell culture of primary
CC tissues; induces tissue of mesodermal origin to differentiate in early
CC embryos; increases or decreases the differentiation or proliferation of
CC embryonic stem cells, besides, haematopoietic lineage; modulates
CC mammalian characteristics, such as, body height, weight, hair colour, eye
CC colour, skin, percentage of adipose tissue, pigmentation, size, and shape
CC (e.g., cosmetic surgery); modulates mammalian metabolism; changes
CC mammal's metal state or physical state by influencing biorhythms,
CC circadian rhythms, depression, tendency for violence, tolerance for pain,
CC reproductive capabilities, hormonal or endocrine levels, appetite,
CC libido, memory, or stress; increases or decreases storage capabilities,
CC fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors
CC or other nutritional components. This sequence encodes a novel human
CC musculoskeletal system antigen.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from the US patent office at
CC ftp.segdata.uspto.gov/sequence.html?DocID=20020147140.
XX
SQ Sequence 2004 BP; 629 A; 429 C; 353 G; 593 T; 0 other;

Query Match 0.1%; Score 23; DB 25; Length 2004;

Best Local Similarity 100.0%; Pred. No. 55;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4250 TTAACATGATGATTTTAA 4272
DB 439 TTAACATGATGATTTTAA 417

RESULT 8
ABX60639/c
ID ABX60639 standard; cDNA; 2004 BP.

XX ABX60639;

DT 26-FEB-2003 (first entry)

XX cDNA encoding novel human musculoskeletal system antigen #2983.

Gene: ss; musculoskeletal system antigen; cancer; metastasis;
re-vascularisation; thrombosis; arteriosclerosis; mineral content;
cardiovascular condition; wound; injury; burn; angiogenesis; ulcer;
post-operative tissue repair; limb regeneration; neuronal growth;
neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
AIDS-related complex; chondrocyte growth; bone regeneration;
periodontal regeneration; tissue transport; bone graft; skin aging;
keratinocyte growth; hair loss; melanocyte growth; cell proliferation;
cell growth; organ transplant; cell differentiation; body height;
weight; hair colour; eye colour; skin; percentage of adipose tissue;
pigmentation; cosmetic surgery; metabolism; biopharm; cardiac rhythm;
depression; tendency for violence; pain; reproductive capability;
hormone level; endocrine level; appetite; libido; memory; stress;
storage capability; fat content; lipid content; protein content;
carbohydrate content; vitamin content; cofactor content;
nutritional component.

XX Homo sapiens.

XX US2002147140-A1.

XX 10-OCT-2002.

XX 17-JAN-2001; 2001US-0764877.

XX 31-JAN-2000; 2000US-179065P.
PR 04-FEB-2000; 2000US-180628P.
PR 28-JUN-2000; 2000US-214886P.
PR 07-JUL-2000; 2000US-216647P.
PR 07-JUL-2000; 2000US-216880P.
PR 11-JUL-2000; 2000US-217487P.
PR 11-JUL-2000; 2000US-217496P.
PR 14-JUL-2000; 2000US-218290P.
PR 26-JUL-2000; 2000US-220963P.
PR 26-JUL-2000; 2000US-220964P.
PR 14-AUG-2000; 2000US-224518P.
PR 14-AUG-2000; 2000US-224519P.
PR 14-AUG-2000; 2000US-225267P.
PR 14-AUG-2000; 2000US-225268P.
PR 14-AUG-2000; 2000US-225270P.
PR 14-AUG-2000; 2000US-225447P.
PR 14-AUG-2000; 2000US-225477P.
PR 14-AUG-2000; 2000US-225758P.
PR 22-AUG-2000; 2000US-226868P.
PR 30-AUG-2000; 2000US-228924P.
PR 01-SEP-2000; 2000US-229287P.
PR 01-SEP-2000; 2000US-229343P.
PR 01-SEP-2000; 2000US-229344P.
PR 01-SEP-2000; 2000US-229345P.
PR 05-SEP-2000; 2000US-229509P.
PR 05-SEP-2000; 2000US-229513P.
PR 08-SEP-2000; 2000US-231413P.
PR 21-SEP-2000; 2000US-234223P.
PR 21-SEP-2000; 2000US-234274P.
PR 25-SEP-2000; 2000US-234979P.

PR 27-SEP-2000; 2000US-235834P.
PR 29-SEP-2000; 2000US-236327P.
PR 29-SEP-2000; 2000US-236367P.
PR 29-SEP-2000; 2000US-236368P.
PR 29-SEP-2000; 2000US-236369P.
PR 29-SEP-2000; 2000US-236370P.
PR 02-OCT-2000; 2000US-236802P.
PR 02-OCT-2000; 2000US-237037P.
PR 02-OCT-2000; 2000US-237038P.
PR 02-OCT-2000; 2000US-237039P.
PR 02-OCT-2000; 2000US-237040P.
PR 13-OCT-2000; 2000US-239935P.
PR 20-OCT-2000; 2000US-240960P.
PR 20-OCT-2000; 2000US-241785P.
PR 20-OCT-2000; 2000US-241809P.
PR 01-NOV-2000; 2000US-244617P.
PR 17-NOV-2000; 2000US-249299P.
PR 08-DEC-2000; 2000US-251856P.
PR 08-DEC-2000; 2000US-251868P.
PR 08-DEC-2000; 2000US-251869P.
PR (ROSE/) ROSEN C A.
PR (RUBE/) RUBEN S M.
PR (BARA/) BARASH S C.
PI Rosen CA, Ruben SM, Barash SC;
PI WPI; 2003-128199/12.
PT Isolated nucleic acid molecules encoding musculoskeletal system
PT associated polypeptides, useful for detecting disorders, e.g. cancer -
PS Disclosure: SEQ ID NO 4016; 321pp; English.
PS
XX
XX The invention describes an isolated nucleic acid molecule comprising a
CC sequence encoding musculoskeletal system associated polypeptides useful
CC for detecting disorders, e.g., cancer or cancer metastases, in animals
CC or humans. The nucleic acid stimulates re-vascularisation of ischemic
CC tissues associated with conditions such as thrombosis, arteriosclerosis,
CC and other cardiovascular conditions; treats wounds due to injuries,
CC burns, post-operative tissue repair, and ulcers; stimulates angiogenesis
CC and limb regeneration; stimulates neuronal growth; can treat and prevent
CC neuronal damage occurring in certain disorders or neurodegenerative
CC conditions, such as, Alzheimer's disease, Parkinson's disease, and
CC AIDS-related complex; stimulates chondrocyte growth, thus they can be
CC used to enhance bone and periodontal regeneration and aid in tissue
CC transports or bone grafts; prevents skin aging due to sunburn by
CC stimulating keratinocyte growth; prevents hair loss, since RGF family
CC members activate hair-forming cells and promotes melanocyte growth;
CC stimulates growth and differentiation of hematopoietic cells and bone
CC marrow cells when used in combination with other cytokines; maintains
CC organs before transplantation or for supporting cell culture of primary
CC tissues; induces tissue of mesodermal origin to differentiate in early
CC embryos; increases or decreases the differentiation or proliferation of
CC embryonic stem cells, besides, haematopoietic lineage; modulates
CC mammalian characteristics, such as, body height, weight, hair colour, eye
CC colour, skin, percentage of adipose tissue, pigmentation, size, and shape
CC (e.g., cosmetic surgery); modulates mammalian metabolism; changes
CC mammal's metal state or physical state by influencing biorythms,
CC circadian rhythms, depression, tendency for violence, tolerance for pain,
CC reproductive capabilities, hormonal or endocrine levels, appetite,
CC libido, memory, or stress; increases or decreases storage capabilities,
CC fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors
CC or other nutritional components. This sequence encodes a novel human
CC musculoskeletal system antigen.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from the US patent office at
CC ftp.segdata.uspto.gov/sequence.html?DocID=20020147140.
SQ Sequence 2004 BP; 632 A; 428 C; 351 G; 593 T; 0 other;

Query Match

0.1%; Score 23; DB 25; Length 2004;

Best Local Similarity 100.0%; Pred. No. 55;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4250 TTAACATGCGATTATTATAA 4272
|||||
DB 439 TTAACATGCGATTATTATAA 417

RESULT 9

AB070267
ID AB070267 standard; DNA: 917 BP.

AC AB070267;

DT 29-AUG-2002 (first entry)

DE Listeria monocytogenes 4b contig DNA sequence #209.

KW Antibacterial; Listeria; food contamination; mutational analysis;
infection; ds.

OS Listeria monocytogenes 4b.

XX WO200228891-A2.

PD 11-APR-2002.

PF 04-OCT-2001; 2001WO-FR03061.

PR 04-OCT-2000; 2000FR-0012697.

PA (INSP) INST PASTEUR.
(CNRS) CNRS CENT NAT RECH SCI.

PI Kunst F, Glaser P;

DR WPI: 2002-332479/37.

PT New genomic sequences from Listeria species, useful for detection,
treatment and prevention of infection, also related polypeptides,
PT antibodies and modulators -

XX Claim 14; SEQ ID 3080; 180pp; French.

CC The present invention relates to nucleic acid sequences

CC (AB067188-AB071212) from Listeria sp. The sequences are useful as probes

CC and primers for identification and/or detection of Listeria (e.g. as

CC contaminants in foods, or mutational analysis) and for analysis of

CC gene expression. Proteins encoded by the nucleic acid sequences can be

CC used to screen for compounds that modulate gene expression, replication

CC and pathogenicity of Listeria (potential therapeutic agents), also for

CC treating infections by Listeria, and are useful as immunogens in

CC anti-Listeria vaccines.

CC Note: The sequence data for this patent did not form part

CC of the printed specification, but was obtained in electronic format

CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 917 BP; 211 A; 178 C; 164 G; 360 T; 4 other;

SO Query Match 0.1%; Score 22; DB 24; Length 917;

Best Local Similarity 100.0%; Pred. No. 1.5e+02;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2808 TATCAGCTTTTGAGTCGCTTG 2829
|||||

DB 279 TATCAGCTTTTGAGTCGCTTG 300

RESULT 10

ABK74889/c
ID ABK74889 standard; DNA: 1393 BP.

XX ABK74889;

XX 13-AUG-2002 (first entry)

DE Bacillus licheniformis genomic sequence tag (GST) #2180.

XX Differential gene expression; genomic sequenced tag; GST;

KW altered culture condition; environmental stress;

KW physiological provocation; ds.

OS Bacillus licheniformis.

XX WO200229113-A2.

PD 11-APR-2002.

PF 05-OCT-2001; 2001WO-US31437.

PR 06-OCT-2000; 2000US-0680598.

PR 27-MAR-2001; 2001US-279526P.

PA (NOVO) NOVOZYMES BIOTECH INC.

XX (NOVO) NOVOZYMES AS.

XX Berka R, Clausen IG;

XX WPI: 2002-416684/44.

PS Claim 4; SEQ ID NO 2180; 200pp; English.

CC The invention describes a method of monitoring differential expression of
CC genes in a first Bacillus cell relative to expression of the genes in
CC other Bacillus cells, comprising hybridising labelled nucleic acid probes

CC isolated from Bacillus cells to a substrate containing array of Bacillus

CC genomic sequenced tags (GST), examining the array, and determining

CC relative gene expression by an observed hybridisation reporter signal of

CC a spot in the array. The method is useful for measuring the expression of

CC genes in a first Bacillus cell relative to expression of the same genes

CC in one or more second Bacillus cells. The method is useful for monitoring

CC global expression of several genes from a Bacillus cell, discovering new

CC genes, identifying possible functions of unknown open reading frames and

CC monitoring gene copy number variation and stability. Monitoring changes

CC in expression of genes may be used to provide a representation of the way

CC in which Bacillus cells adapt to changes in culture conditions,

CC environmental stress or other physiological provocation. Extensive

CC follow-up characterisation is unnecessary, when one spot on an array

CC equals one gene or one open reading frame, since sequence information is

CC available. This sequence represents a genomic sequence tag (GST) used in

CC the method of the invention.

CC Note: The sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic format directly from WIPO

XX at ftp.wipo.int/pub/published_pct_sequences.

SO Sequence 1393 BP; 346 A; 319 C; 352 G; 375 T; 1 other;

SO Query Match 0.1%; Score 22; DB 24; Length 1393;

Best Local Similarity 100.0%; Pred. No. 1.5e+02;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7457 TCCGTGATGGCCAGCTCTCG 7478
|||||

DB 393 TCCGTGATGGCCAGCTCTCG 372

RESULT 11

ABLA9345
ID ABLA9345 standard; DNA: 19233 BP.

XX

AC ABL49345;
 XX
 DT 01-MAY-2002 (first entry)
 XX
 DE Human polynucleotide associated with DNA replication SEQ ID NO 45.
 XX
 KW Human: cytosolic; neuroprotective; nootropic; immunostimulant;
 KW ERCC3; SNRPB; RAD50; Lig2; cytosine methylation; Ataxia telangiectasia;
 KW ATR-X; Bloom's syndrome; tumour; cancer; methylation; gene; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200177377-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-EP03971.
 XX
 PR 06-APR-2000; 2000DE-1019058.
 PR 07-APR-2000; 2000DE-1019173.
 PR 30-JUN-2000; 2000DE-1032529.
 PR 01-SEP-2000; 2000DE-1043826.
 XX
 PA (EPIC-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI: 2002-017471/02.
 XX
 PT New nucleic acid sequences from chemically modified genes associated
 PT with DNA replication, useful for analysing cytosine methylations for
 PT diagnosis and therapy of diseases e.g. Ataxia telangiectasia
 XX
 PS Claim 1: SEQ ID NO 45; 23pp + Sequence Listing: English.
 XX
 CC The invention relates to nucleic acid sequences comprising at least 18
 CC bases of a chemically pretreated gene associated with gene regulation,
 CC selected from 94 genes (ABL49301-ABL49394) and/or complementary sequences
 CC associated with DNA replication, CENPB, DNAL2, ATR, CHD1L, ERCC3, SNRPB,
 CC RAD50 and Lig2. The chemical pretreatment converts cytosine bases
 CC unethylated at the 5-position to uracil or another base with
 CC hybridisation behaviour dissimilar to cytosine, to enable analysis of
 CC cytosine methylations. The DNA sequences and method are useful in the
 CC diagnosis of diseases (or predisposition to diseases) associated with DNA
 CC replication and in therapy of such diseases, by enabling analysis of the
 CC cytosine methylation patterns of such genes. They are especially useful
 CC in diagnosis and therapy of e.g. Ataxia telangiectasia, ATR-X, Bloom's
 CC syndrome, solid tumours and cancer.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification and was supposed to be available directly from WIPO at
 CC ftp.wipo.int/pub/published_pat_sequences. However, the sequence data did
 CC not correspond to that referred to in the specification. The present data
 CC is taken from EPO data for the patent.
 XX
 SO Sequence 19233 BP; 4336 A; 489 C; 4429 G; 9848 T; 131 other;
 Query Match 0.1%; Score 22; DB 24; Length 19233;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1152 AATTGAGTATTGATTTT 1173
 DB 12221 AATTGAGTATTGATTTT 12242

XX Nucleotide sequence of the FK-520 biosynthetic gene cluster.
 DE
 XX FK-520; polyketide synthase; PKS; gene cluster; immunosuppressant;
 KW Streptomyces hygroscopicus var. ascomiteticus; immunophilin;
 KW FK-506 binding protein; polyketide compound; transplant rejection;
 KW graft-versus-host disease; uveitis; alopecia universalis;
 KW autoimmune chronic active hepatitis; inflammatory bowel disease;
 KW multiple sclerosis; primary biliary cirrhosis; scleroderma;
 KW neurite outgrowth; nerve regrowth; Parkinson's disease;
 KW Alzheimer's disease; stroke; traumatic spinal cord; brain injury;
 KW peripheral neuropathy; ss.
 XX
 OS Streptomyces hygroscopicus.
 XX
 FH Location/Qualifiers
 FT complement (412..1836)
 FT CDS
 FT /tag= a
 FT /note= "fkbw gene"
 FT complement (2020..3579)
 FT CDS
 FT /tag= b
 FT /note= "fkbv gene"
 FT 3969..4496
 FT CDS
 FT /tag= c
 FT /note= "fkbr2 gene"
 FT complement (4595..5488)
 FT CDS
 FT /tag= d
 FT /note= "fkbr1 gene"
 FT 5601..6818
 FT CDS
 FT /tag= e
 FT /note= "fkbe gene"
 FT 6808..8052
 FT CDS
 FT /tag= f
 FT /note= "fkbf gene"
 FT 8156..8824
 FT CDS
 FT /tag= g
 FT /note= "fkbg gene"
 FT complement (9122..9883)
 FT CDS
 FT /tag= h
 FT /note= "fkhh gene"
 FT complement (9894..10994)
 FT CDS
 FT /tag= i
 FT /note= "fkbi gene"
 FT complement (10987..11247)
 FT CDS
 FT /tag= j
 FT /note= "fkbi gene"
 FT complement (11244..12092)
 FT CDS
 FT /tag= k
 FT /note= "fkbi gene"
 FT complement (12113..13150)
 FT CDS
 FT /tag= l
 FT /note= "fkbl gene"
 FT complement (13212..23988)
 FT CDS
 FT /tag= m
 FT /note= "fkbc gene"
 FT complement (13452..13662)
 FT misc_feature
 FT /tag= n
 FT /note= "ACP6"
 FT complement (13761..14394)
 FT misc_feature
 FT /tag= o
 FT /note= "KR6"
 FT complement (14517..15294)
 FT misc_feature
 FT /tag= p
 FT /note= "ER6"
 FT complement (15438..16587)
 FT misc_feature
 FT /tag= q
 FT /note= "dehydratase domain (DH) 6"
 FT complement (16587..17820)
 FT misc_feature
 FT /tag= r
 FT /note= "acyltransferase domain (AT) 6"
 FT complement (17820..19053)
 FT misc_feature
 FT /tag= s
 FT /note= "KSc"

```

FT misc-feature complement (19116..19326)
FT /tag- t
FT /note- "ACP5"
FT complement (19464..20097)
FT /tag- u
FT /note- "KR5"
FT complement (20241..21420)
FT /tag- v
FT /note- "DH5"
FT complement (21420..22653)
FT /tag- w
FT /note- "AT5"
FT complement (22653..23892)
FT /tag- x
FT /note- "KS5"
FT complement (23992..46573)
FT /tag- y
FT /note- "fkb gene"
FT complement (24163..24373)
FT /tag- z
FT /note- "ACP4"
FT complement (24997..26146)
FT /tag- aa
FT /note- "DH4 (inactive)"
FT complement (26146..27430)
FT /tag- ab
FT /note- "AT4"
FT complement (27430..28684)
FT /tag- ac
FT /note- "KS4"
FT complement (28750..28960)
FT /tag- ad
FT /note- "ACP3"
FT complement (29092..29740)
FT /tag- ae
FT /note- "KR3"
FT complement (29869..31018)
FT /tag- af
FT /note- "DH3 (inactive)"
FT complement (31018..32185)
FT /tag- ag
FT /note- "AT3"
FT complement (32185..33439)
FT /tag- ah
FT /note- "KS3"
FT complement (33505..33715)
FT /tag- ai
FT /note- "ACP2"
FT complement (33823..34480)
FT /tag- aj
FT /note- "KR2"
FT complement (34606..35749)
FT /tag- ak
FT complement (28750..28960)
FT /tag- al
FT /note- "DH2 (inactive)"
FT complement (35749..37144)
FT /tag- am
FT /note- "AT2"
FT complement (37145..38296)
FT /tag- an
FT /note- "KS2"
FT complement (38371..38581)
FT /tag- ao
FT /note- "ACP1"
FT complement (38677..39307)
FT /tag- ap
FT /note- "KR1"
FT complement (39442..40609)
FT /tag- aq
FT /note- "DH1"
FT complement (40609..41842)
FT /tag- ar

```

```

FT /note- "AT1"
FT complement (41842..43093)
FT /tag- as
FT /note- "KS of extender module 1 (KS1)"
FT complement (43144..43660)
FT /tag- at
FT /note- "ACP of loading domain"
FT complement (43777..44629)
FT /tag- au
FT /note- "ER of loading domain"
FT complement (44974..46573)
FT /tag- av
FT /note- "CoA ligase of loading domain"
FT complement (46754..47788)
FT /tag- aw
FT /note- "fkb gene"
FT complement (47785..52272)
FT /tag- ax
FT /note- "fkb gene"
FT complement (52275..52716)
FT /tag- ay
FT /note- "fkb gene"
FT complement (52362..53576)
FT /tag- az
FT /note- "KS7"
FT complement (53577..54716)
FT /tag- ba
FT /note- "AT7"
FT complement (54717..55871)
FT /tag- bb
FT /note- "DH7"
FT complement (56019..56819)
FT /tag- bc
FT /note- "ER7"
FT complement (56943..57575)
FT /tag- bd
FT /note- "KR7"
FT complement (57710..57920)
FT /tag- be
FT /note- "ACP7"
FT complement (57990..59243)
FT /tag- bf
FT /note- "KS8"
FT complement (59244..60398)
FT /tag- bg
FT /note- "AT8"
FT complement (60399..61412)
FT /tag- bh
FT /note- "DH8 (inactive)"

```

Query Match 0.1%: Score 22: DB 21: Length 77536:
 Best Local Similarity 100.0%: Pred. No. 1e+02:
 Matches 22: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

```

Qy 23444 GCCCGCGTGGCGCTTCGCA 23465
   |||
DB 64419 GCCCGCGTGGCGCTTCGCA 64440

```

```

RESULT 13
AA14651/c
ID AAA14651 standard; DNA: 77536 BP.
XX
AC AAA14651;
XX
DT 08-AUG-2000 (first entry)
XX
DE Nucleotide sequence of the FK-520 biosynthetic gene cluster.
XX
KW FK-520: polyketide synthase; PKS: gene cluster; immunosuppressant;
KW Streptomyces hygroscopicus var. ascomyceticus; immunophilin;
KW FK-506 binding protein; polyketide compound; transplant rejection;
KW graft-versus-host disease; uveitis; alopecia universalis;

```



```

FT misc-feature complement (43777..44629)
FT /tag- au
FT /note- "ER of loading domain"
FT misc-feature complement (44974..46573)
FT /tag- av
FT /note- "CoA ligase of loading domain"
FT CDS
FT /tag- aw
FT /note- "fxbo gene"
FT CDS
FT /tag- ax
FT /note- "fxbp gene"
FT CDS
FT /tag- ay
FT /note- "fxba gene"
FT misc-feature
FT /tag- az
FT /note- "KS7"
FT misc-feature
FT /tag- bc
FT /note- "ER7"
FT misc-feature
FT /tag- bd
FT /note- "KR7"
FT misc-feature
FT /tag- be
FT /note- "ACP7"
FT misc-feature
FT /tag- bf
FT /note- "KS8"
FT misc-feature
FT /tag- bg
FT /note- "Ar8"
FT misc-feature
FT /tag- bh
FT /note- "DH8 (inactive)"

Query Match
Best Local Similarity 100.0%; Score 22; DB 21; Length 77536;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23444 GCCCGCGTGTGGCCTTCGCA 23465
DB 22086 GCCCGCGTGTGGCCTTCGCA 22065

RESULT 14
AB067196/C
ID AB067196 standard; DNA; 684707 BP.
AC AB067196;
XX
XX 29-AUG-2002 (first entry)
DE Listeria innocua contig DNA sequence #9.
XX
XX Antibacterial; Listeria; food contamination; mutational analysis;
XX infection; ds.
OS Listeria innocua.
XX
XX WO200228891-A2.
PN
XX 11-APR-2002.
PD
XX 04-OCT-2001; 2001WO-FR03061.
XX

```

```

PR 04-OCT-2000; 2000FR-0012697.
XX
XX (INSP ) INST PASTEUR.
PA (CNRS ) CNRS CENT NAT RECH SCI.
XX
XX Kunst F, Glaser P;
PI
XX WPI; 2002-332479/37.
XX
XX New genomic sequences from Listeria species, useful for detection,
PT treatment and prevention of infection, also related polypeptides,
PT antibodies and modulators
XX
XX Claim 5; SEQ ID 9; 180pp; French.
XX
XX The present invention relates to nucleic acid sequences
CC (AB067188-AB071212) from Listeria sp. The sequences are useful as probes
CC and primers for identification and/or detection of Listeria (e.g. as
CC contaminants in foods, or mutational analysis) and for analysis of
CC gene expression. Proteins encoded by the nucleic acid sequences can be
CC used to screen for compounds that modulate gene expression, replication
CC and pathogenicity of Listeria (potential therapeutic agents), also for
CC treating infections by Listeria, and are useful as immunogens in
CC anti-Listeria vaccines.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 684707 BP; 213423 A; 126375 C; 133438 G; 211468 T; 3 other:

Query Match
Best Local Similarity 100.0%; Score 22; DB 24; Length 684707;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2808 TATCAGCTTTTGACCTGCTTC 2829
DB 47940 TATCAGCTTTTGACCTGCTTC 47919

RESULT 15
AAK20248/C
ID AAK20248 standard; DNA; 910715 BP.
XX
XX AAK20248;
AC
XX
XX 04-MAY-1999 (first entry)
DE Borrelia burgdorferi polynucleotide sequence #1.
XX
XX Borrelia burgdorferi; spirochete; bacterium; pathogen; Lyme disease;
KW epidemic relapsing fever; endemic relapsing fever; Lyme borreliosis;
KW infection; diagnosis; characterisation; detection; ds.
XX
XX Borrelia burgdorferi.
OS
XX
XX WO9858943-A1.
PN
XX 30-DEC-1998.
PD
XX 18-JUN-1998; 98WO-US12764.
PF
XX 03-SEP-1997; 97US-0057483.
PR 20-JUN-1997; 97US-0050359.
PR 22-JUL-1997; 97US-0053344.
PR 22-JUL-1997; 97US-0053377.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
PA (MEDI-) MEDIMUNE INC.
XX
XX Clayton R, Dougherty BA, Fraser C, Lathigra R, Smith HO;
PI White OR;
XX
XX WPI; 1999-081217/07.
XX

```

XX New isolated *Borrelia burgdorferi* nucleic acids - used to develop
PT products for the detection, diagnosis, characterisation, prevention
PT and therapy of infections, particularly Lyme disease
XX
PS Claim 1: Page 157-671, 1128pp; English.
XX
CC AAX20248 to AAX20402 represent polynucleotide sequences isolated from
CC *Borrelia burgdorferi* (Bb). Products derived from Bb can be used for
CC the detection, diagnosis, characterisation, prevention and therapy of
CC Bb infections, e.g. Lyme disease. They can also be used for the
CC production of biosynthetic products, e.g. enzymes. *Borrelia* belongs
CC to a family of motile, spiral-shaped bacteria called Spirochetes.
CC Spirochetes are pathogenic in humans and *Borrelia* causes epidemic and
CC endemic relapsing fever, and Lyme borreliosis, more commonly known as
CC Lyme disease.
XX
SQ Sequence 910715 BP; 327171 A; 129646 C; 130753 G; 323091 T; 54 other:
Query Match 0.1%; Score 22; DB 20; Length 910715;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 29735 AAAAATTTAACTTACGAC 29756
DB 77874 AAAAATTTAACTTACGAC 77853
RESULT 16
ABA03041
ID ABA03041 standard; DNA; 2944528 BP.
XX
AC ABA03041:
XX
DT 05-FEB-2002 (first entry)
XX
DE *Listeria monocytogenes* EGD-e genome sequence.
XX
KM Antihacterial; gene therapy; vaccine; biosynthesis; biodegradation;
KM vitamin B12; bacterial infection; disease; ds.
XX
OS *Listeria monocytogenes*.
XX
PN WO200177335-A2.
XX
PD 18-OCT-2001.
XX
PF 11-APR-2001; 2001WO-FR01118.
XX
PR 11-APR-2000; 2000FR-0004629.
XX
PA (INSP) INST PASTEUR.
XX
PI Buchrieser C, Frangeul L, Couve E, Rusnick C, Fsihl H, Dehoux P;
PI Dussurget O, Chetouani F, Nedjati H, Glaser P, Kunst F, Cossart P;
PI Daniels J, Goebel W, Kreft J, Kuhn M, Ng E, Vazquez-Poland JA;
PI Dominguez-Bernal G, Garrido-Garcia P, Tierrez-Martinez A, Amend A;
PI Chakraborty T, Dommann E, Hain T, Berche P, Charbit A, Durant L;
PI Perez-Diaz J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N;
PI Madueno E, De Pablos B, Wehlant J, Kaerst U, Ertian K, Hauf J;
PI Rose M, Voss H;
XX
DR WPI: 2002-010914/01.
XX
XX Genomic sequence for *Listeria monocytogenes*, useful e.g. for treatment
PT and prevention of *Listeria* and related bacterial infections, and
PT related polypeptides -
XX
PS Claim 1: SEQ ID No 1: 192pp; French.
XX
CC The present sequence is the genome sequence of *Listeria monocytogenes*
CC EGD-e. This sequence and fragments of this sequence are useful for
CC selecting probes and primers for detecting genes in *L. monocytogenes* and

CC related organisms, and to study genetic polymorphisms and other genomes.
CC Proteins (AB067297-AB0670149) expressed from the present sequence are
CC useful for raising specific antibodies, identification of *L.*
CC *monocytogenes* and related organisms, and for biosynthesis and
CC biodegradation, especially biosynthesis of vitamin B12. This sequence and
CC proteins encoded by it are also useful for selecting compounds that
CC regulate gene expression and cell replication and modulate *L.*
CC *monocytogenes*-related diseases. In addition, this sequence and proteins
CC encoded by it are useful in pharmaceutical and vaccine compositions for
CC the treatment or prevention of infections by *L. monocytogenes* and related
CC organisms.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 2944528 BP; 914202 A; 563301 C; 555061 G; 911964 T; 0 other:
Query Match 0.1%; Score 22; DB 24; Length 2944528;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 2808 TATCAGCTTTTGGAGCTGCTTG 2829
DB 2709929 TATCAGCTTTTGGAGCTGCTTG 2709950
RESULT 17
AB069245
ID AB069245 standard; DNA; 3011208 BP.
XX
AC AB069245:
XX
DT 29-AUG-2002 (first entry)
XX
DE *Listeria innocua* DNA sequence #684.
XX
KM Antihacterial; *Listeria*; food contamination; mutational analysis;
KM infection; ds.
XX
OS *Listeria innocua*.
XX
PN WO200228891-A2.
XX
PD 11-APR-2002.
XX
PF 04-OCT-2001; 2001WO-FR03061.
XX
PR 04-OCT-2000; 2000FR-0012697.
XX
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
XX
PI Kunst F, Glaser P;
XX
DR WPI: 2002-332479/37.
XX
XX New genomic sequences from *Listeria* species, useful for detection,
PT treatment and prevention of infection, also related polypeptides,
PT antibodies and modulators -
XX
PS Claim 5: SEQ ID 2058; 180pp; French.
XX
XX The present invention relates to nucleic acid sequences
CC (AB067188-AB071212) from *Listeria* sp. The sequences are useful as probes
CC and primers for identification and/or detection of *Listeria* (e.g. as
CC contaminants in foods, or mutational analysis) and for analysis of
CC gene expression. Proteins encoded by the nucleic acid sequences can be
CC used to screen for compounds that modulate gene expression, replication
CC and pathogenicity of *Listeria* (potential therapeutic agents), also for
CC treating infections by *Listeria*, and are useful as immunogens in
CC anti-*Listeria* vaccines.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic format

CC directly from WIP0 at ftp.wipo.int/pub/published_pct_sequences.

SQ Sequence 3011208 BP; 941651 A; 568176 C; 559189 G; 942192 T; 0 other;

Query Match 0.1%; Score 22; DB 24; Length 3011208;

Best Local Similarity 100.0%; Pred. No. 68;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2808 TATCAGCTTTTGAGCTGCTTG 2829

DB 2800874 TATCAGCTTTTGAGCTGCTTG 2800895

RESULT 18

ABLO1517/c

ID ABL01517 standard; DNA: 496 BP.

AC ABL01517;

DT 15-MAR-2002 (first entry)

DE Murine apoptosis related DNA sequence #182.

KM Apoptosis; mouse; cancer; autoimmune disease; viral infection;

KM Alzheimer's disease; Parkinson's disease; Huntington's disease;

KM reperfusion injury; stroke; liver disease; dilatory cardiomyopathy;

KM transgenic animal; hepatocarcinoma; antialcoholism; cytostatic;

KM immunosuppressive; vitreous; neoplastic; neuroprotective; vasotropic;

KM antiparkinsonian; cerebroprotective; ds.

OS Mus sp.

XX DE10126344-A1.

XX 24-JAN-2002.

XX 30-MAY-2001; 2001DE-1026344.

XX 14-JUL-2000; 2000DE-1034303.

XX (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.

XX Grimm S, Schoenfeld N, Braziulis E, Cramer U, Gewies A, Voss F;

XX Mund T, Albayrak T, Gille H, Klein M;

XX WPI; 2002-115563/16.

XX New Apoptosis-associated nucleic acid sequences and polypeptides,

XX useful for diagnosis, treatment and prevention of e.g. tumors and

XX neurodegeneration -

XX Claim 1; Page 206; 227pp; German.

XX The present invention relates to nucleic acids from the mouse, where the

XX nucleic acid is associated with apoptosis. The sequences can be used in

XX the diagnosis, treatment and prevention of diseases associated with

XX excessive or inadequate apoptosis, including tumours, autoimmune

XX diseases, viral infections, degenerative diseases (Alzheimer's,

XX Parkinson's and Huntington's diseases), reperfusion injury, stroke and

XX alcohol-induced injury to the liver, for identifying agents for treating

XX these diseases, and to prepare transgenic animals in which expression of

XX an apoptosis related sequence is altered. These are useful for genetic

XX and/or pharmacological investigations of apoptosis and related diseases,

XX including dilatory cardiomyopathy. The present sequence is one of the

XX apoptosis related sequences of the invention.

XX Sequence 496 BP; 101 A; 121 C; 87 G; 108 T; 79 other;

SQ Query Match 0.1%; Score 21; DB 24; Length 496;

Best Local Similarity 100.0%; Pred. No. 4,2e+02;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5346 TGCGCTGTTCAGGCAAGT 5366

DB 150 TGCGCTGTTCAGGCAAGT 130

RESULT 19

ABV59094

ID ABV59094 standard; cDNA: 597 BP.

AC ABV59094;

DT 13-SEP-2002 (first entry)

DE Human prostate expression marker cDNA 59085.

XX Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;

XX pharmacogenomic marker; gene; ss.

XX Homo sapiens.

XX WO200160860-A2.

XX 23-AUG-2001.

XX 20-FEB-2001; 2001WO-US05171.

XX 17-FEB-2000; 2000US-183319P.

XX 16-MAR-2000; 2000US-189862P.

XX 25-MAY-2000; 2000US-207454P.

XX 09-JUN-2000; 2000US-211314P.

XX 18-JUL-2000; 2000US-219007P.

XX 13-DEC-2000; 2000US-255281P.

XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

XX Schlegel R, Endege WO, Monahan JE;

XX WPI; 2001-662795/76.

XX Novel isolated nucleic acid molecule associated with cancerous state of

XX prostate cells and correlating with presence of prostate cancer, useful

XX for detecting presence of prostate cancer, stage of prostate cancer -

XX Claim 1; Page 11330; 11750pp; English.

XX The invention relates to an isolated nucleic acid molecule (I) comprising

XX a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the

XX specification or its complement. (I) is useful for:

XX (a) assessing whether a patient is afflicted with prostate cancer;

XX (b) monitoring the progression of prostate cancer in a patient;

XX (c) assessing the efficacy of a test compound to inhibit prostate

XX cancer in a patient;

XX (d) assessing the efficacy of a therapy for inhibiting prostate cancer

XX in a patient;

XX (e) selecting a composition for inhibiting prostate cancer in a patient;

XX (f) assessing the prostate cell carcinogenic potential of a compound;

XX (g) determining whether prostate cancer has metastasized in a patient;

XX (h) assessing the aggressiveness or indolence of prostate cancer in a

XX patient;

XX (I) is also useful as a pharmacodynamic or pharmacogenomic marker.

XX Sequence 597 BP; 195 A; 86 C; 94 G; 221 T; 1 other;

SQ Query Match 0.1%; Score 21; DB 23; Length 597;

Best Local Similarity 100.0%; Pred. No. 4,1e+02;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4268 TTAAGTTGTTATTTTAAAT 4288

DB 66 TTAAGTTGTTATTTTAAAT 86

RESULT 20

AB253947

ID AB253947 standard; cDNA: 626 BP.
 XX
 AC AB253947;
 XX
 DT 28-MAR-2003 (first entry)
 XX
 DE Aspergillus oryzae polynucleotide SEQ ID NO 3060.
 XX
 KW Aspergillus oryzae; fermentation; fungus; industrial; EST;
 KM expressed sequence tag; gene; ss.
 XX
 OS Aspergillus oryzae.
 XX
 PN WO200279476-A1.
 XX
 PD 10-OCT-2002.
 XX
 PF 22-MAR-2002; 2002WO-1B00890.
 XX
 PR 30-MAR-2001; 2001JP-0098371.
 XX
 PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
 PA (NARE-) NAT RES INST BREWING.
 PA (NORO) NAT FOOD RES INST MIN AGRIC.
 XX
 PI Machida M, Akita O, Kashiwagi Y, Kitamoto K, Horiuchi H;
 PI Takeuchi M, Kobayashi T, Kitamoto N, Gomi K, Abe K;
 XX
 DR WPI: 2003-046817/04.
 XX
 PT Detection of expression of specific Aspergillus genes for monitoring
 PT the fermentation and growth conditions of the fungus, using DNA probes
 PT
 PS Claim 1: SEQ ID NO 3060; 48bp + Sequence Listing; Japanese.
 XX
 CC The invention relates to a polynucleotide having any of 6006 specific
 CC sequences (AB250888-AB256893), which are expressed by a fungus under
 CC specific culture conditions including one or more of eutrophic,
 CC oligotrophic, solid, early germination, alkaline, high temperature, low
 CC temperature or maltose culture or polynucleotides stringently hybridising
 CC to these sequences. The polynucleotides are useful for monitoring the
 CC progress of fermentation and the growth conditions of a fungus,
 CC especially of Aspergillus oryzae which is widely used in industrial
 CC fermentation. Also monitoring for fungal contamination.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SO Sequence 626 BP; 146 A; 182 C; 140 G; 158 T; 0 other;
 QY
 Query Match 0.1%; Score 21; DB 25; Length 626;
 Best Local Similarity 100.0%; Pred. No. 4.1e+02;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 23198 GTCCTATCTCCACGCGCTTCG 23218
 316 GTCCTATCTCCACGCGCTTCG 336
 RESULT 21
 AAS22986/c
 ID AAS22986 standard; DNA: 713 BP.
 XX
 AC AAS22986;
 XX
 DT 24-OCT-2001 (first entry)
 XX
 DE DNA encoding novel bone marrow polypeptide #80.
 XX
 KW bone marrow; diagnostic; therapeutic; gene therapy; antigenic;
 KW haematopoiesis; myeloid; lymph cell disorder; tissue regeneration;
 KW wound healing; nutritional supplement; immune disorder;

KW severe combined immunodeficiency; SCID; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200157187-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 05-FEB-2001; 2001WO-US03782.
 XX
 PR 03-FEB-2000; 2000US-0496914.
 PR 20-JUN-2000; 2000US-0598075.
 PR 19-JUL-2000; 2000US-0620325.
 PR 30-NOV-2000; 2000US-0230683.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Ford JE, Boyle RJ, Tang YT, Liu C, Asundi V, Zhou P, Xue AJ;
 PI Ren F, Dmanac RT;
 XX
 DR WPI: 2001-488875/53.
 DR P-PSDB; AAU14681.
 XX
 PT Nucleic acids encoding bone marrow polypeptides, useful in diagnostic
 PT and gene therapy -
 PT
 PS Claim 1; Page 193; 392pp; English.
 XX
 CC AAS22907-AAS23099 represent nucleic acids encoding novel bone marrow
 CC polypeptides. The nucleic acids and corresponding proteins may be used
 CC in the prevention, diagnosis and treatment of diseases associated with
 CC inappropriate bone marrow polypeptide expression. For example, to treat
 CC disorders associated with decreased expression by rectifying mutations
 CC or deletions in a patient's genome that affect the activity of the
 CC polypeptides by expressing inactive proteins or to supplement the
 CC patient's own production of the polypeptide. Additionally, the nucleic
 CC acids may be used to produce the polypeptides, by inserting the nucleic
 CC acids into a host cell and culturing the cell to express the protein.
 CC The nucleic acid and its complementary sequences may also be used as
 CC probes in diagnostic assays to detect and quantitate the presence of
 CC similar nucleic acid sequences in samples, and therefore which patients
 CC may be in need of restorative therapy. The proteins may also be used as
 CC antigens in the production of antibodies against bone marrow proteins
 CC and in assays to identify modulators of their expression and activity.
 CC The anti-bone marrow protein antibodies and antagonists may also be used
 CC to down regulate expression and activity. The antibodies may also be used
 CC as diagnostic agents for detecting the presence of the protein in samples
 CC (e.g. by enzyme linked immunosorbent assay (ELISA)). The proteins
 CC may be used to regulate haematopoiesis activity, and consequently in the
 CC treatment of myeloid or lymph cell disorders, and tissue regeneration,
 CC such as wound healing, as a nutritional supplement, and in treatment of
 CC immune disorders such as severe combined immunodeficiency (SCID).
 XX
 SO Sequence 713 BP; 133 A; 184 C; 243 G; 153 T; 0 other;
 QY
 Query Match 0.1%; Score 21; DB 22; Length 713;
 Best Local Similarity 100.0%; Pred. No. 4.1e+02;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 10823 TCCCGGTCGCGATGTCAT 10843
 21 TCCCGGTCGCGATGTCAT 1
 RESULT 22
 AAA76268
 ID AAA76268 standard; cDNA: 1098 BP.
 XX
 AC AAA76268;
 XX
 DT 25-JAN-2001 (first entry)
 XX
 DE Maize glutathione-S-transferase coding sequence fragment SEQ ID NO: 35.

XX Maize; glutathione-S-transferase; GST; plant detoxification;
KW herbicide metabolism; ss.
XX
OS Zea mays.
XX
PN US6096504-A.
PD 01-AUG-2000.
XX
PF 10-FEB-1999; 99US-0248335.
XX
PR 05-SEP-1997; 97US-0924759.
XX
PA (DUPO) DU PONT DE NEMOURS & CO E I.
XX
PI McConigle B, O'Keefe DP;
XX
DR WPI; 2000-523870/47.
DR P-PSDB; AAB22117.
XX
PT New nucleic acid fragment encoding maize glutathione-S-transferase
PT enzyme for detoxifying xenobiotic compounds in plants and seeds,
XX comprises a specific nucleotide sequence -
XX
PS Claim 2; Column 69-72; 62pp; English.
XX
CC The present invention concerns the isolation of a number of maize
CC glutathione-S-transferase (GST) fragments and their coding sequences. The
CC coding sequences were isolated from a number of different clones, leading
CC to the identification of a number of different protein sequences. The
CC protein is involved in the detoxification of xenobiotic compounds in
CC plants and seeds, and has been implicated in the detoxification of
CC herbicides. The gene can thus be used to produce herbicide-resistant
CC transgenic plants. The gene and protein can also be used in screening for
CC GST inhibitors and the identification of GST substrates, to aid in the
CC mapping of plant genomes and as signal sequences to direct molecules to
CC the plant vacuole.
XX
SQ Sequence 1098 BP; 368 A; 213 C; 238 G; 279 T; 0 other;
XX
Query Match 0.1%; Score 21; DB 21; Length 1098;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1340 AGAAGATGATGATGATGATGATGAT 1360
DB 419 AGAAGATGATGATGATGATGATGAT 439
XX
RESULT 23
AB083863/C
ID AB083863 standard; DNA; 4912 BP.
XX
AC AB083863;
XX
DT 04-FEB-2003 (first entry)
XX
DE Human MDDT-5 encoding cDNA SEQ ID NO:28.
XX
KW Human; MDDT; molecules for disease detection and treatment; anti-HIV;
KW antiallergic; antiinflammatory; antianaemic; antiparinsonian; nootropic;
KW anticonvulsant; antileptin; antileptin; antileptin; antileptin;
KW immunosuppressive; antithyroid; cytostatic; hepatotropic; dermatological;
KW antidiabetic; nephrotoxic; antitumor; thymine; neuroprotective;
KW osteopathic; ophthalmological; antiparasitic; antihelminthic; antiparasitic;
KW urticaria; protozoa; fungicide; gene therapy; cell proliferative;
KW cancer; developmental disorder; neurological disorder; infection; gene;
KW reproductive disorder; autoimmune disorder; inflammatory disorder; ss.
XX
OS Homo sapiens.
XX

FH Key Location/Qualifiers
FT CDS 171..4742
FT /tag= a
FT /product= "MDDT-5"
FT /note= "molecule for disease detection and treatment"
XX
XX W0200278420-A2.
XX
XX 10-OCT-2002.
XX
XX 29-MAR-2002; 2002WO-US09809.
XX
XX 30-MAR-2001; 2001US-280387P.
XX 05-APR-2001; 2001US-282335P.
XX 13-APR-2001; 2001US-283663P.
XX 19-APR-2001; 2001US-285484P.
XX 18-JAN-2002; 2002US-350702P.
XX 25-JAN-2002; 2002US-351743P.
XX
XX (INCY-) INCYTE GENOMICS INC.
XX
XX Lu DAM, Arvizu CS, Gandhi AR, Hafalla AJA, Dang L, Lu Y;
PI Rankumar J, Swarnakar A, Tang YT, Yue H, Tran B, Lee ST;
PI Warren BA, Nguyen DB, Thangavelu K, Yao MG, Elliott VS, Baughn MR;
PI Emerling BM, Lal PG, Gietzen KJ, Becha SD, Marquis JP, Kable AE;
XX
XX WPI; 2003-058385/05.
XX P-PSDB; ABP55396.
XX
XX New human molecules for disease detection and treatment, useful for
XX diagnosing, treating or preventing autoimmune or inflammatory disorders
XX (e.g. AIDS, allergy or anemia), multiple sclerosis, osteoarthritis,
XX cancer or hepatitis -
XX
XX Claim 5; Page 218-220; 238pp; English.
XX
XX The present invention describes 23 human molecules for disease detection
XX and treatment (MDDT-1 to 23) (see ABP55392 to ABP55414). The human
XX MDDT-1 to 23 proteins (I) are encoded by the sequences given in AB083859
XX to AB083881. (I) can have various activities depending on the cells and
XX tissues in which they are expressed. These activities include: anti-HIV;
XX antiallergic; antiinflammatory; antianaemic; antiparinsonian; nootropic;
XX anticonvulsant; antileptin; antileptin; antileptin; antileptin;
XX immunosuppressive; antithyroid; cytostatic; hepatotropic; dermatological;
XX antidiabetic; nephrotoxic; antitumor; thymine; neuroprotective;
XX osteopathic; ophthalmological; antiparasitic; antihelminthic; antiparasitic;
XX urticaria; protozoa; fungicide; gene therapy; cell proliferative;
XX cancer; developmental disorder; neurological disorder; infection; gene;
XX reproductive disorder; autoimmune disorder; inflammatory disorder; ss.
XX
SQ Sequence 4912 BP; 1082 A; 1318 C; 1804 G; 708 T; 0 other;
XX
Query Match 0.1%; Score 21; DB 25; Length 4912;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 10823 TCCCGCTCCGATGATGATGATGAT 10843
DB 4082 TCCCGCTCCGATGATGATGATGAT 4062
XX
RESULT 24
AAS46706
ID AAS46706 standard; DNA; 5242 BP.
XX

KW antiarteriosclerotic; antihaemic; cytosstatic; nootropic;
KW neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
KW antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
KW antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
KW acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
KW neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
KW gene; ds.
XX
OS Homo sapiens.
PN WO200200928-A2.
PD 03-JAN-2002.
XX
PF 02-JUL-2001; 2001WO-EP07537.
XX
PR 30-JUN-2000; 2000DE-1032529.
PR 01-SEP-2000; 2000DE-1043826.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2002-130909/17.
XX
PT Nucleic acid comprising fragment of chemically modified gene, useful
PT for diagnosis and treatment of diseases associated with abnormal
PT cytosine methylation -
XX
PS Claim 1; SEQ ID NO 1317; 32pp + Sequence Listing; German.
XX
CC The present invention provides a number of human immune system associated
CC genes which are modified by the methylation of cytosines. The sequences
CC can be used in the diagnosis and treatment of immune system disorders,
CC including eye diseases such as retinopathy, neovascular glaucoma and
CC macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid
CC leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,
CC rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
CC diseases. The present sequence is a gene of the invention.
XX
SQ Sequence 17674 BP; 4897 A; 481 C; 4073 G; 8223 T; 0 other;
XX
Query Match 0.1%; Score 21; DB 24; Length 17674;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4268 TTAAGTGTATTATTATTAAT 4288
DB 9363 TTAAGTGTATTATTATTAAT 9383
XX
RESULT 27
ID AAK89452/C
XX AAK89452 standard; DNA; 32192 BP.
XX
AC AAK89452;
XX
DT 05-NOV-2001 (first entry)
XX
DE Human digestive system antigen genomic sequence SEQ ID NO: 3028.
XX
XX Human; digestive system antigen; gene therapy; cancer; appendicitis;
KW ulcerative colitis; infection; Hirschsprung's disease; chronic colitis;
KW digestive system disorder; Meckel's diverticulum; ds.
XX
OS Homo sapiens.
PN WO200155314-A2.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01324.
XX

PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180668.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226868.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.

PR 02-OCT-2000; 2000US-0237037.
 PR 02-OCT-2000; 2000US-0237038.
 PR 02-OCT-2000; 2000US-0237039.
 PR 02-OCT-2000; 2000US-0237040.
 PR 13-OCT-2000; 2000US-0239935.
 PR 13-OCT-2000; 2000US-0239937.
 PR 20-OCT-2000; 2000US-0240960.
 PR 20-OCT-2000; 2000US-0241221.
 PR 20-OCT-2000; 2000US-0241785.
 PR 20-OCT-2000; 2000US-0241786.
 PR 20-OCT-2000; 2000US-0241787.
 PR 20-OCT-2000; 2000US-0241808.
 PR 20-OCT-2000; 2000US-0241809.
 PR 20-OCT-2000; 2000US-0241826.
 PR 01-NOV-2000; 2000US-0244617.
 PR 08-NOV-2000; 2000US-0246474.
 PR 08-NOV-2000; 2000US-0246475.
 PR 08-NOV-2000; 2000US-0246476.
 PR 08-NOV-2000; 2000US-0246477.
 PR 08-NOV-2000; 2000US-0246478.
 PR 08-NOV-2000; 2000US-0246523.
 PR 08-NOV-2000; 2000US-0246524.
 PR 08-NOV-2000; 2000US-0246525.
 PR 08-NOV-2000; 2000US-0246526.
 PR 08-NOV-2000; 2000US-0246527.
 PR 08-NOV-2000; 2000US-0246528.
 PR 08-NOV-2000; 2000US-0246532.
 PR 08-NOV-2000; 2000US-0246609.
 PR 08-NOV-2000; 2000US-0246610.
 PR 08-NOV-2000; 2000US-0246611.
 PR 08-NOV-2000; 2000US-0246613.
 PR 17-NOV-2000; 2000US-0249207.
 PR 17-NOV-2000; 2000US-0249208.
 PR 17-NOV-2000; 2000US-0249209.
 PR 17-NOV-2000; 2000US-0249210.
 PR 17-NOV-2000; 2000US-0249211.
 PR 17-NOV-2000; 2000US-0249212.
 PR 17-NOV-2000; 2000US-0249213.
 PR 17-NOV-2000; 2000US-0249214.
 PR 17-NOV-2000; 2000US-0249215.
 PR 17-NOV-2000; 2000US-0249216.
 PR 17-NOV-2000; 2000US-0249217.
 PR 17-NOV-2000; 2000US-0249218.
 PR 17-NOV-2000; 2000US-0249244.
 PR 17-NOV-2000; 2000US-0249245.
 PR 17-NOV-2000; 2000US-0249264.
 PR 17-NOV-2000; 2000US-0249265.
 PR 17-NOV-2000; 2000US-0249297.
 PR 17-NOV-2000; 2000US-0249299.
 PR 17-NOV-2000; 2000US-0249300.
 PR 01-DEC-2000; 2000US-0250160.
 PR 01-DEC-2000; 2000US-0250391.
 PR 05-DEC-2000; 2000US-0251030.
 PR 05-DEC-2000; 2000US-0251888.
 PR 05-DEC-2000; 2000US-0256719.
 PR 06-DEC-2000; 2000US-0251479.
 PR 08-DEC-2000; 2000US-0251856.
 PR 08-DEC-2000; 2000US-0251868.
 PR 08-DEC-2000; 2000US-0251869.
 PR 08-DEC-2000; 2000US-0251989.
 PR 11-DEC-2000; 2000US-0254097.
 PR 05-JAN-2001; 2001US-0253678.
 PA (HUMA-) HUMAN GENOME SCI INC.
 PI Rosen CA, Barash SC, Ruben SM;
 XX WPI; 2001-502630/55.
 DR
 XX
 PT Polynucleotides encoding digestive system antigens, useful for
 PT diagnosing, treating, preventing and/or prognosing disorders of the
 PT digestive system, particularly cancer and cancer metastases -

XX Disclosure; SEQ ID NO 3028; 986bp; English.
 PS
 XX
 CC The present invention provides the protein and coding sequences of a
 CC number of human digestive system antigens. These can be used in the
 CC diagnosis, treatment and prevention of digestive system disorders,
 CC including cancer, Meckel's diverticulum, bacterial or parasitic
 CC infections, appendicitis, Hirschsprung's disease, chronic colitis or
 CC ulcerative colitis. The present sequence is a genomic DNA fragment
 CC encoding a digestive system antigen of the invention.
 XX
 SQ Sequence 32192 BP; 8394 A; 7707 C; 7605 G; 8486 T; 0 other;
 QY
 DB 2647 TGCCCGCGTCACGGCCTTG 2667
 24796 TGCCCGCGTCACGGCCTTG 24776
 Query Match 0.1%; Score 21; DB 22; Length 32192;
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 RESULT 28
 ID AB067197 standard; DNA; 1163020 BP.
 XX
 AC AB067197;
 XX
 DT 29-AUG-2002 (first entry)
 XX
 DE Listeria innocua contig DNA sequence #10.
 XX
 KW Antibacterial; Listeria; food contamination; mutational analysis;
 KW infection; ds.
 XX
 OS Listeria innocua.
 XX
 PN WO200228891-A2.
 XX
 PD 11-APR-2002.
 XX
 PF 04-OCT-2001; 2001MO-FR03061.
 XX
 PR 04-OCT-2000; 2000FR-0012697.
 XX
 PA (INSP) INST PASTEUR.
 PA (CNRS) CNRS CENT NAT RECH SCI.
 XX
 PI Kunst F, Glaser P;
 XX
 DR WPI; 2002-332479/37.
 XX
 PT New genomic sequences from Listeria species, useful for detection,
 PT treatment and prevention of infection, also related polypeptides,
 PT antibodies and modulators -
 XX
 PS Claim 5; SEQ ID 10; 180bp; French.
 PS
 XX
 CC The present invention relates to nucleic acid sequences
 CC (AB067188-AB071212) from Listeria sp. The sequences are useful as probes
 CC and primers for identification and/or detection of Listeria (e.g. as
 CC contaminants in foods, or mutational analysis) and for analysis of
 CC gene expression. Proteins encoded by the nucleic acid sequences can be
 CC used to screen for compounds that modulate gene expression, replication
 CC and pathogenicity of Listeria (potential therapeutic agents), also for
 CC treating infections by Listeria, and are useful as immunogens in
 CC anti-Listeria vaccines.
 CC Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pat_sequences.
 XX
 SQ Sequence 1163020 BP; 388339 A; 197589 C; 235612 G; 341474 T; 6 other;

Query Match 0.1%; Score 21; DB 24; Length 1163020;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4488 AGCCAGTTTTTCATTCCAG 4508
|||||
DB 389074 AGCCAGTTTTTCATTCCAG 389054

RESULT 29
AB069245/c
ID AB069245 standard; DNA; 3011208 BP.
XX
AC AB069245;
XX
XX 29-AUG-2002 (first entry)
DT
XX Listeria innocua DNA sequence #684.
DE
XX Listeria innocua DNA sequence #684.
XX
XX Antibacterial; Listeria; food contamination; mutational analysis;
KM infection; ds.
XX
OS Listeria innocua.
XX
XX WO200228891-A2.
PN
XX 11-APR-2002.
PD
XX 04-OCT-2001; 2001WO-FR03061.
PF
XX 04-OCT-2000; 2000FR-0012697.
PR
XX (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
XX
PI Kunst F, Glaeser P;
XX
XX WPI; 2002-332479/37.
DR
XX
XX New genomic sequences from Listeria species, useful for detection,
PT treatment and prevention of infection, also related polypeptides,
PT antibodies and modulators -
XX
XX Claim 5; SEQ ID 2058; 180pp; French.
PS
XX
XX The present invention relates to nucleic acid sequences
CC (AB067188-AB071212) from Listeria sp. The sequences are useful as probes
CC and primers for identification and/or detection of Listeria (e.g. as
CC contaminants in foods, or mutational analysis) and for analysis of
CC gene expression. Proteins encoded by the nucleic acid sequences can be
CC used to screen for compounds that modulate gene expression, replication
CC and pathogenicity of Listeria (potential therapeutic agents), also for
CC treating infections by Listeria, and are useful as immunogens in
CC anti-Listeria vaccines.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pcl_sequences.
XX
XX Sequence 3011208 BP; 941651 A; 568176 C; 559189 G; 942192 T; 0 other;

Query Match 0.1%; Score 21; DB 24; Length 3011208;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4488 AGCCAGTTTTTCATTCCAG 4508
|||||
DB 479340 AGCCAGTTTTTCATTCCAG 479320

RESULT 30
ABN71329/c
ID ABN71329 standard; DNA; 114 BP.
XX

AC ABN71329;
XX
DT 01-JUL-2002 (first entry)
XX
XX Streptococcus polynucleotide SEQ ID NO 10571.
DE
XX
XX Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae;
KM group A streptococcus; Streptococcus pyogenes; antibacterial; gene;
XX antiinflammatory; infection; vaccine; meningitis; gene therapy; ds.
XX
OS Streptococcus agalactiae.
XX
XX WO200234771-A2.
PN
XX
XX 02-MAY-2002.
PD
XX
XX 29-OCT-2001; 2001WO-GB04789.
PF
XX
XX 27-OCT-2000; 2000GB-0026333.
PR 24-NOV-2000; 2000GB-0028727.
PR 07-MAR-2001; 2001GB-0005640.
XX
XX (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
XX
XX Telford J, Maignant V, Margalit Ros YI, Grandi G, Fraser C;
PI Tetelin H;
XX
XX WPI; 2002-352536/38.
DR P-PDB; ABP30698.
XX
XX New Streptococcus protein for the treatment or prevention of infection
PT or disease caused by Streptococcus bacteria, such as meningitis, and
PT for detecting a compound that binds to the protein -
XX
XX Claim 7; Page 4173; 4525pp; English.
PS
XX
XX The invention relates to a protein (ABP25413-ABP30895) from group B
CC streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS
CC (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in
CC the specification. The proteins have antibacterial and antiinflammatory
CC activity. (1), nucleic acids encoding (1), ABN6044-ABN71526 and
CC antibodies that bind (1) are used in the manufacture of medicaments for
CC the treatment or prevention of infection or disease caused by
CC Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.
CC Nucleic acids encoding (1) are used to detect Streptococcus in a
CC biological sample. (1) is used to determine whether a compound binds to
CC (1). A composition comprising (1) or a nucleic acid encoding (1), may be
CC used as a vaccine or diagnostic composition. The disease caused by
CC Streptococcus that is prevented or treated may be meningitis. Nucleic
CC acid encoding (1) may be used to recombinantly produce (1) and may be
CC used in gene therapy. Antibodies to (1) are used for affinity
CC chromatography, immunoassays, and distinguishing/identifying
CC Streptococcus proteins.
XX
XX Sequence 114 BP; 40 A; 25 C; 9 G; 40 T; 0 other;

Query Match 0.1%; Score 20; DB 24; Length 114;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28442 AGAATGTAACCAATTAA 28461
|||||
DB 101 AGAATGTAACCAATTAA 82

RESULT 31
ABL15723/c
ID ABL15723 standard; cDNA; 371 BP.
XX
XX ABL15723;
AC
XX 26-MAR-2002 (first entry)
DT

XX Drosophila melanogaster expressed polynucleotide SEQ ID NO 41651.
DE
XX Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical; gene; ss.
XX Drosophila melanogaster.
XX WO200171042-A2.
PN
XX
XX 27-SEP-2001.
PD
XX 23-MAR-2001; 2001WO-US09231.
PE
XX 23-MAR-2000; 2000US-191637P.
PR
XX 11-JUL-2000; 2000US-0614150.
PR
XX (PEKE) PE CORP NY.
PA
XX
PI Venter JC, Adams M, Li PWD, Myers EW;
PI
XX WPI: 2001-656860/75.
DR
XX P-PSDB; ABB71620.
DR
XX
PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
PT
XX
PS Claim 1; SEQ ID NO 41651; 21pp + Sequence Listing; English.
XX
XX The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (AB16176-AB130511), expressed DNA
CC sequences (AB101840-AB16175) and the encoded proteins
CC (ABB57737-ABB72072).
CC (ABB57737-ABB72072).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
CC
XX
SQ Sequence 371 BP; 95 A; 89 C; 110 G; 77 T; 0 other;

Query Match 0.1%; Score 20; DB 23; Length 371;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 27422 CATGCCACCGTGACCGGT 27441
DB 137 CATGCCACCGTGACCGGT 118
|||||

RESULT 32
AA193665
ID AA193665 standard; cDNA; 406 BP.
XX
AC AA193665;
XX
DT 06-NOV-2001 (first entry)
XX
XX Human polynucleotide SEQ ID NO 13725.
DE
XX
XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorders; arthritis; inflammation; ss.
XX
XX Homo sapiens.
OS
XX
XX WO200164835-A2.
PN
XX
PD 07-SEP-2001.

XX 26-FEB-2001; 2001WO-US04927.
PF
XX
XX 28-FEB-2000; 2000US-0515126.
PR
XX 18-MAY-2000; 2000US-0577409.
PR
XX
PA (HYSE-) HYSEQ INC.
XX
XX
PI Tang YF, Liu C, Drmanac RT;
PI
XX WPI: 2001-514838/56.
DR
XX P-PSDB; AAO13734.
DR
XX
XX Isolated nucleic acids and polypeptides, useful for preventing
PT diagnosing and treating e.g. leukaemia, inflammation and immune
PT disorders -
PT
XX
PS Claim 1; SEQ ID NO 13725; 1399pp + Sequence Listing; English.
XX
XX The invention relates to human polynucleotides (AA179941-AA193841) and
CC the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
CC
XX
SQ Sequence 406 BP; 104 A; 104 C; 74 G; 124 T; 0 other;

Query Match 0.1%; Score 20; DB 22; Length 406;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9083 TAAAAATGTGTAAACCAA 9102
DB 275 TAAAAATGTGTAAACCAA 294
|||||

RESULT 33
AA191552/C
ID AA191552 standard; cDNA; 443 BP.
XX
AC AA191552;
XX
DT 06-NOV-2001 (first entry)
XX
XX Human polynucleotide SEQ ID NO 11612.
DE
XX
XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorders; arthritis; inflammation; ss.
XX
XX Homo sapiens.
OS
XX
XX WO200164835-A2.
PN
XX
XX 07-SEP-2001.
PD
XX
XX 26-FEB-2001; 2001WO-US04927.
PE
XX
XX 28-FEB-2000; 2000US-0515126.
PR
XX 18-MAY-2000; 2000US-0577409.
PR
XX
PA (HYSE-) HYSEQ INC.
XX

PI Tang YT, Liu C, Drmanac RT;
 XX
 DR WPI: 2001-514838/56.
 DR P-PDB; AAO11621.
 XX
 PT Isolated nucleic acids and polypeptides, useful for preventing
 PT diagnosing and treating e.g. leukaemia, inflammation and immune
 disorders -
 XX
 PS Claim 1: SEQ ID NO 11612; 1399pp + Sequence Listing: English.
 XX
 CC The invention relates to human polynucleotides (AA179941-AA193841) and
 CC the encoded proteins (AA000010-AA013910) that exhibit activity elating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activity/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 CC
 XX Sequence 443 BP; 120 A; 100 C; 100 G; 122 T; 1 other;
 SQ
 Query Match 0.1%; Score 20; DB 22; Length 443;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 15215 AGTTGCTCTCGCCAGG 15234
 DB 50 AGTTGCTCTCGCCAGG 31
 RESULT 34
 ABR80077/c
 ID ABR80077 standard; DNA; 492 BP.
 XX
 AC ABR80077;
 XX
 DT 13-AUG-2002 (first entry)
 XX
 DE Bacillus clausii genomic sequence tag (GST) #2920.
 XX
 KW Differential gene expression; genomic sequenced tag; GST;
 KW altered culture condition; environmental stress;
 KW physiological provocation; ds.
 XX
 OS Bacillus clausii.
 XX
 PN WO200229113-A2.
 XX
 PD 11-APR-2002.
 XX
 PF 05-OCT-2001; 2001WO-US31437.
 XX
 PR 06-OCT-2000; 2000US-0680598.
 PR 27-MAR-2001; 2001US-279526P.
 XX
 PA (NOVO) NOVOZYMES BIOTECH INC.
 PA (NOVO) NOVOZYMES AS.
 XX
 PI Berka R, Clausen IG;
 XX
 DR WPI: 2002-416684/44.
 XX
 PT Monitoring differential expression of several genes in first Bacillus
 PT cell relative to expression of same genes in one or more second
 PT Bacillus cells, by using substrate containing Bacillus genomic
 PT sequenced tag array -

XX
 PS Claim 11: SEQ ID NO 7368; 200pp; English.
 XX
 CC The invention describes a method of monitoring differential expression of
 CC genes in a first Bacillus cell relative to expression of the genes in
 CC other Bacillus cells, comprising hybridising labeled nucleic acid probes
 CC isolated from Bacillus cells to a substrate containing array of Bacillus
 CC genomic sequenced tags (GST), examining the array, and determining
 CC relative gene expression by an observed hybridisation reporter signal of
 CC a spot in the array. The method is useful for measuring the expression of
 CC genes in a first Bacillus cell relative to expression of the same genes
 CC in one or more second Bacillus cells. The method is useful for monitoring
 CC global expression of several genes from a Bacillus cell, discovering new
 CC genes, identifying possible functions of unknown open reading frames and
 CC monitoring gene copy number variation and stability. Monitoring changes
 CC in expression of genes may be used to provide a representation of the way
 CC in which Bacillus cells adapt to changes in culture conditions,
 CC environmental stress or other physiological provocation. Extensive
 CC follow-up characterisation is unnecessary, when one spot on an array
 CC equals one gene or one open reading frame, since sequence information is
 CC available. This sequence represents a genomic sequence tag (GST) used in
 CC the method of the invention.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at
 CC ftp.wipo.int/pub/published_pct_sequences.
 CC
 XX Sequence 492 BP; 144 A; 102 C; 118 G; 127 T; 1 other;
 SQ
 Query Match 0.1%; Score 20; DB 24; Length 492;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 9348 TCCTATAAATCTTCATT 9367
 DB 248 TCCTATAAATCTTCATT 229
 RESULT 35
 AAF09895
 ID AAF09895 standard; cDNA; 628 BP.
 XX
 AC AAF09895;
 XX
 DT 13-MAR-2001 (first entry)
 XX
 DE Fusarium venenatum EST Seq ID NO:2418.
 XX
 KW Multiple gene expression; filamentous fungal cell; EST;
 KW expressed sequence tag; Fusarium venenatum; Aspergillus niger;
 KW Aspergillus oryzae; Trichoderma reesei; identification; recombination;
 KW culture condition; environmental stress; spore morphogenesis;
 KW metabolic pathway engineering; catabolic pathway engineering; ss.
 XX
 OS Fusarium venenatum.
 XX
 PN WO200056762-A2.
 XX
 PD 28-SEP-2000.
 XX
 PF 22-MAR-2000; 2000WO-US07781.
 XX
 PR 22-MAR-1999; 99US-0273623.
 XX
 PA (NOVO) NOVO NORDISK BIOTECH INC.
 PA (NOVO) NOVO NORDISK AS.
 XX
 PI Berka RM, Rey MW, Shuster JR, Kaupinen S, Clausen IG, Olsen PB;
 XX
 DR WPI: 2000-594572/56.
 XX
 PT Monitoring differential expression of genes in filamentous fungal cells
 PT uses fluorescence-labeled nucleic acids isolated from the cells and a

PT substrate of expressed sequence tags -
XX
XX Claim 86; Page 1272; 3161pp; English.
PS
XX The present invention describes a method for monitoring differential
CC expression of genes in a first filamentous fungal (FF) cell relative to
CC expression of the same genes in one or more second filamentous fungal
CC cells. The method uses fluorescence-labeled nucleic acids isolated from
CC FF cells and a substrate of expressed sequence tags (EST). The ESTs
CC are used in the methods for monitoring differential expression of genes
CC in a first filamentous fungal (FF) cell relative to expression of the
CC same genes in one or more second filamentous fungal cells. Monitoring
CC the global expression of genes from FF cells allows the production
CC potential of the microorganisms to be improved. New genes may be
CC discovered, possible functions of unknown open reading frames can be
CC identified and gene copy number variation and stability can be
CC monitored. The expression of genes can be used to study how FF cells
CC adapt to changes in culture conditions, environmental stress, spore
CC morphogenesis, recombination, metabolic or catabolic pathway
CC engineering. Using ESTs provides several advantages over genomic or
CC random cDNA clones including elimination of redundancy as one spot on an
CC array equals one gene or open reading frame, and organisation of the
CC microarrays based on function of the gene products to facilitate
CC analysis of the results. AAF07478 to AAF11247 represents ESTs from
CC *Fusarium venenatum*; AAF11248 to AAF11853 represents ESTs from *Aspergillus*
CC *niger*; AAF11854 to AAF14878 represents ESTs from *Aspergillus oryzae*; and
CC AAF14879 to AAF15337 represents ESTs from *Trichoderma reesei*, which are
CC all specifically claimed in the present invention.
XX
SQ Sequence 628 BP; 146 A; 156 C; 146 G; 176 T; 4 other;
Query Match 0.1%; Score 20; DB 21; Length 628;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 31189 ACGACGATGCGATATCCGCC 31208
DB 197 ACGACGATGCGATATCCGCC 216
|||||
RESULT 36
ABT07203
ID ABT07203 standard; DNA; 676 BP.
XX
AC ABT07203;
XX
DT 07-NOV-2002 (first entry)
XX
DE Human CpG island rich DNA sequence SEQ ID No 20.
XX
KW CpG island; methylated; methylation-sensitive restriction enzyme; cancer;
KW malignant cell; tumour; human; ds.
XX
XX Homo sapiens.
OS
XX WO200260318-A2.
PN
PD 08-AUG-2002.
XX
XX 31-JAN-2002; 2002WO-US03077.
PF
XX 31-JAN-2001; 2001US-0775398.
PR
XX (OHIS) UNIV OHIO STATE RES FOUND.
PA
XX Plass C;
PI
XX WPI; 2002-627436/67.
DR
XX Identifying methylated CpG islands in malignant cells, useful for
PT diagnosing or classifying cancer, comprises the use of infrequent
PT cleaving, methylation-sensitive restriction enzymes and gel
PT electrophoresis

XX
PS Claim 15; Page 76; 133pp; English.
XX
XX The invention relates to a method for identifying CpG islands which are
CC preferentially methylated in malignant cells, which comprises obtaining
CC genomic DNA from malignant and non-malignant cells, digesting this DNA
CC with infrequently-cutting, methylation sensitive restriction enzymes to
CC form restriction fragments, electrophoresing these fragments and
CC comparing the intensity of these patterns to control cell restriction
CC fragments. The method is useful in diagnosing cancer, in classifying
CC tumours, in providing prognoses for cancer patients, and in identifying
CC new DNA clones within a library based on the methylation status of CpG
CC dinucleotides. The isolated polynucleotides and oligonucleotides can also
CC be used as probes to identify genes whose expression is increased or
CC decreased in cancerous tissues. This polynucleotide sequence represents a
CC CpG-island rich DNA sequence relating to the invention.
XX
SQ Sequence 676 BP; 104 A; 248 C; 261 G; 59 T; 4 other;
Query Match 0.1%; Score 20; DB 24; Length 676;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 19852 CCGACCGTCAGCCTCCGCC 19871
DB 277 CCGACCGTCAGCCTCCGCC 296
|||||
RESULT 37
AAH92965/C
ID AAH92965 standard; DNA; 700 BP.
XX
AC AAH92965;
XX
DT 09-OCT-2001 (first entry)
XX
DE Human inflammatory bowel disease related gene fragment IGR3258a.
XX
XX Human; inflammatory bowel disease; Crohn's disease; ulcerative colitis;
KW single nucleotide polymorphism; SNP; chromosome 19p13; paternity test;
KW chromosome 5q31-33; forensic test; gene therapy; ds.
XX
XX Homo sapiens.
OS
XX WO200142511-A2.
PN
XX 14-JUN-2001.
PD
XX 11-DEC-2000; 2000WO-US33632.
PF
XX 10-DEC-1999; 99US-0170257.
PR
XX 10-APR-2000; 2000US-0196046.
PR
XX (WHEED) WHITEHEAD INST BIOMEDICAL RES.
PA (ELIT-) ELIIPSIS BIOTHERAPEUTICS CORP.
XX
XX Daly M, Hudson TJ, Lander ES, Rioux J, Siminovitch K;
PI
XX WPI; 2001-367874/38.
DR
XX Testing for the presence of polymorphisms associated with inflammatory
PT bowel disease, using a hybridization assay -
PT
XX Disclosure; Page 366; 463pp; English.
PS
XX The present invention describes a method for detecting the presence of
CC polymorphisms associated with inflammatory bowel diseases such as
CC ulcerative colitis and Crohn's disease. The methods can be used to detect
CC the presence of genetic polymorphisms associated with inflammatory bowel
CC disease and correlating their occurrence with disease states. They may be
CC used in this way for phenotypic correlations, forensics, paternity
CC testing, medicine and genetic analysis. The present sequence is a gene
CC containing a polymorphic site described in the exemplification of the

CC Invention.
 XX Sequence 700 BP; 168 A; 139 C; 152 G; 241 T; 0 other;
 SQ Query Match 0.1%; Score 20; DB 22; Length 700;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4244 ATAAATTTAAACATGCGAT 4263
 ID AAO53372/c
 XX AAO53372 standard; DNA; 720 BP.

AC AAO53372;
 XX 25-MAR-2003 (updated)
 DT 03-JUN-1994 (first entry)
 XX

DE Sequence encoding glutathione peroxidase.
 XX Glutathione peroxidase; Schistosoma mansoni; schistosome;
 KW diagnosis; vaccine; ss.
 XX Schistosoma mansoni.
 OS

FT Key Location/Qualifiers
 FT CDS 16..525.
 FT /tag= a
 FT /product= glutathione peroxidase.
 FT misc_difference 142..144
 FT /tag= b
 FT /note= "this stop codon is ignored due to a
 FT suppressor tRNA inserting a selenocysteine
 FT residue into the amino acid sequence."
 FT misc_difference 304..306
 FT /tag= c
 FT /transl_except= CAA encodes glutamic acid.
 FT

XX FR2689906-A1.
 XX
 PD 15-OCT-1993.
 XX
 PF 10-APR-1992; 92FR-0004406.
 XX
 PR 10-APR-1992; 92FR-0004406.
 XX
 PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
 PA (INSP) INST. PASTEUR.
 PA (INSP) INST PASTEUR LILLE.
 XX
 PI Capron A, Pierce R, Williams D;
 XX
 DR WPI; 1993-388582/49.
 DR P-PSDB; AAR44988.
 XX
 PT Nucleic acid encoding schistosome glutathione peroxidase - and
 PT derived peptide, useful in diagnostic reagents and vaccines, also
 PT related vectors, transformed cells, etc.
 XX
 XX Claim 2; Page 10; 15pp; French.
 XX
 CC The glutathione peroxidase is immunogenic and is used as a
 CC diagnostic reagent and in the preparation of vaccines.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 CC
 SQ Sequence 720 BP; 233 A; 129 C; 146 G; 212 T; 0 other;
 XX
 XX Query Match 0.1%; Score 20; DB 14; Length 720;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16698 CATCTCCTGAGTTGGCGAT 16717
 ID
 DB 183 CATCTCCTGAGTTGGCGAT 164

RESULT 39
 ID AA24801/c
 XX AA24801 standard; DNA; 852 BP.
 XX
 AC AA24801;
 XX
 DT 07-DEC-1999 (first entry)
 XX
 DE Vibrio cholerae thya coding region sequence.
 XX
 KW Wild type; thya; enzyme; thymidilate synthase; non-toxicogenic; mutation;
 KW attenuation; immunization; cholera; hemagglutinin protease; biosafety;
 KW auxotrophism; replication; vaccine; ss.
 XX
 OS Vibrio cholerae.
 XX
 PN W09935271-A2.
 XX
 PD 15-JUL-1999.
 XX
 PF 30-DEC-1998; 98WO-CU00008.
 XX
 PR 30-DEC-1997; 97CU-0000142.
 XX
 PA (NAIN-) CENT NACIONAL INVESTIGACIONES CIENTIFICAS.
 XX
 PI Campos Gomez J, Fando Calzada RA, Rodriguez Gonzalez BL;
 PI Ledon Perez TV, Valle Diaz E, Silva Cabrera AJ, Benitez Robles JA;
 XX
 DR WPI; 1999-430398/36.
 DR P-PSDB; AAY26895.
 XX
 PT Producing strains of Vibrio cholerae with inactivated gene for
 PT hemagglutinin protease, useful in vaccines against cholera -
 XX
 PS Claim 18; Page 30; 30pp; Spanish.
 XX
 CC This sequence represents the wild type coding region of the thya gene
 CC from Vibrio cholerae, which encodes the enzyme thymidilate synthase.
 CC The invention relates to the production, from a non-toxicogenic strain
 CC of V. cholerae, of attenuated strains of V. cholerae suitable for
 CC immunization against cholera. The attenuation comprises inactivating
 CC the gene for hemagglutinin protease (HP), either by deletion, insertion
 CC or some other defined and irreversible genetic manipulation. Additional
 CC biosafety of the attenuated strains is generated by mutating the thya
 CC gene, resulting in auxotrophic mutants unable to replicate in the
 CC environment. The new strains are used to produce anticholera vaccines.
 XX
 SQ Sequence 852 BP; 217 A; 177 C; 216 G; 242 T; 0 other;

QY 30846 GTGACGTCAAAATCATCCAA 30865
 ID
 DB 806 GTGACGTCAAAATCATCCAA 787

RESULT 40
 ID ABQ40312/c
 XX ABQ40312 standard; DNA; 913 BP.
 AC ABQ40312;
 XX
 DT 12-JUL-2002 (first entry)

DE	Oligonucleotide for detecting cytosine methylation SEQ ID NO 26903.
XX	
XX	Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
KW	drug; side effect; cancer; central nervous system; cardiovascular;
KW	gastrointestinal; respiratory system; single nucleotide polymorphism;
CC	SNP; cell differentiation; ds.
XX	
OS	Homo sapiens.
XX	
PN	WO200218632-A2.
XX	
PD	07-MAR-2002.
XX	
PF	01-SEP-2001; 2001WO-EP10074.
XX	
PR	01-SEP-2000; 2000DE-1043826.
XX	
PR	05-SEP-2000; 2000DE-1044543.
XX	
PA	(EP1G-) EPIGENOMICS AG.
XX	
PI	Olek A, Piepenbrock C, Berlin K, Guetig D;
XX	
DR	WPI: 2002-371829/40.
XX	
PT	Determining the degree of cytosine methylation in genomic DNA, useful
PT	for diagnosis and prognosis, comprises selective hybridization of
PT	amplicons from chemically treated DNA -
XX	
PS	Claim 12; 56pp + Sequence Listing; 56pp; German.
XX	
CC	This invention describes a novel method for determining the degree of
CC	methylation of a particular cytosine in a motif 5'-CpG-3', present in a
CC	genomic sample of DNA. The sample is treated chemically to convert
CC	cytosine (C) but not methylation C, to uracil, then part of the genomic
CC	DNA that contains the target C is amplified to form a labeled amplicon.
CC	The amplicon is hybridised to two classes, each with at least one
CC	member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers
CC	and the degree of hybridisation to both classes is determined from the
CC	label on the amplicon. From the ratio of labels hybridised to the two
CC	classes of oligomers, the degree of methylation is calculated. The method
CC	is used: (i) for diagnosis and/or prognosis of side effects of
CC	therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders
CC	of the central nervous, cardiovascular, gastrointestinal and respiratory
CC	systems etc., particularly by detecting mutations or single nucleotide
CC	polymorphisms (SNP's); and (ii) for differentiation of cell or tissue
CC	types and for investigating cell differentiation. The method allows the
CC	methylation status of many C residues to be determined simultaneously.
CC	AB013410-AB051121 represent genomic DNA sequences used to illustrate the
CC	method for determining the degree of cytosine methylation described in
CC	the disclosure of the invention.
XX	
SO	Sequence 913 BP; 145 A; 114 C; 288 G; 366 T; 0 other;
XX	
Query Match	0.1%; Score 20; DB 24; Length 913;
Best Local Similarity	100.0%; Pred. No. 1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Y	30467 CCTAACGCGAATTCACGCCG 30486
DB	
	119 CCTAACGCGAATTCACGCCG 100
XX	
RESULT 41	
ABQ40313	
ID	ABQ40313 standard; DNA; 913 BP.
XX	
AC	ABQ40313;
XX	
DT	12-JUL-2002 (first entry)
XX	
DE	Oligonucleotide for detecting cytosine methylation SEQ ID NO 26904.

Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
drug; side effect; cancer; central nervous system; cardiovascular;
gastrointestinal; respiratory system; single nucleotide polymorphism;
SNP; cell differentiation; ds.

OS Homo sapiens.
PN WO200218632-A2.
PD
PP 07-MAR-2002.
PE 01-SEP-2001; 2001WO-EPI0074.
PR 01-SEP-2000; 2000DE-1043826.
PR 05-SEP-2000; 2000DE-1044543.
XX
PA (EPIC-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K, Guetig D;
PI
DR WPI; 2002-371829/40.
XX

Determining the degree of cytosine methylation in genomic DNA, useful
for diagnosis and prognosis, comprises selective hybridization of
PT amplicons from chemically treated DNA -
PS
PP

Claim 12; 56pp + Sequence Listing; 56pp; German.

This invention describes a novel method for determining the degree of
methylation of a particular cytosine in a motif 5'-CpG-3', present in a
genomic sample of DNA. The sample is treated chemically to convert
cytosine (C) but not methylated C, to uracil, then part of the genomic
DNA that contains the target C is amplified to form a labeled amplicon.
The amplicon is hybridised to two classes, each with at least one
member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers
and the degree of hybridisation to both classes is determined from the
label on the amplicon. From the ratio of labels hybridised to the two
classes of oligomers, the degree of methylation is calculated. The method
is used as (1) for diagnosis and/or prognosis of side effects of
therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders
of the central nervous, cardiovascular, gastrointestinal and respiratory
systems etc., particularly by detecting mutations or single nucleotide
polymorphisms (SNPs); and (11) for differentiation of cell or tissue
types and for investigating cell differentiation. The method allows the
methylation status of many C residues to be determined simultaneously.
ABQ31410-ABQ54121 represent genomic DNA sequences used to illustrate the
method for determining the degree of cytosine methylation described in
the disclosure of the invention.

Sequence 913 BP; 366 A; 288 C; 114 G; 145 T; 0 other;

Query Match 0.1%; Score 20; DB 24; Length 913;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0

OY 30467 CCTAACGGGAATTACGCCG 30486
|||||
DB 795 CCTAAGCGGAATTCGCCG 814

RESULT 42
AAC48637
ID AAC48637 standard; DNA; 1016 BP.
XX
AC AAC48637;
XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 58206.
XX
KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.

XX Arabidopsis thaliana.
OS
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 28-APR-1999; 99US-0130891.
PR 30-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 04-MAY-1999; 99US-0132407.
PR 05-MAY-1999; 99US-0132484.
PR 06-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 06-MAY-1999; 99US-0132487.
PR 07-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.

PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144684.
PR 21-JUL-1999; 99US-0144614.
PR 21-JUL-1999; 99US-0145086.
PR 22-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151080.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151338.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.

```
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154033.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0158655.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161922.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 0.1%; Score 20; DB 21; Length 1016;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 11796 AATCTCATTTCTGTAATCT 11815
    |||||||
DB 106 AATCTCATTTCTGTAATCT 125
```

```
RESULT 43
AAS81345/c
ID AAS81345 standard; cDNA; 1285 BP.
XX
AC AAS81345;
XX
DT 13-FEB-2002 (first entry)
XX
DE DNA encoding novel human diagnostic protein #17149.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US08631.
```

```
XX 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX
XX (HYSE-) HYSEQ INC.
PI Dmanac RT, Liu C, Tang YT;
XX WPI; 2001-639362/73.
DR P-PSDB; ABG17158.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
PS Claim 1; SEQ ID NO 17149; 103pp; English.
```

The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations and responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

Sequence 1285 BP; 342 A; 327 C; 327 G; 289 T; 0 other;

```
Query Match 0.1%; Score 20; DB 23; Length 1285;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 23671 GATGTTAAGTTTACGAC 23690
    |||||||
DB 457 GATGTTAAGTTTACGAC 438
```

```
RESULT 44
ABA19992
ID ABA19992 standard; DNA; 1845 BP.
XX
AC ABA19992;
XX
DT 23-JAN-2002 (first entry)
XX
DE Human nervous system related polynucleotide SEQ ID NO 12323.
XX
KW Human; nootropic; neuroprotective; cytosolic; dermatological; virucide;
KW immunosuppressive; anti-infectious; anti-HIV; antibacterial; vulnerrary;
KW antiparkinsonian; antistickling; antianemic; antitarrtic; cancer;
KW antirheumatic; hepatotropic; cerebroprotective; antinflammatory;
KW antiallergic; antidiabetic; antileuc; anticonvulsant; antifungal;
KW antiparasitic; cardiac; immune disorder; cardiovascular disorder;
KW neurological disease; infection; nephrotropic; gene therapy; vaccine; ds.
XX
OS Homo sapiens.
XX
PN WO200159063-A2.
XX
```

PD 16-AUG-2001.
XX 17-JAN-2001; 2001WO-US01334.
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 14-AUG-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226686.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.

PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240360.
PR 20-OCT-2000; 2000US-0241826.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 20-OCT-2000; 2000US-0242221.
PR 01-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249267.
PR 17-NOV-2000; 2000US-0249287.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250391.
PR 01-DEC-2000; 2000US-0251160.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251038.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 06-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.

(HUMA-) HUMAN GENOME SCI INC.
PA Rosen CA, Barash SC, Ruben SM;
PI
XX WPI; 2001-541565/60.
XX

XX Nucleic acids encoding 3224 human nervous system antigen polypeptides,
 PT useful for preventing, diagnosing and/or treating nervous system
 PT cancers and metastases -
 PS Disclosure: SEQ ID NO 12323; 1701bp + Sequence Listing; English.

CC The invention relates to novel genes (AB11004-AB21534) and proteins
 CC (AB114678-AB18001) useful for preventing, treating or ameliorating
 CC medical conditions e.g. by protein or gene therapy. The genes are
 CC isolated from a range of human tissues disclosed in the specification.
 CC The nucleic acids, proteins, antibodies and (anti)agonists are useful
 CC in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast
 CC and ovarian cancer and other cancers of the adrenal gland, bone, bone
 CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
 CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune
 CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
 CC colitis; (c) cardiovascular disorders such as myocardial ischaemia;
 CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
 CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
 CC and parasitic infections.
 CC Note: The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pcl_sequences.
 CC
 SQ Sequence 1845 BP; 589 A; 309 C; 289 G; 658 T; 0 other;

Query Match 0.1%; Score 20; DB 22; Length 1845;
 Best Local Similarity 100.0%; Pred. No. 9.7e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16789 ATTTTCAGATAGTGTGCTCA 16808
 ||||||||||||||||||||
 DB 583 ATTTTCAGATAGTGTGCTCA 602

RESULT 45
 AAS72850
 ID AAS72850 standard; cDNA; 1983 BP.
 XX
 AC AAS72850;
 XX
 DT 13-FEB-2002 (first entry)
 XX
 DE DNA encoding novel human diagnostic protein #8654.
 XX
 KW Human: Chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200175067-A2.
 XX
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US08631.
 XX
 PR 31-MAR-2000; 2000US-0540217.
 PR 23-AUG-2000; 2000US-0649167.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Drmanac RT, Liu C, Tang YT;
 XX
 DR WPI: 2001-639362/73.
 DR P-PSDB; ABG08663.
 XX
 XX New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity -
 XX

PS Claim 1: SEQ ID NO 8654; 103bp; English.

XX
 CC The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping; and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. AAS64197-AAS94564 represent novel human
 CC diagnostic coding sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pcl_sequences.
 CC
 SQ Sequence 1983 BP; 804 A; 422 C; 368 G; 389 T; 0 other;

Query Match 0.1%; Score 20; DB 23; Length 1983;
 Best Local Similarity 100.0%; Pred. No. 9.6e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6232 GTACTGGAACAAACATTGA 6251
 ||||||||||||||||||||
 DB 1607 GTACTGGAACAAACATTGA 1626

Search completed: September 29, 2003, 23:47:02
 Job time : 7702 secs